

Endophyte Project Report

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1 Introduction

The data set we have analyzed seeks to understand the effect of various fungal treatments and how they affect the growth of different soybean plants when they are affected by different types of worms. These worms “stress” the plant, and can represent different conditions that the plant might be under. There are three different “stressors” or species of worms in this experiment that we subjected to different fungal treatments. In addition to fungal treatment, there is a control treatment, which corresponds to not applying any treatment. Each soybean plant is grown in a greenhouse. In the data set these are represented by the “id” category. There are many ways to assess how well a plant is growing. You can look at how tall the plant is, the weight of the larva of the worms, or the area of the leaves. A particular way that measures how the plant is growing is called a “metric”, and there are 7 different metrics that are recorded. Our goal is to find which “fungal treatment” is best for the plant overall.

There are 7 different metrics that we're too explore. The metrics are "Plant Height", "Shoot Fresh Weight", "Root Fresh Weight", "Cysts and Females", "Larval Weight", "Leaf Area", and "Leaf Weight". Each metric is not measured on every stressor type. The worms affect the plants in different areas, and as a result the metrics are observed in a fashion that is appropriate. For instance, it would be inappropriate to look at the plant height for a worm that primarily impacts the root of the plant. All of the metrics are observed for either 1 or 2 types of stressors.

There are three different types of "worms" or stressors. They are: "Heterodera glycines", "Chrysodeixis includens", and "Trichoplusia ni". Not every stressor was run on every treatment. There are many treatments that were not touched by some stressors. We analyzed only treatments that were tried on every stressor. There were too many different types of treatments on the different types of stressors to run all the different experiment types in the same greenhouse. As a result, there are several greenhouses with different treatments in each greenhouse. Every greenhouse has a control treatment though, which corresponds to observing how the plant does without any fungal treatment.

We pruned the data set to only include treatments that have different been done on every stressor type. In the appendix, we have included R code that preprocesses the data. In addition, some greenhouses were observed that only had the control treatment, and some treatments that were not applied to every stressor type. We removed these greenhouses from our sample as well.

We now proceed to analyzing the processed data set and discussing our results.

2 Exploratory Analysis

One of the questions we first wanted to know, is if the stressor type affects how well the treatment is doing. If the stressor type does not, then answering the question on which treatment type is best is simpler, we can just pick the treatment that does the best across all treatments. If the stressor type affects which treatment is best, then we would have to consider which treatment does best for particular stressor types. We would like to add that this is only a concern for metrics with 2 types of stressors. There were some metrics that did best for only 1 type of stressor.

2.1 Looking for interaction between stressor type and treatment

The following interaction plots let us see if the stressor type changes how well a treatment does. The interaction plot shows the average value of the metric for a particular treatment under a particular stressor type. The lines connect the treatments that share the same stressor types.

If it appears that all the lines change at roughly the same rate when changing treatments, that means there is no interaction, the effect of the treatment is the same across both stressors. If the lines do not change at roughly the same rate when changing treatments, that means the effect of the treatment differs across both stressors.

```
prunedat %>% dim()

## [1] 6843    5

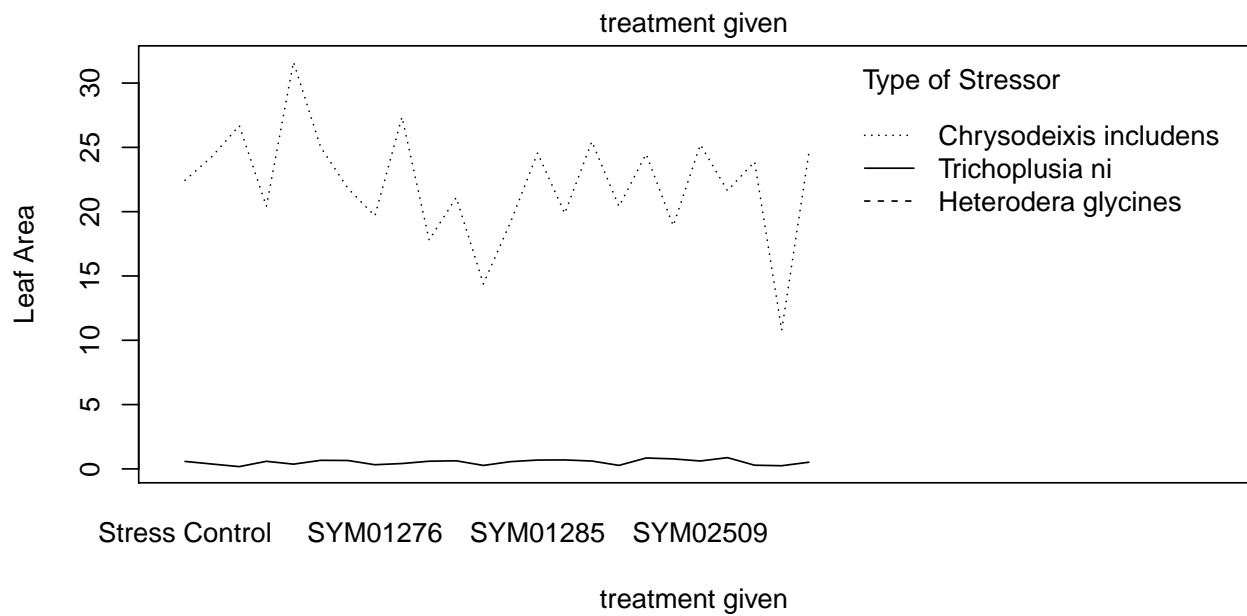
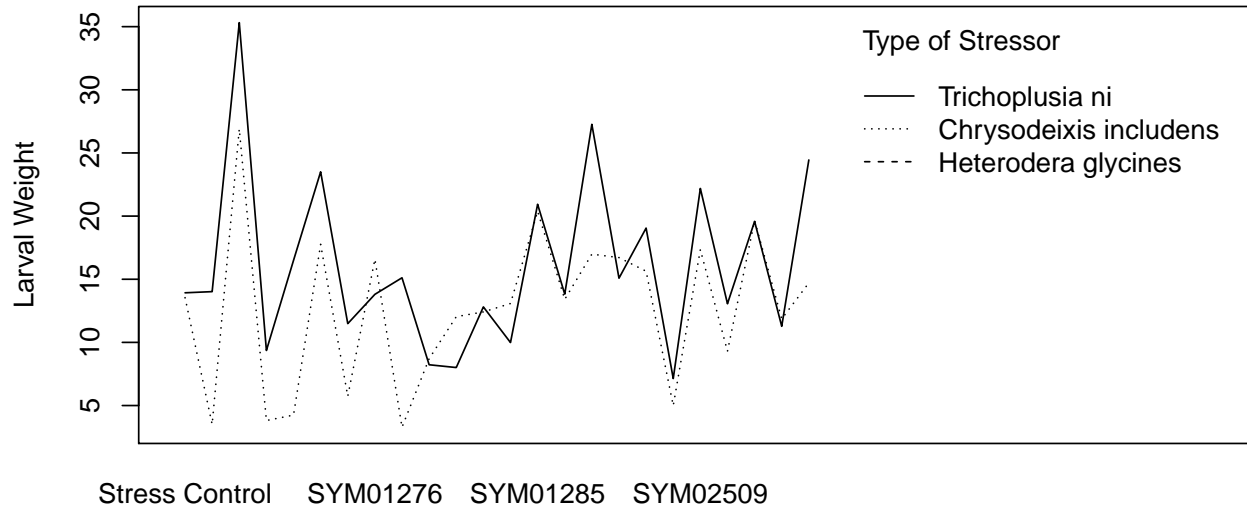
prunedat %>% colnames()

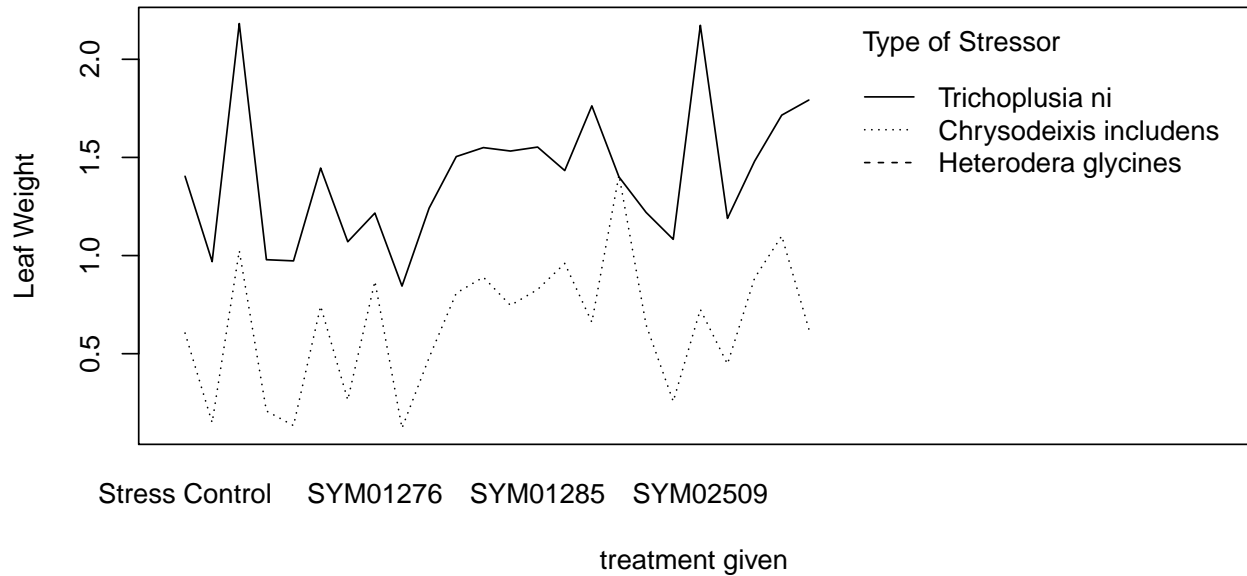
## [1] "id"      "type"    "metric"  "trt"     "value"

prunedat %>% pull(metric) %>% table()

## .
## Cysts and Females      Larval Weight      Leaf Area      Leaf Weight
##           638           1417           1460           1414
## Plant Height Root Fresh Weight Shoot Fresh Weight
```

```
##                                638                                638                                638
for(j in which(n.type == 2))
{
  interaction.plot(response = prunedat.list[[j]]$value, as.factor(prunedat.list[[j]]$trt),
                  as.factor(prunedat.list[[j]]$type),
                  xlab = "treatment given", ylab = metrics[j], trace.label = "Type of Stressor")
}
```

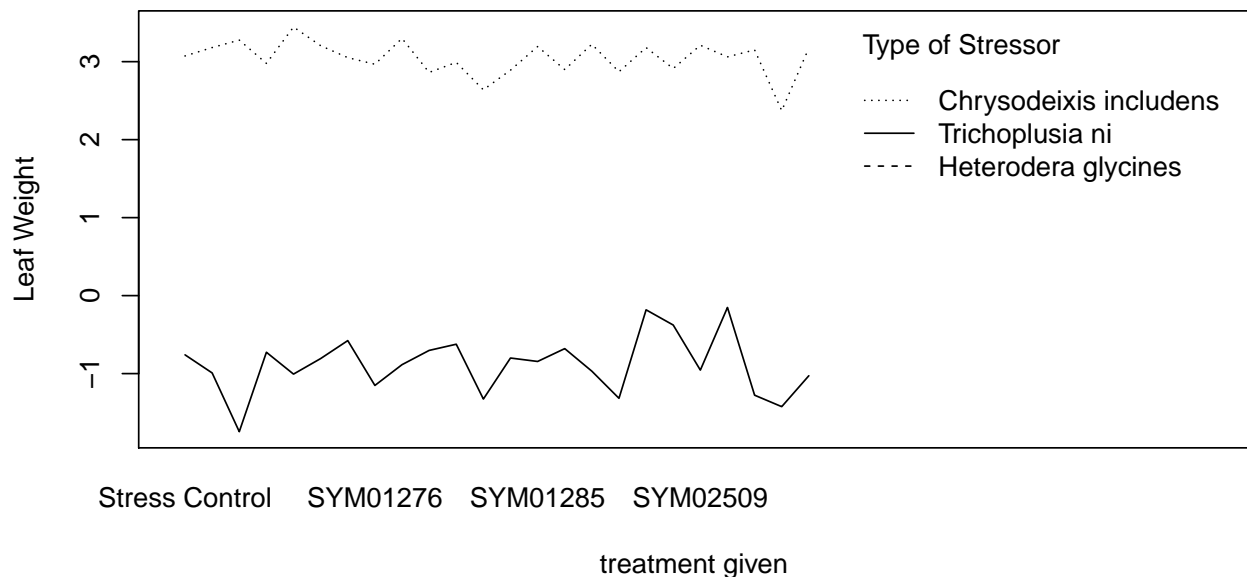




We note the following from the plots.

It appears that the stressor type does indeed impact the effectiveness of the fungal treatment. We will take this into account when we make our model. We also note the leaf area graph looks different compared to the other plots. The leaf area varies a lot more under “Chrysodeixis includens” then it does for “Heterodera Glycines”. We took the log transformation of the leaf area instead to stabilize the variances, and then re-examined the interaction plot.

```
interaction.plot(response = log(prunedat.list[[2]]$value), as.factor(prunedat.list[[2]]$trt),
                 as.factor(prunedat.list[[2]]$type),
                 xlab = "treatment given", ylab = metrics[j], trace.label = "Type of Stressor")
```



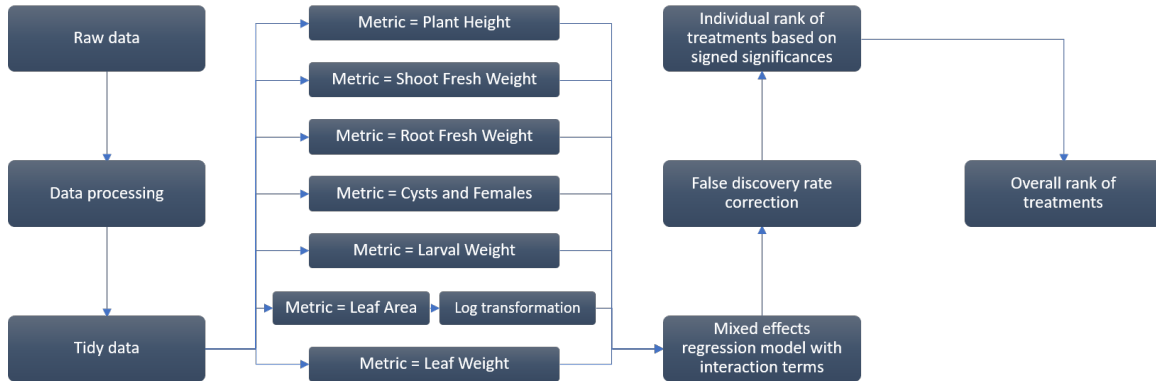
It appears that even after taking the log, the treatments affect the leaf weight value differently under different stressors. We should take this in to account for leaf area as well.

The final thing we’d like to note, is that we can’t really take the effect of the greenhouses in to account easily. Since the treatments are different for each of the greenhouses, and not all greenhouses have all treatments, we can’t say if the treatments or the greenhouses are more responsible for causing changes in the metrics. The two are inherently confounded. However, we do know that we’re more interested in the treatment effect

than the effect of the greenhouses. As a result we'll treat the greenhouse that we got observations from to be a random effect. This means we think that the greenhouses have an effect, but we're not very interested in estimating it.

3 A Road Map for Our Analysis

The following figure illustrates our plan for analyzing this data set.



4 Methodology

We begin with an overview of our methodology to get the overall rankings of treatments. Our method proceeds in the following four steps.

1. For each metric, we fit a linear mixed effect model to estimate the treatment effect. As described in the previous section, we take into account that the value for the metric for a particular treatment is effected by which stressor type was applied. We also keep the “greenhouse” or “id” effect as a random effect.
2. For each metric, we test whether all treatment effects are zero simultaneously. The false discovery rate (FDR) is controlled in this multiple testing procedure. This is necessary because we’re testing many things to see if they’re equal to 0. If we do this too many times without controlling the FDR, we’ll say a treatment is important when it’s not.
3. For each metric, we establish a ranking of treatments based on the signs of estimated treatment effects and the significance of the multiple testing.
4. We finally combine the rankings for each metric to obtain an overall ranking based on the relative importance of metrics.

We discuss each step more in the below subsections.

4.1 Linear mixed effect models

For each metric, we fit a linear mixed effect model using the measured values of the metric as responses. We include treatments and greenhouse IDs as regression covariates. For those metrics with two different stressor types, we also use stressor types as covariates. Considering that the effect of a treatment varies under different stressor types, we also include interaction terms between treatments and stressor types.

The treatments and stressor type effects (and their interaction) are modeled as fixed effects, and the greenhouse effect is treated as a random effect. Section 7.2 in Appendix discusses the models in more technical details.

4.2 False discovery rate correction

Let θ_{jk} represent the effect of treatment j under a particular stressor type k , which is the average difference of the metric values between the treatment j and the control under the same stressor k (also see Section 7.2 for how we obtain it from the regression models). To see which treatment is effective under stressor type k , we are interested in testing the hypotheses $H_0 : \theta_{jk} = 0$ versus $H_1 : \theta_{jk} \neq 0$ for $j = 1, \dots, J$. We used R package `emmeans` (Lenth 2020) to test each individual hypothesis.

Since we would like to test all hypotheses simultaneously, it is desired to control the probability that at least one null hypothesis is incorrectly rejected (type-I error). In our case, we need to test $J = 23$ hypotheses simultaneously for each metric and each stressor type. The Bonferroni correction is one such method, and it involves testing our hypothesis at level $\frac{.05}{23} = .002$ for each metric. However, using this procedure results in all treatments being found as having no effect, which provides no information.

Instead, we control the false discovery rate (FDR), defined as the expected proportion of rejected null hypotheses that are incorrectly rejected. The classic Benjamini-Hochberg procedure (Benjamini and Hochberg 1995) for FDR control assumes independent test statistics, which may not be true in our case since all test statistics are based on coefficient estimators of a regression model. The Benjamini-Yekutieli procedure (Benjamini and Yekutieli 2001) is its extension that allows for arbitrary dependency among test statistics. We adopt this procedure for FDR control in our case. Specifically, for each metric and stressor type, we first obtained the p -value of each individual test using `emmeans`, and then adjusted them by the Benjamini-Yekutieli procedure using the R function `p.adjust()` in the `stats` package (R Core Team 2019). The code for this method can also be found in the appendix.

4.3 Individual rankings

Given the adjusted p -values and the coefficient estimates, we construct a ranking of treatments for each metric under each stressor associated with this metric. For each of them, we define a rank variable $\mathbf{r}_k = (r_{1k}, \dots, r_{Jk})$ with the rank for the j th treatment under the k th stressor given by

$$r_{jk} = \begin{cases} 1, & \text{if } \hat{\theta}_{jk} > 0 \text{ and } p_{jk} < 0.05 \\ -1, & \text{if } \hat{\theta}_{jk} < 0 \text{ and } p_{jk} < 0.05, \\ 0, & \text{otherwise} \end{cases} \quad (1)$$

where $\hat{\theta}_{jk}$ is the estimated treatment effect from the model, and p_{jk} is the adjusted p -value for testing $H_0 : \theta_{jk} = 0$. Intuitively, $r_{jk} = 1$ means the j th treatment has a significant positive impact (i.e., it increases the value) on that metric under the k th stressor, while $r_{jk} = -1$ means it has a significant negative impact (i.e., it decreases the value). If $r_{jk} = 0$, then the treatment effect is too tiny to be deemed significant. Hence, $r_{jk} > r_{jk'}$ means the j th treatment has more positive impact on the metric than the j' th one does under the k th stressor.

4.4 Overall rankings

Our goal is to combine the individual rankings to get an overall ranking of treatments that measures which treatments are best in terms of improving plant growth. An overall rank variable $\mathbf{R}_k = (R_{1k}, \dots, R_{Jk})$ under the k th stressor type takes the form

$$\mathbf{R}_k = \sum_{m=1}^M \delta^{(m)} \mathbf{r}_k^{(m)}, \quad (2)$$

where $\mathbf{r}_k^{(m)}$ is the individual rank for metric m under stressor k , and $\delta^{(m)} \in [-1, 1]$ is the weight for metric m that satisfies $\sum_{m=1}^M |\delta^{(m)}| = 1$. The weights $\{\delta^{(m)}\}$ measure the relative importance of the metrics. Note that $\delta^{(m)}$ can be positive or negative. If a metric is positively related to plant growth, i.e., higher value of the

metric means better growth, then we set $\delta^{(m)} > 0$; otherwise, we set $\delta^{(m)} < 0$. $R_{jk} > R_{j'k}$ means that the j th treatment is better at improving plant growth than the j' th one under the k th stressor type.

We first combine rankings for the first group of metrics, which have one associated stressor type. The weights are shown in the following table.

Metric	Weight	Metric	Weight
Cysts and Females	−4/10	Plant Height	1/10
Root Fresh Weight	3/10	Shoot Fresh Weight	2/10

For the second group of metrics that have two levels of stressor types, we obtain an overall ranking for each level, denoted as \mathbf{R}_1 and \mathbf{R}_2 , respectively. We use a same set of weights shown in the following table.

Metric	Weight	Metric	Weight
Larval Weight	−2/6	Leaf Area	−3/6
Leaf Weight	−1/6		

It is also possible to combine the rankings for both levels of stressor types by taking a weighted sum of \mathbf{R}_1 and \mathbf{R}_2 . Here we use 0.5 for both weights.

Finally, we remark that it is possible to use other weights to combine the rankings if desired.

5 Ranking Results

This section presents individual rankings of fungal treatments for metrics and overall ranking of fungal treatments.

Results from the linear mixed-effects models with interaction terms can be found in the appendix.

Based on the findings described in this section, the following observations can be made:

- Taking into account the correction of multiple comparisons, we apparently have only a few significant effects of fungal treatments.
- Individual rankings of fungal treatments vary in terms of metrics. Nevertheless, we suggest that there is a reasonable way to rank the effects of fungal treatments if there is a need for overall ranking of them.

The following subsections provide further details about the analysis. Subsection 5.1 presents fitting results of the linear mixed-effects models. Individual rankings of effects of the fungal treatments for different metrics are provided in Subsection 5.2. In Subsection 5.3, we offer an overall ranking of the fungal treatments.

5.1 Individual rankings of fungal treatments for metrics

In this subsection, we rank the effects of the fungal treatments using different metrics. There are many zeros in the individual rankings, which implies that it is required to consider the correction for multiple testings (or comparisons). For each of the metrics ‘Larval Weight,’ ‘Leaf Area,’ and ‘Leaf Weight,’ two different individual rankings of the fungal treatments are presented, since there are two different stressors (*Chrysodeixis includens* and *Trichoplusia ni*). The ranking columns `rankings1` and `rankings2` are for *Chrysodeixis includens* and *Trichoplusia ni*, respectively. The rest of the metrics only had 1 stressor type, so this isn’t present there.

We show a glimpse of what each of these individual rankings look like. The full individual rankings, as well as the R code used to make them, will be in the appendix.

Some of the individual rankings for larval weight.

##		rankings1	rankings2
##	SYM01261 - Stress Control	0	0
##	SYM01262 - Stress Control	0	0
##	SYM01263 - Stress Control	0	0
##	SYM01264 - Stress Control	0	-1
##	SYM01273 - Stress Control	0	0
##	SYM01275 - Stress Control	0	-1

Some of the individual rankings for Leaf area.

##		rankings1	rankings2
##	SYM01261 - Stress Control	0	0
##	SYM01262 - Stress Control	0	0
##	SYM01263 - Stress Control	0	0
##	SYM01264 - Stress Control	0	0
##	SYM01273 - Stress Control	0	0
##	SYM01275 - Stress Control	0	1

Some of the individual rankings for Leaf Weight

##		rankings1	rankings2
##	SYM01261 - Stress Control	0	0
##	SYM01262 - Stress Control	0	0
##	SYM01263 - Stress Control	0	0
##	SYM01264 - Stress Control	0	0
##	SYM01273 - Stress Control	0	0
##	SYM01275 - Stress Control	0	0

Some of the individual rankings for Cysts and Females

##	SYM01261 - Stress Control	SYM01262 - Stress Control	SYM01263 - Stress Control
##	0	0	-1
##	SYM01264 - Stress Control	SYM01273 - Stress Control	SYM01275 - Stress Control
##	-1	0	0

Some of the individual rankings for Plant Height

##	SYM01261 - Stress Control	SYM01262 - Stress Control	SYM01263 - Stress Control
##	0	0	-1
##	SYM01264 - Stress Control	SYM01273 - Stress Control	SYM01275 - Stress Control
##	0	0	0

Some of the individual rankings for Root Fresh Weight

##	SYM01261 - Stress Control	SYM01262 - Stress Control	SYM01263 - Stress Control
##	0	0	0
##	SYM01264 - Stress Control	SYM01273 - Stress Control	SYM01275 - Stress Control
##	0	1	0

Some of the individual rankings for Shoot Fresh Weight

##	SYM01261 - Stress Control	SYM01262 - Stress Control	SYM01263 - Stress Control
##	0	0	0
##	SYM01264 - Stress Control	SYM01273 - Stress Control	SYM01275 - Stress Control
##	0	0	0

5.2 Overall ranking of fungal treatments

Our goal was to make rankings for the fungal treatments for two different classes of metrics. One of the overall rankings was based on the following metrics: Leaf Weight, Leaf Area, and Larval Weight. The other overall ranking was based on the Cysts and females metric, the Root Fresh Weight metric, the Shoot Fresh Weight metric, and the Plant Height metric. We obtained an overall ranking score of the fungal treatments based on the individual rankings obtained above after taking in to account that there are two partial orders of importance of metrics. These can be briefly described as follows: (1) Leaf Area > Larval Weight > Leaf Weight and (2) Cysts and Females > Root Fresh Weight > Shoot Fresh Weight > Plant Height.

We include a list of the treatments alongside the ranks that they had for both of the overall rankings. We will include the full table in the appendix, alongside the r code used to generate these rankings.

```
overall_rank
```

##	Treatment	Rank1	Rank2
## 1	SYM02498	2	2
## 2	SYM02477	7	1
## 3	SYM01279	2	7
## 4	SYM01273	8	2
## 5	SYM01287	8	2
## 6	SYM01285	4	7
## 7	SYM01275	5	7
## 8	SYM02512	8	5
## 9	SYM02522	8	6
## 10	SYM01261	8	7
## 11	SYM01262	8	7
## 12	SYM01284	8	7
## 13	SYM01286	8	7
## 14	SYM02496	1	19
## 15	SYM02513	5	15
## 16	SYM01276	8	15
## 17	SYM01283	8	15
## 18	SYM02509	8	15
## 19	SYM02521	8	19
## 20	SYM01277	21	7
## 21	SYM01263	8	23
## 22	SYM01264	21	19
## 23	SYM01281	21	19

It seems that, for instance, the fungal treatment **SYM02498** is most effective compared to others. But we do not hesitate to say that one also need to take the treatments **SYM02477** and **SYM02496** into consideration.

6 Conclusions

We have obtained overall rankings for fungal treatments as well as created a model that portrays the effects of the fungal treatments after taking in to account how they vary across stressor types.

7 Appendix and Supplements

7.1 Additional exploratory data analysis and pruning the data set

7.1.1 R libraries

```
library(lme4)
library(dplyr)
library(readr)
library(emmeans)
library(ggplot2)
library(lmerTest)
library(stats)
library(readxl)
library(tibble)
library(ggpubr)
library(lattice)
library(gridExtra)
```

7.1.2 R code for data set pruning and exploration

```
rawdat <- read_xlsx(path = "Rivera Vega_Raw Data All.xlsx",
                    sheet = 1, col_names = TRUE, col_types = "text") %>% tbl_df()

## New names:
## * `` -> ...6

glimpse(rawdat)

## Observations: 9,539
## Variables: 6
## $ Treatment      <chr> "SYM01273", "SYM01273", "SYM01273", "SYM01273", ...
## $ Experiment_Unit_ID <chr> "SCT0001", "SCT0001", "SCT0001", "SCT0001", "SCT...
## $ Stress_Type     <chr> "Heterodera glycines", "Heterodera glycines", "H...
## $ Metric          <chr> "Plant Height", "Plant Height", "Plant Height", ...
## $ Value           <chr> "20.5", "22", "16.5", "24", "18.5", "14", "15.5"...
## $ ...6            <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, ...

datasetlist = list()
rawdat$Metric[which(rawdat$Metric == "Larval weight")] <- "Larval Weight"
rawdat$Metric[which(rawdat$Metric == "Leaf area")] <- "Leaf Area"
rawdat$Metric[which(rawdat$Metric == "Weight_leaf")] <- "Leaf Weight"
rawdat$Metric[which(rawdat$Metric == "weight_leaf")] <- "Leaf Weight"

# index of observations of which Value is missing
ind.na <- rawdat %>% pull(Value) %>% as.numeric() %>% is.na() %>% which()
ind.na

## [1] 8106 8166 8190
```

There are 3 indices that are missing in the full data set. After discussing this with Dr. Vega, we opt to completely remove these data points and continue our analysis without these points.

```

# Remove the redundant column X
rawdat <- rawdat %>% select(Treatment, Experiment_Unit_ID, Stress_Type, Metric, Value)
rawdat <- rawdat[-ind.na, ]

rawdat %>% pull(Treatment) %>% unique()

## [1] "SYM01273"      "SYM02493"      "SYM02486"      "SYM01261"
## [5] "SYM01268"      "SYM02477"      "SYM02500"      "Stress Control"
## [9] "SYM01279"      "SYM01284"      "SYM01285"      "SYM01287"
## [13] "SYM02498"      "SYM02521"      "SYM02522"      "SYM01263"
## [17] "SYM01264"      "SYM01272"      "SYM01275"      "SYM01276"
## [21] "SYM01280"      "SYM01283"      "SYM01281"      "SYM02492"
## [25] "SYM02494"      "SYM02496"      "SYM34594"      "SYM34596"
## [29] "SYM34603"      "SYM34616"      "SYM34642"      "SYM34643"
## [33] "SYM34646"      "SYM34703"      "SYM01262"      "SYM01269"
## [37] "SYM01277"      "SYM01286"      "SYM02507"      "SYM02509"
## [41] "SYM02512"      "SYM02513"      "Abamectin"      "SYM02523"
## [45] "SYM02511"      "SYM02491"      "SYM02495"      "SYM02478"
## [49] "SYM02508"      "SYM02490"      "SYM01278"      "SYM01282"

rawdat %>% pull(Experiment_Unit_ID) %>% unique()

## [1] "SCT0001"  "SCT0002"  "SCT0003"  "SCT0004"  "SCT0005"  "SCT0006_1"
## [7] "SCT0007_1" "SLT0001"  "SLT0002"  "SLT0003"  "SLT0004"  "SLT0005"
## [13] "SLT0006"  "SLT0007"  "SLT0008"  "SLT0009"  "SLT0010"  "GH13"
## [19] "GH12"     "GH10"     "GH9"      "GH6"      "GH7"      "GH8"

rawdat %>% pull(Stress_Type) %>% unique()

## [1] "Heterodera glycines"  "Chrysodeixis includens" "Trichoplusia ni"

rawdat %>% pull(Metric) %>% unique() # Capital!

## [1] "Plant Height"      "Shoot Fresh Weight" "Root Fresh Weight"
## [4] "Cysts and Females" "Larval Weight"      "Leaf Area"
## [7] "Leaf Weight"

tempvec <- rawdat$Metric
tempvec[which(tempvec == "Larval weight")] <- "Larval Weight"
tempvec[which(tempvec == "Leaf area")] <- "Leaf Area"
tempvec[which(tempvec == "Weight_leaf")] <- "Leaf Weight"
tempvec[which(tempvec == "weight_leaf")] <- "Leaf Weight"
rawdat$Metric <- tempvec

level <- rawdat %>% pull(Treatment) %>% unique()
level <- sort(level)
level <- c("Stress Control", level[-which(level == "Stress Control")])
rawdat$Treatment <- factor(rawdat$Treatment, levels = level)

level <- rawdat %>% pull(Experiment_Unit_ID) %>% unique()
temp1 <- level[which(substring(level, 1, 2) == "SC")] %>% sort()
temp2 <- level[which(substring(level, 1, 2) == "SL")] %>% sort()
temp3 <- level[which(substring(level, 1, 2) == "GH")]
temp3 <- temp3[substring(temp3, 3) %>% as.numeric() %>% order()]
level <- c(temp1, temp2, temp3) ; rm(temp1, temp2, temp3)
rawdat$Experiment_Unit_ID <- factor(rawdat$Experiment_Unit_ID, levels = level)

```

```
# rawdat$Stress_Type <- factor(rawdat$Stress_Type)

rawdat[, "Value"] <- rawdat %>% pull(Value) %>% as.numeric()

rawdat <- rawdat %>% tbl_df()

rawdat <- rawdat %>% rename(trt = Treatment, id = Experiment_Unit_ID,
                           type = Stress_Type, metric = Metric, value = Value)

##### EDA #####

name.metric <- rawdat %>% pull(metric) %>% unique()
name.metric
```

```
## [1] "Plant Height"      "Shoot Fresh Weight" "Root Fresh Weight"
## [4] "Cysts and Females"  "Larval Weight"      "Leaf Area"
## [7] "Leaf Weight"
```

It looks like there are 7 different metrics that we're too explore. The metrics are "Plant Height", "Shoot Fresh Weight", "Root Fresh Weight", "Cysts and Females", "Larval Weight", "Leaf Area", and "Leaf Weight".

```
dat.list <- list()
for(i in 1:length(name.metric)) {
  ind <- which(rawdat$metric == name.metric[i])
  dat.list[[i]] <- rawdat[ind, , drop = FALSE] %>% select(-metric)
}
names(dat.list) <- name.metric

n.trt <- c()
n.id <- c()
n.type <- c()
for(i in 1:length(name.metric)) {
  n.trt[i] <- dat.list[[i]] %>% pull(trt) %>% unique() %>% length()
  n.id[i] <- dat.list[[i]] %>% pull(id) %>% unique() %>% length()
  n.type[i] <- dat.list[[i]] %>% pull(type) %>% unique() %>% length()
}
n.trt
```

```
## [1] 43 42 42 42 37 37 37
```

```
n.id
```

```
## [1] 7 7 7 7 17 17 17
```

```
n.type
```

```
## [1] 1 1 1 1 2 2 2
```

It appears that each metric is not measured on every stressor type. After some discussion, this is reasonable.

The worms affect the plants in different areas, and as a result the metrics are observed in a fashion that is appropriate. For instance, it would be inappropriate to look at the plant height for a worm that primarily impacts the root of the plant. All of the metrics are observed for either 1 or 2 types of stressors.

```
unique(rawdat$type)
```

```
## [1] "Heterodera glycines"      "Chrysodeixis includens" "Trichoplusia ni"
```

```
trt_hg <- rawdat %>% filter(type == 'Heterodera glycines') %>%
  pull(trt) %>% as.character() %>% unique()
trt_ci <- rawdat %>% filter(type == 'Chrysodeixis includens') %>%
  pull(trt) %>% as.character() %>% unique()
trt_tn <- rawdat %>% filter(type == 'Trichoplusia ni') %>%
  pull(trt) %>% as.character() %>% unique()
```

trt_hg

```
## [1] "SYM01273"      "SYM02493"      "SYM02486"      "SYM01261"
## [5] "SYM01268"      "SYM02477"      "SYM02500"      "Stress Control"
## [9] "SYM01279"      "SYM01284"      "SYM01285"      "SYM01287"
## [13] "SYM02498"      "SYM02521"      "SYM02522"      "SYM01263"
## [17] "SYM01264"      "SYM01272"      "SYM01275"      "SYM01276"
## [21] "SYM01280"      "SYM01283"      "SYM01281"      "SYM02492"
## [25] "SYM02494"      "SYM02496"      "SYM34594"      "SYM34596"
## [29] "SYM34603"      "SYM34616"      "SYM34642"      "SYM34643"
## [33] "SYM34646"      "SYM34703"      "SYM01262"      "SYM01269"
## [37] "SYM01277"      "SYM01286"      "SYM02507"      "SYM02509"
## [41] "SYM02512"      "SYM02513"      "Abamectin"
```

trt_ci

```
## [1] "Stress Control" "SYM01273"      "SYM02477"      "SYM02509"
## [5] "SYM02513"      "SYM02522"      "SYM02523"      "SYM01269"
## [9] "SYM01272"      "SYM02511"      "SYM02512"      "SYM02491"
## [13] "SYM02492"      "SYM02494"      "SYM02495"      "SYM02496"
## [17] "SYM01275"      "SYM01261"      "SYM02478"      "SYM01263"
## [21] "SYM01277"      "SYM01264"      "SYM02498"      "SYM01279"
## [25] "SYM02508"      "SYM01283"      "SYM01284"      "SYM01286"
## [29] "SYM02521"      "SYM01276"      "SYM02490"      "SYM01278"
## [33] "SYM01281"      "SYM01282"      "SYM01262"      "SYM01285"
## [37] "SYM01287"
```

trt_tn

```
## [1] "Stress Control" "SYM01275"      "SYM02491"      "SYM02496"
## [5] "SYM02498"      "SYM01279"      "SYM02512"      "SYM02522"
## [9] "SYM02523"      "SYM01278"      "SYM01281"      "SYM02509"
## [13] "SYM01284"      "SYM01285"      "SYM01286"      "SYM01287"
## [17] "SYM01273"      "SYM01262"      "SYM01276"      "SYM02490"
## [21] "SYM01282"      "SYM02513"      "SYM01261"      "SYM02478"
## [25] "SYM01263"      "SYM01277"      "SYM01264"      "SYM02508"
## [29] "SYM02477"      "SYM01283"      "SYM02521"
```

There are three different types of “worms” or stressors. They are: “*Heterodera glycines*”, “*Chrysodeixis includens*”, and “*Trichoplusia ni*”.

trt_hg, trt_ci, and trt_tn contain the different treatments each of the stressors have. It turns out, not every stressor was run on every treatment. There are quite a few treatments that were not touched by some stressors. After discussing this with Dr. Vega, we analyzed only treatments that were tried on every stressor. We go ahead and prune the data set to only include the treatments.

But before that, lets look at the number of plants that are stored in a greenhouse.

```
trt_inter = intersect(intersect(trt_hg, trt_ci), trt_tn)
```

```
data_pruned = subset(rawdat, trt %in% trt_inter)

##### Remove ids that have control group only #####
# get number of treatment in each group (id, type, metric)
n_trt = aggregate(trt ~ id + type + metric, data = data_pruned,
                  FUN = function(x) length(unique(x)))

n_trt
```

##	id	type	metric	trt
## 1	SCT0001	Heterodera glycines	Cysts and Females	4
## 2	SCT0002	Heterodera glycines	Cysts and Females	8
## 3	SCT0003	Heterodera glycines	Cysts and Females	6
## 4	SCT0004	Heterodera glycines	Cysts and Females	3
## 5	SCT0005	Heterodera glycines	Cysts and Females	1
## 6	SCT0006_1	Heterodera glycines	Cysts and Females	7
## 7	SCT0007_1	Heterodera glycines	Cysts and Females	6
## 8	SLT0001	Chrysodeixis includens	Larval Weight	6
## 9	SLT0002	Chrysodeixis includens	Larval Weight	2
## 10	SLT0003	Chrysodeixis includens	Larval Weight	2
## 11	SLT0004	Chrysodeixis includens	Larval Weight	6
## 12	SLT0005	Chrysodeixis includens	Larval Weight	5
## 13	SLT0006	Chrysodeixis includens	Larval Weight	6
## 14	SLT0007	Chrysodeixis includens	Larval Weight	5
## 15	SLT0008	Chrysodeixis includens	Larval Weight	7
## 16	SLT0009	Chrysodeixis includens	Larval Weight	8
## 17	SLT0010	Chrysodeixis includens	Larval Weight	7
## 18	GH6	Trichoplusia ni	Larval Weight	6
## 19	GH7	Trichoplusia ni	Larval Weight	5
## 20	GH8	Trichoplusia ni	Larval Weight	6
## 21	GH9	Trichoplusia ni	Larval Weight	5
## 22	GH10	Trichoplusia ni	Larval Weight	7
## 23	GH12	Trichoplusia ni	Larval Weight	8
## 24	GH13	Trichoplusia ni	Larval Weight	7
## 25	SLT0001	Chrysodeixis includens	Leaf Area	6
## 26	SLT0002	Chrysodeixis includens	Leaf Area	2
## 27	SLT0003	Chrysodeixis includens	Leaf Area	2
## 28	SLT0004	Chrysodeixis includens	Leaf Area	6
## 29	SLT0005	Chrysodeixis includens	Leaf Area	5
## 30	SLT0006	Chrysodeixis includens	Leaf Area	6
## 31	SLT0007	Chrysodeixis includens	Leaf Area	5
## 32	SLT0008	Chrysodeixis includens	Leaf Area	7
## 33	SLT0009	Chrysodeixis includens	Leaf Area	8
## 34	SLT0010	Chrysodeixis includens	Leaf Area	7
## 35	GH6	Trichoplusia ni	Leaf Area	6
## 36	GH7	Trichoplusia ni	Leaf Area	5
## 37	GH8	Trichoplusia ni	Leaf Area	6
## 38	GH9	Trichoplusia ni	Leaf Area	5
## 39	GH10	Trichoplusia ni	Leaf Area	7
## 40	GH12	Trichoplusia ni	Leaf Area	8
## 41	GH13	Trichoplusia ni	Leaf Area	7
## 42	SLT0001	Chrysodeixis includens	Leaf Weight	6
## 43	SLT0002	Chrysodeixis includens	Leaf Weight	2
## 44	SLT0003	Chrysodeixis includens	Leaf Weight	2

```

## 45 SLT0004 Chrysodeixis includens      Leaf Weight  6
## 46 SLT0005 Chrysodeixis includens      Leaf Weight  5
## 47 SLT0006 Chrysodeixis includens      Leaf Weight  6
## 48 SLT0007 Chrysodeixis includens      Leaf Weight  5
## 49 SLT0008 Chrysodeixis includens      Leaf Weight  7
## 50 SLT0009 Chrysodeixis includens      Leaf Weight  8
## 51 SLT0010 Chrysodeixis includens      Leaf Weight  7
## 52      GH6      Trichoplusia ni      Leaf Weight  6
## 53      GH7      Trichoplusia ni      Leaf Weight  5
## 54      GH8      Trichoplusia ni      Leaf Weight  6
## 55      GH9      Trichoplusia ni      Leaf Weight  5
## 56     GH10      Trichoplusia ni      Leaf Weight  7
## 57     GH12      Trichoplusia ni      Leaf Weight  8
## 58     GH13      Trichoplusia ni      Leaf Weight  7
## 59 SCT0001  Heterodera glycines      Plant Height  4
## 60 SCT0002  Heterodera glycines      Plant Height  8
## 61 SCT0003  Heterodera glycines      Plant Height  6
## 62 SCT0004  Heterodera glycines      Plant Height  3
## 63 SCT0005  Heterodera glycines      Plant Height  1
## 64 SCT0006_1 Heterodera glycines      Plant Height  7
## 65 SCT0007_1 Heterodera glycines      Plant Height  6
## 66 SCT0001  Heterodera glycines Root Fresh Weight  4
## 67 SCT0002  Heterodera glycines Root Fresh Weight  8
## 68 SCT0003  Heterodera glycines Root Fresh Weight  6
## 69 SCT0004  Heterodera glycines Root Fresh Weight  3
## 70 SCT0005  Heterodera glycines Root Fresh Weight  1
## 71 SCT0006_1 Heterodera glycines Root Fresh Weight  7
## 72 SCT0007_1 Heterodera glycines Root Fresh Weight  6
## 73 SCT0001  Heterodera glycines Shoot Fresh Weight  4
## 74 SCT0002  Heterodera glycines Shoot Fresh Weight  8
## 75 SCT0003  Heterodera glycines Shoot Fresh Weight  6
## 76 SCT0004  Heterodera glycines Shoot Fresh Weight  3
## 77 SCT0005  Heterodera glycines Shoot Fresh Weight  1
## 78 SCT0006_1 Heterodera glycines Shoot Fresh Weight  7
## 79 SCT0007_1 Heterodera glycines Shoot Fresh Weight  6

```

`n_trt` represents the different types of treatments in a particular greenhouse.

Even across all the greenhouses, it doesn't seem that all the treatments are in each greenhouse, there can sometimes be only 2 different types of treatments in a greenhouse.

A bit more exploring reveals that there is at least always a control group in each greenhouse, alongside at least one treatment. This makes dealing with this data set tricky. Since we don't have all types of treatments in each greenhouse, we will have trouble distinguishing between the effect of the individual greenhouse, and the effect of the treatment.

However, we're not really interested in the greenhouse. Since its a random factor and we're less interested in it, we can try to walk around this problem by modeling the greenhouse effect as a random effect. The following r code creates the pruned data file.

```

colnames(n_trt)[ncol(n_trt)] = 'n_trt'
data_pruned2 = merge(data_pruned, n_trt, by = c("id", "type", "metric"))
data_pruned2 = subset(data_pruned2, n_trt > 1)
data_pruned2 = data_pruned2[, -ncol(data_pruned2)]

#write.csv(data_pruned2, file = "pruned_data2.csv", row.names = F)

```

7.1.3 Frequency table plots

```
prunedat = read.csv(file = "pruned_data2.csv")
#glimpse(prunedat)
metrics = unique(prunedat$metric) # unique values of metrics
n.metric = length(metrics)
prunedat.list = list()
for(i in 1:n.metric) {
  m = metrics[i]
  prunedat.list[[i]] = filter(prunedat, metric == m)
}

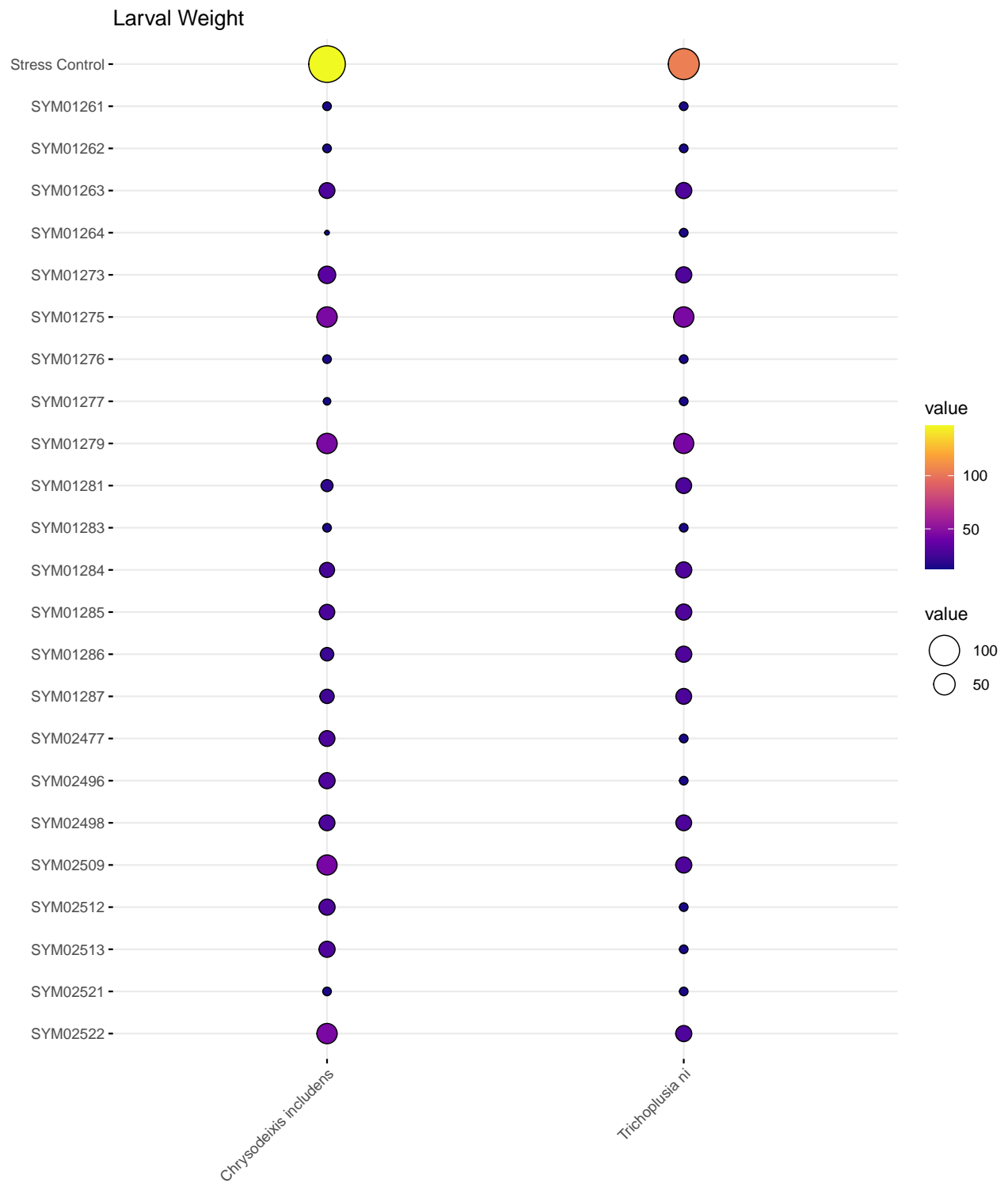
n.trt      <- sapply(X = prunedat.list, FUN = function(x) pull(x, trt) %>% unique() %>% length())
n.id       <- sapply(X = prunedat.list, FUN = function(x) pull(x, id) %>% unique() %>% length())
n.type     <- sapply(X = prunedat.list, FUN = function(x) pull(x, type) %>% unique() %>% length())
fq.trt.type <- list()
fq.trt.id  <- list()
fq.type.id <- list()
for(i in 1:length(metrics)) {
  vis_dat <- prunedat.list[[i]] %>% group_by(trt, type) %>%
    summarize(n = n()) %>% tidyr::spread(type, n) %>% column_to_rownames(var = "trt")
  fq.trt.type[[i]] <- vis_dat %>% ggballoonplot(fill = "value") +
    scale_fill_viridis_c(option = "C") + ggtitle(metrics[i])

  vis_dat <- prunedat.list[[i]] %>% group_by(trt, id) %>%
    summarize(n = n()) %>% tidyr::spread(id, n) %>% column_to_rownames(var = "trt")
  fq.trt.id[[i]] <- vis_dat %>% ggballoonplot(fill = "value") +
    scale_fill_viridis_c(option = "C") + ggtitle(metrics[i])

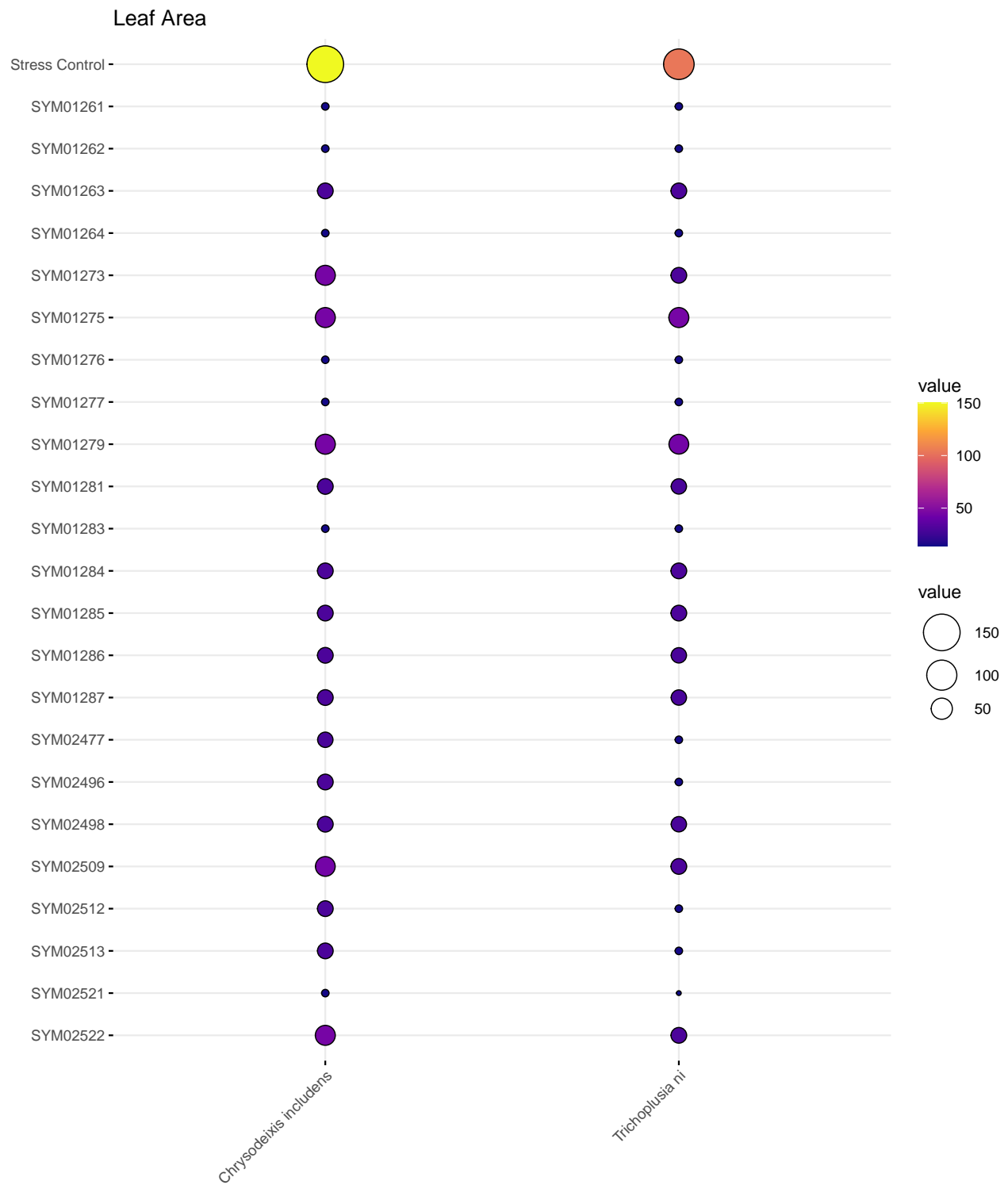
  vis_dat <- prunedat.list[[i]] %>% group_by(type, id) %>%
    summarize(n = n()) %>% tidyr::spread(id, n) %>% column_to_rownames(var = "type")
  fq.type.id[[i]] <- vis_dat %>% ggballoonplot(fill = "value") +
    scale_fill_viridis_c(option = "C") + ggtitle(metrics[i])
} ; rm(i)

print(fq.trt.type)

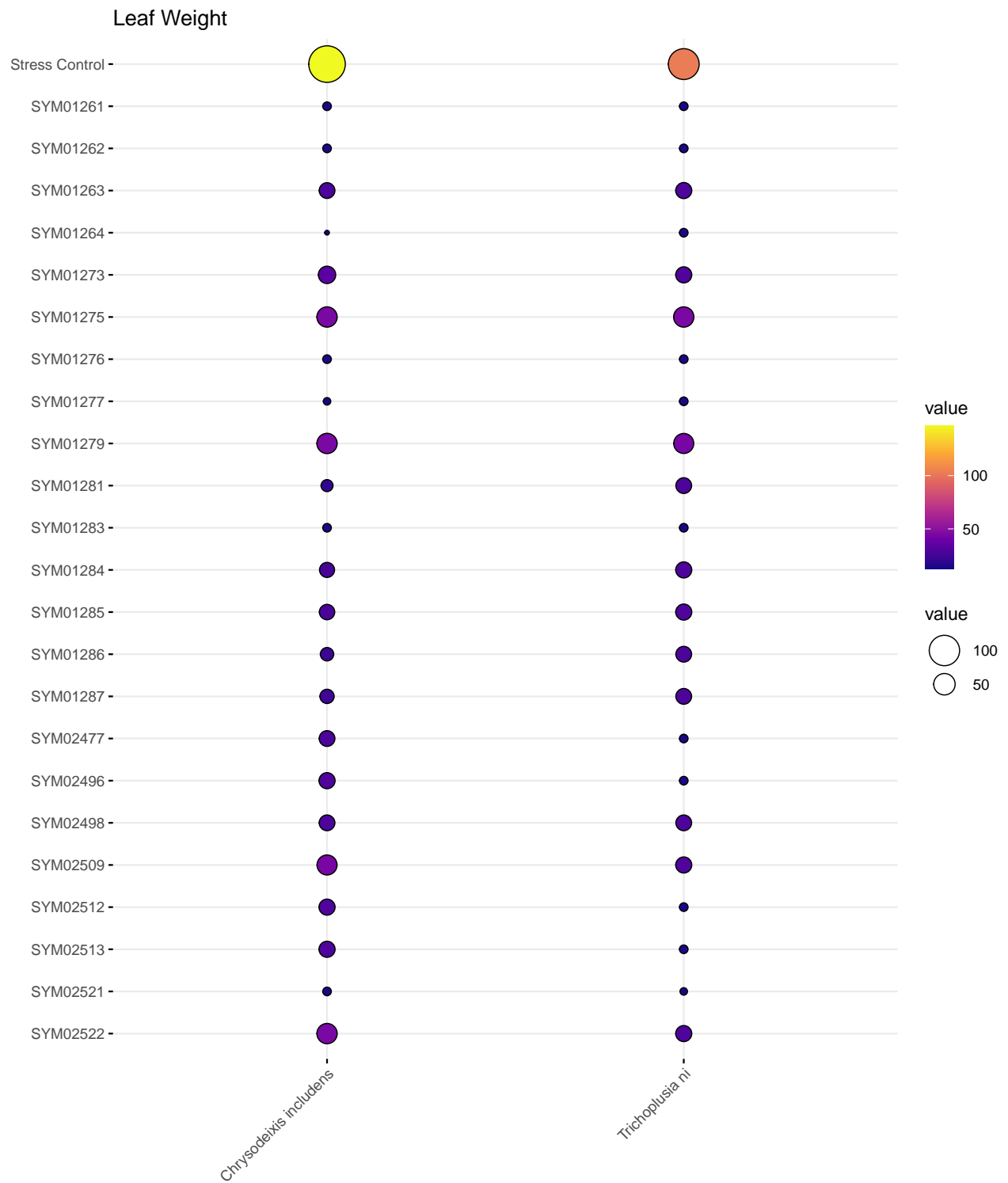
## [[1]]
```

[[2]]

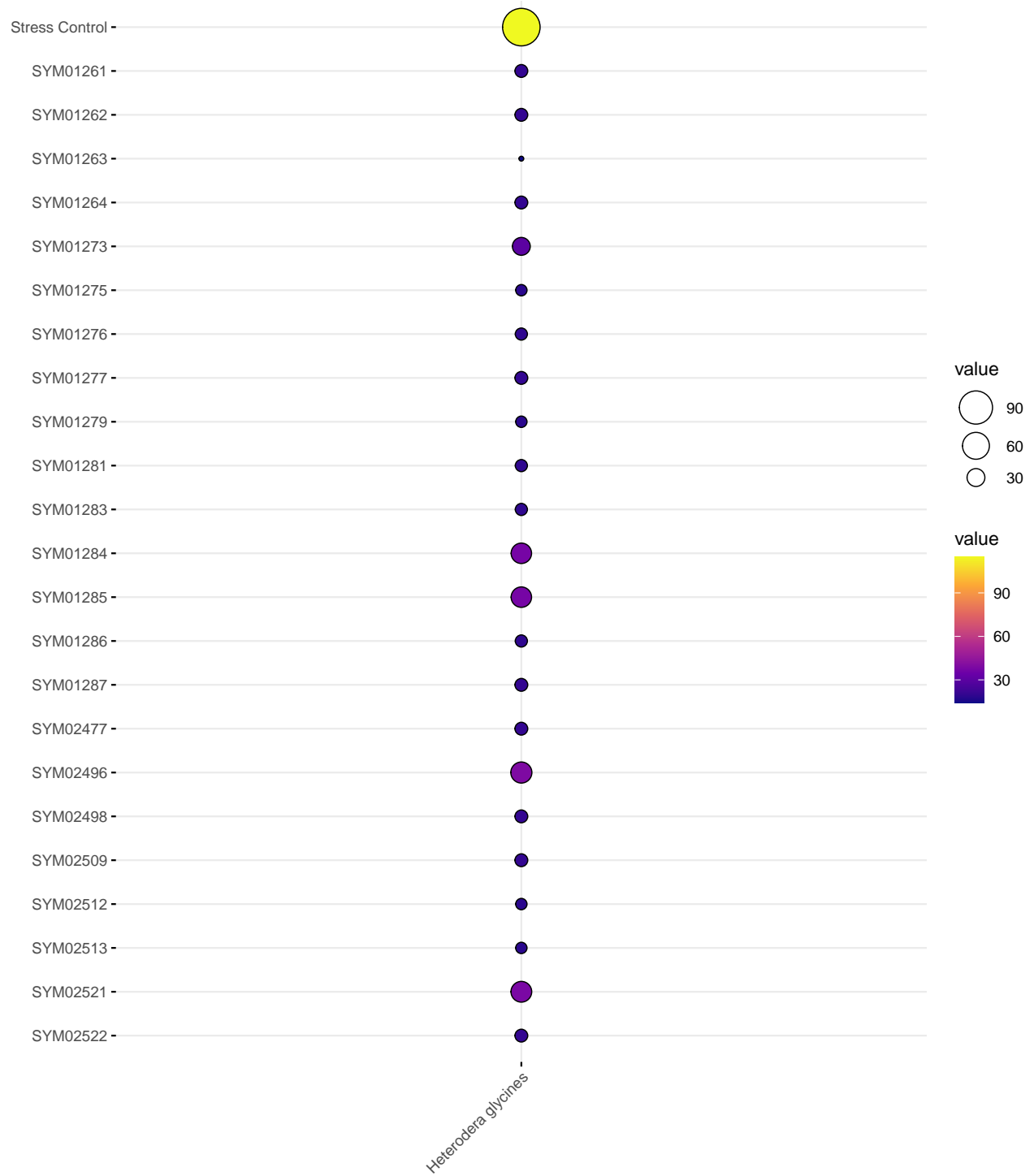


[[3]]

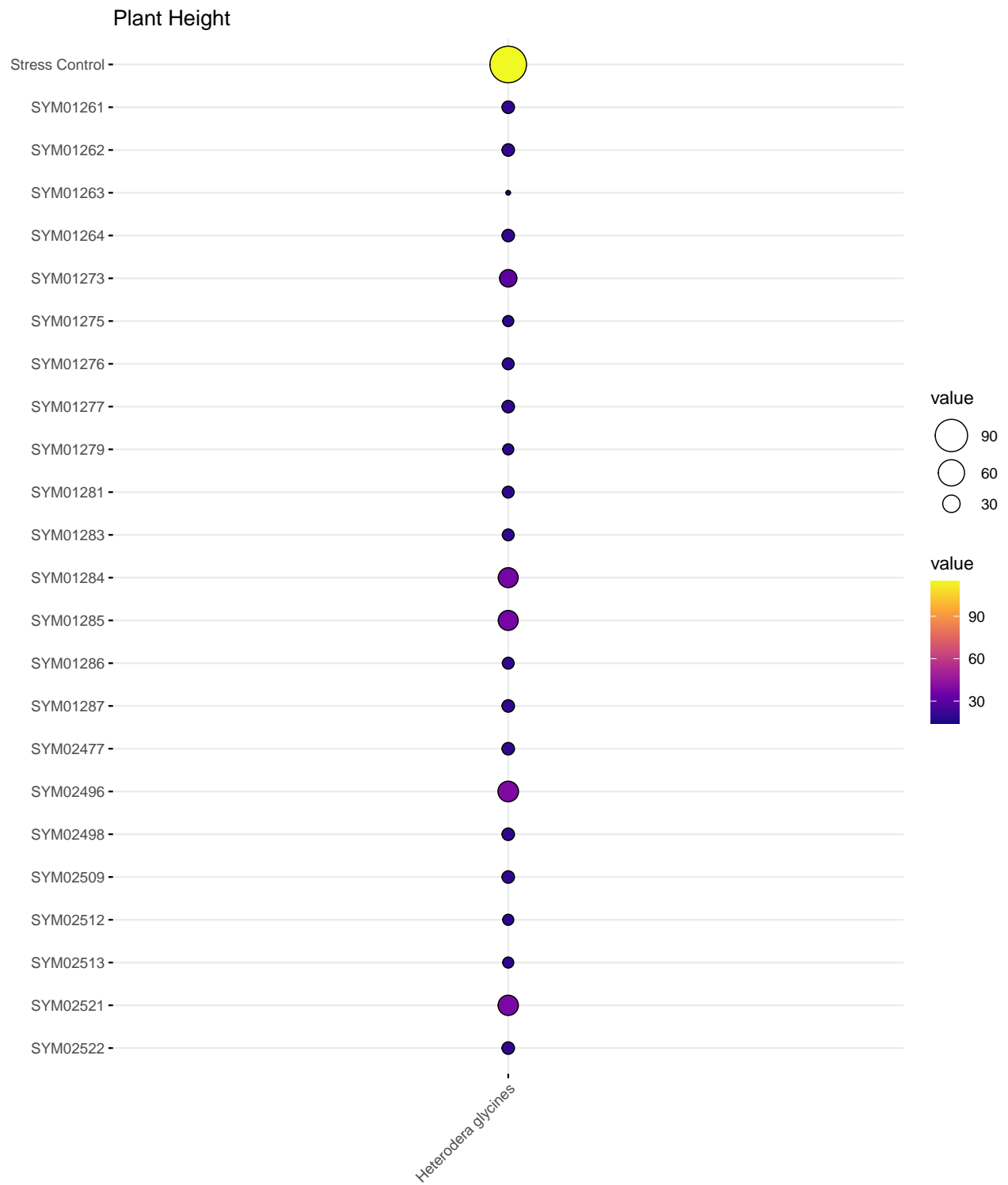


[[4]]

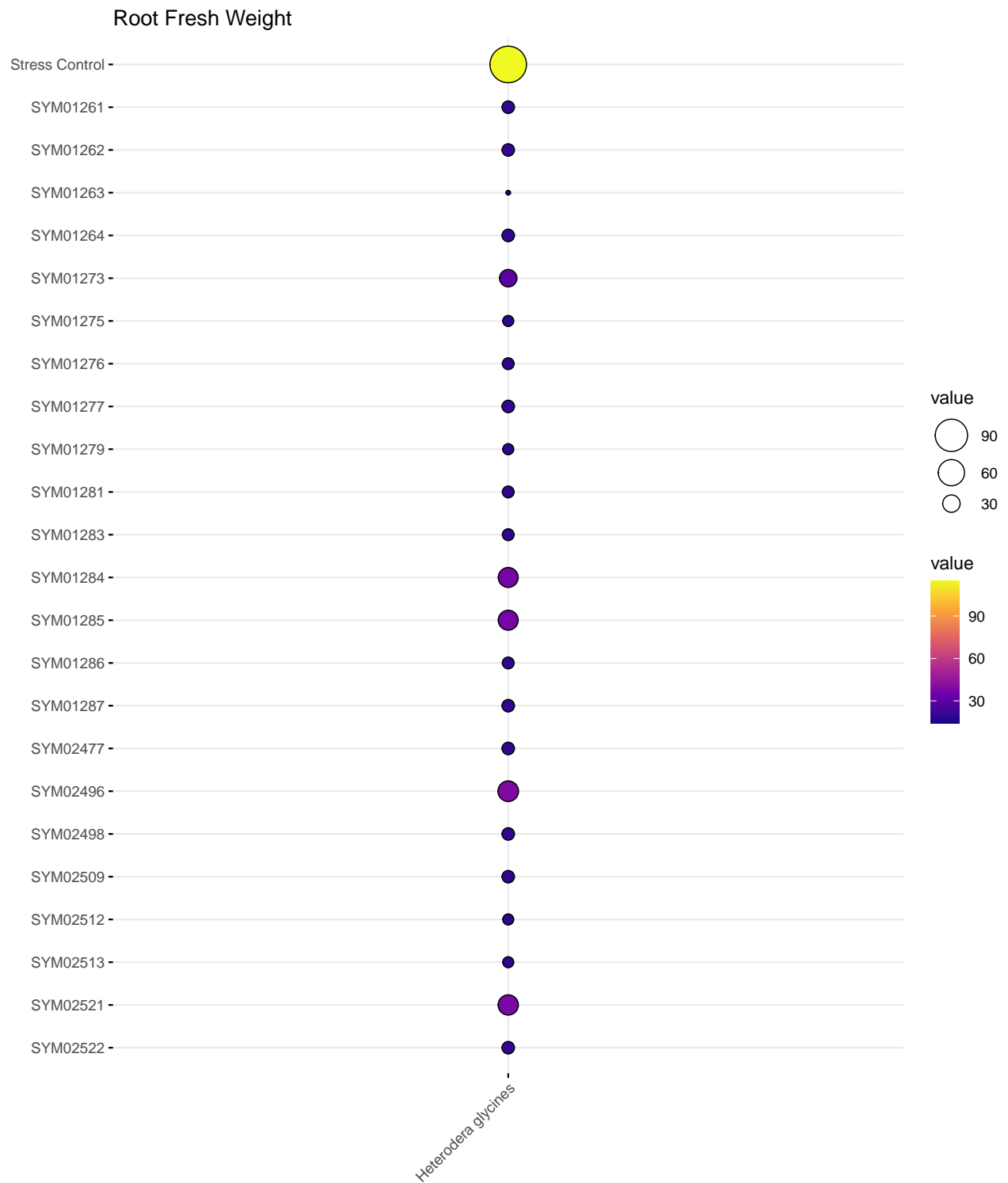
Cysts and Females



[[5]]

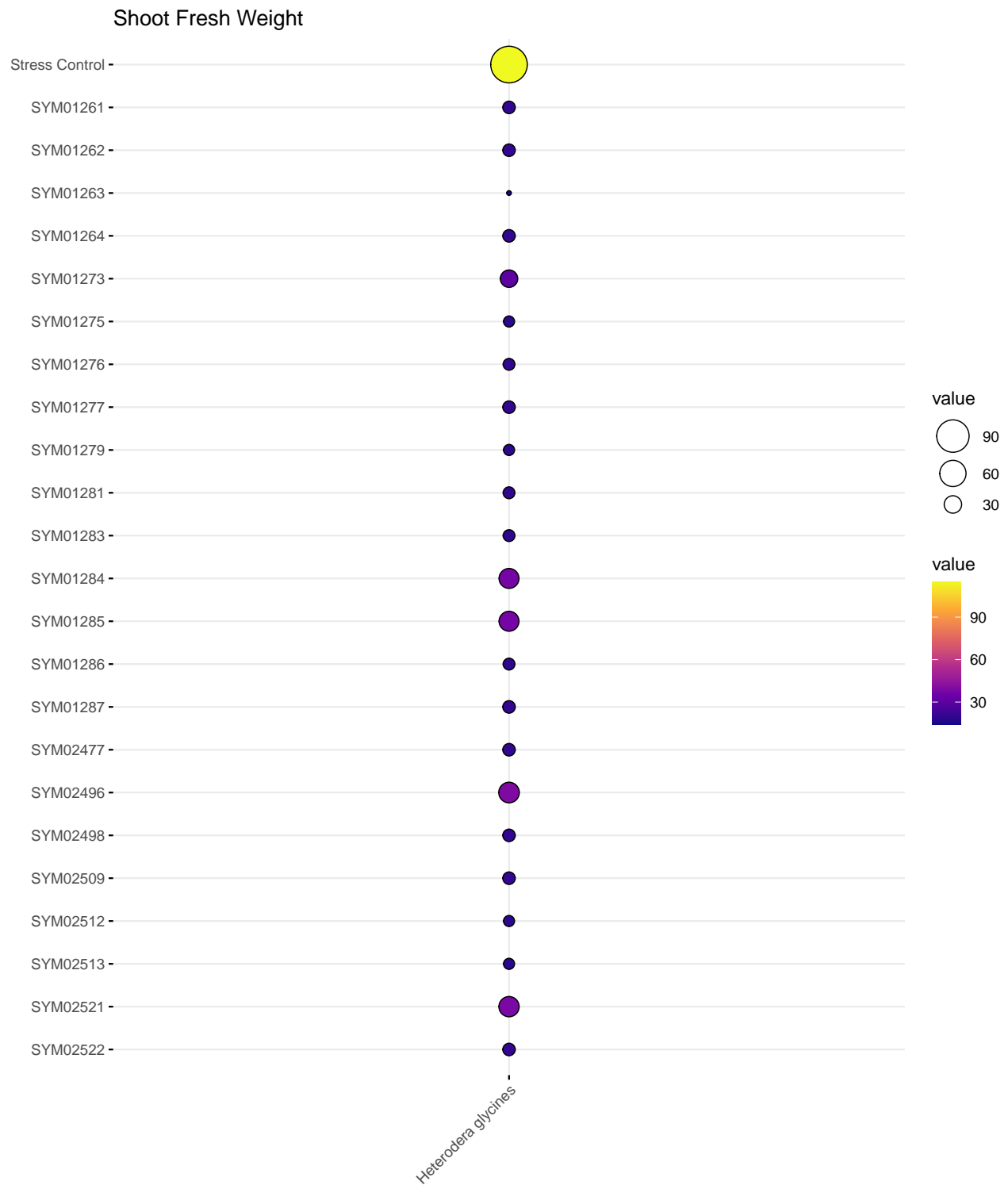


[[6]]



##

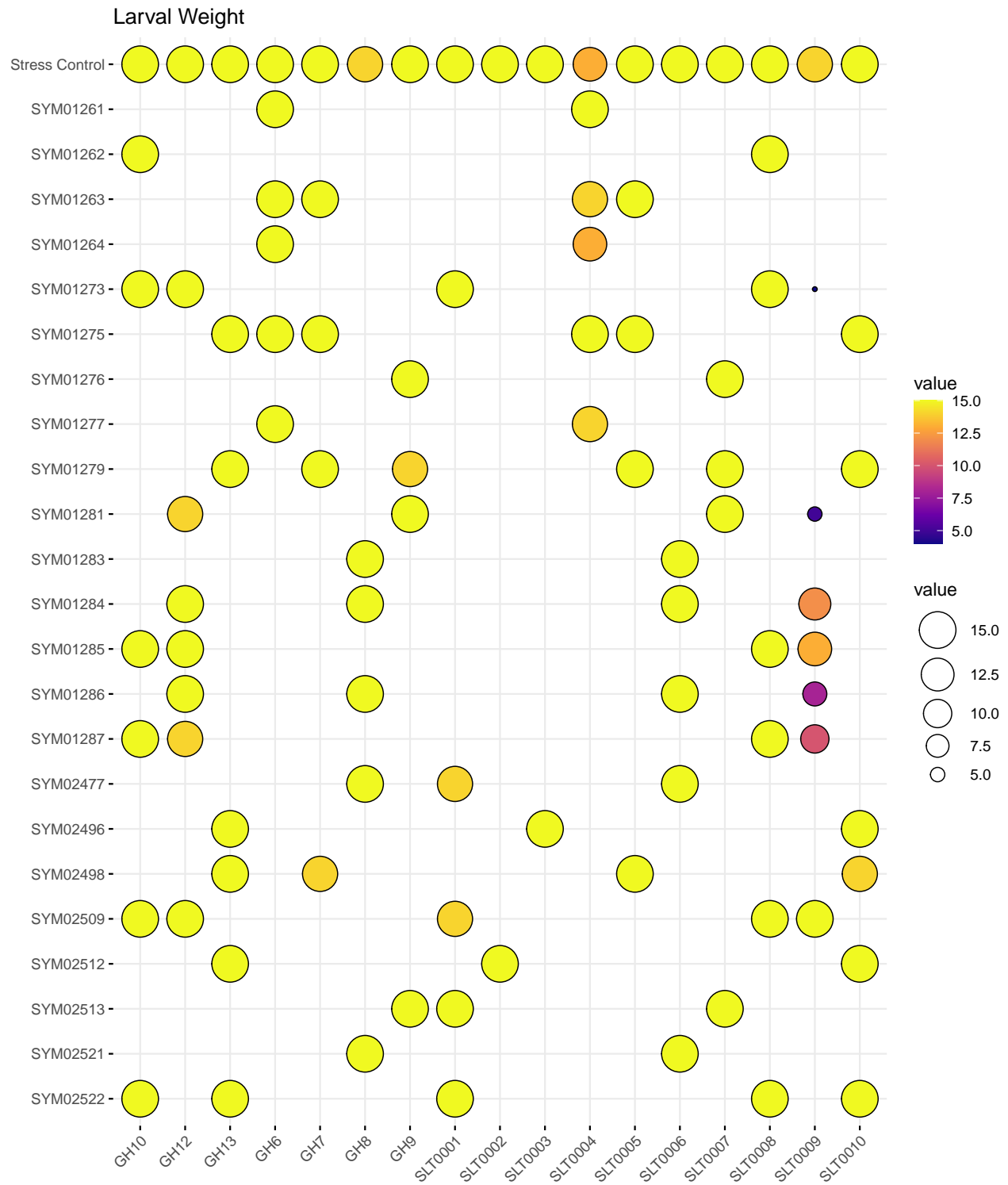
[[7]]



```
print(fq.trt.id)
```

```
## [[1]]
```

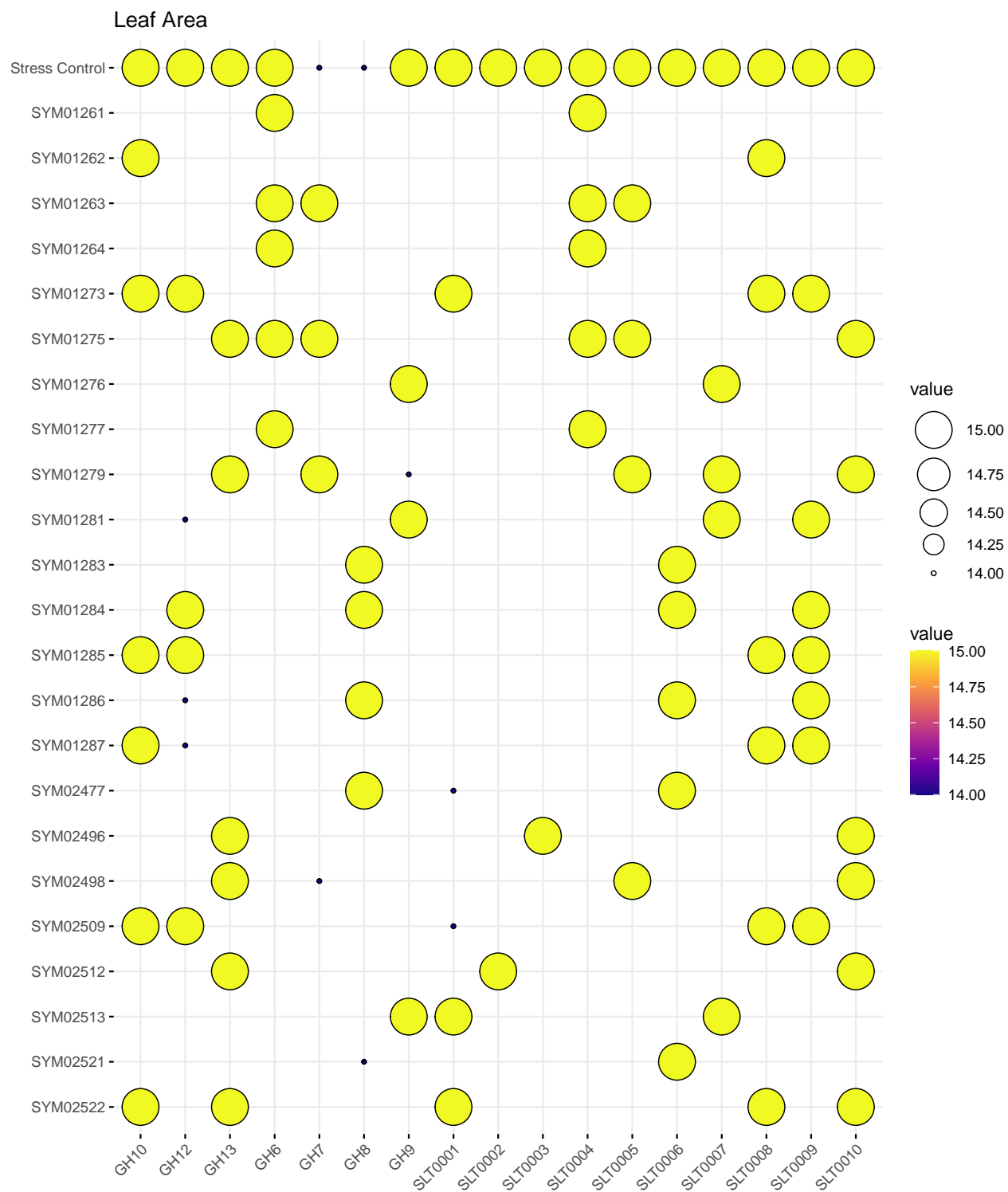
```
## Warning: Removed 310 rows containing missing values (geom_point).
```



```
##
```

```
## [[2]]
```

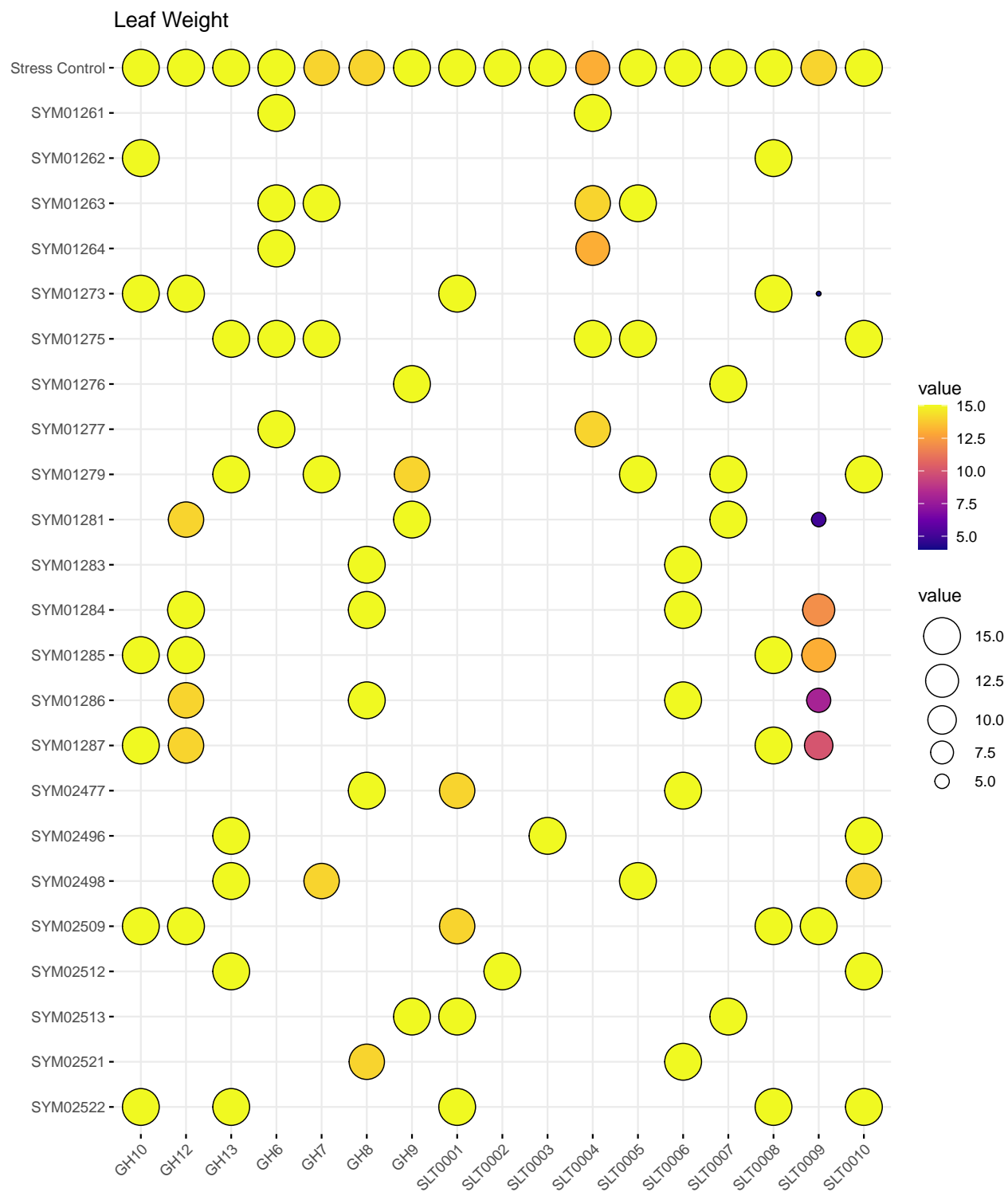
```
## Warning: Removed 310 rows containing missing values (geom_point).
```

##

[[3]]

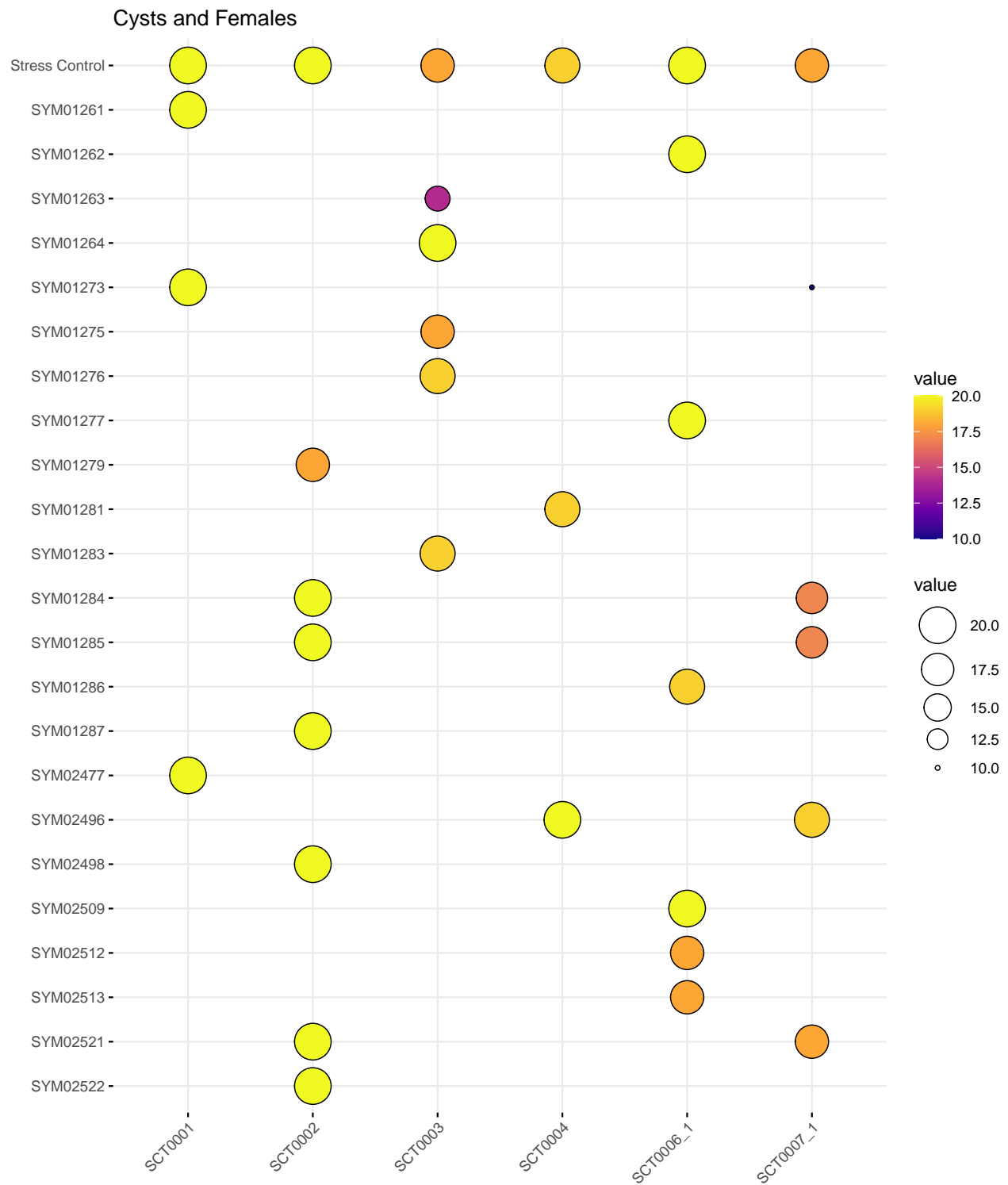
Warning: Removed 310 rows containing missing values (geom_point).



```
##
```

```
## [[4]]
```

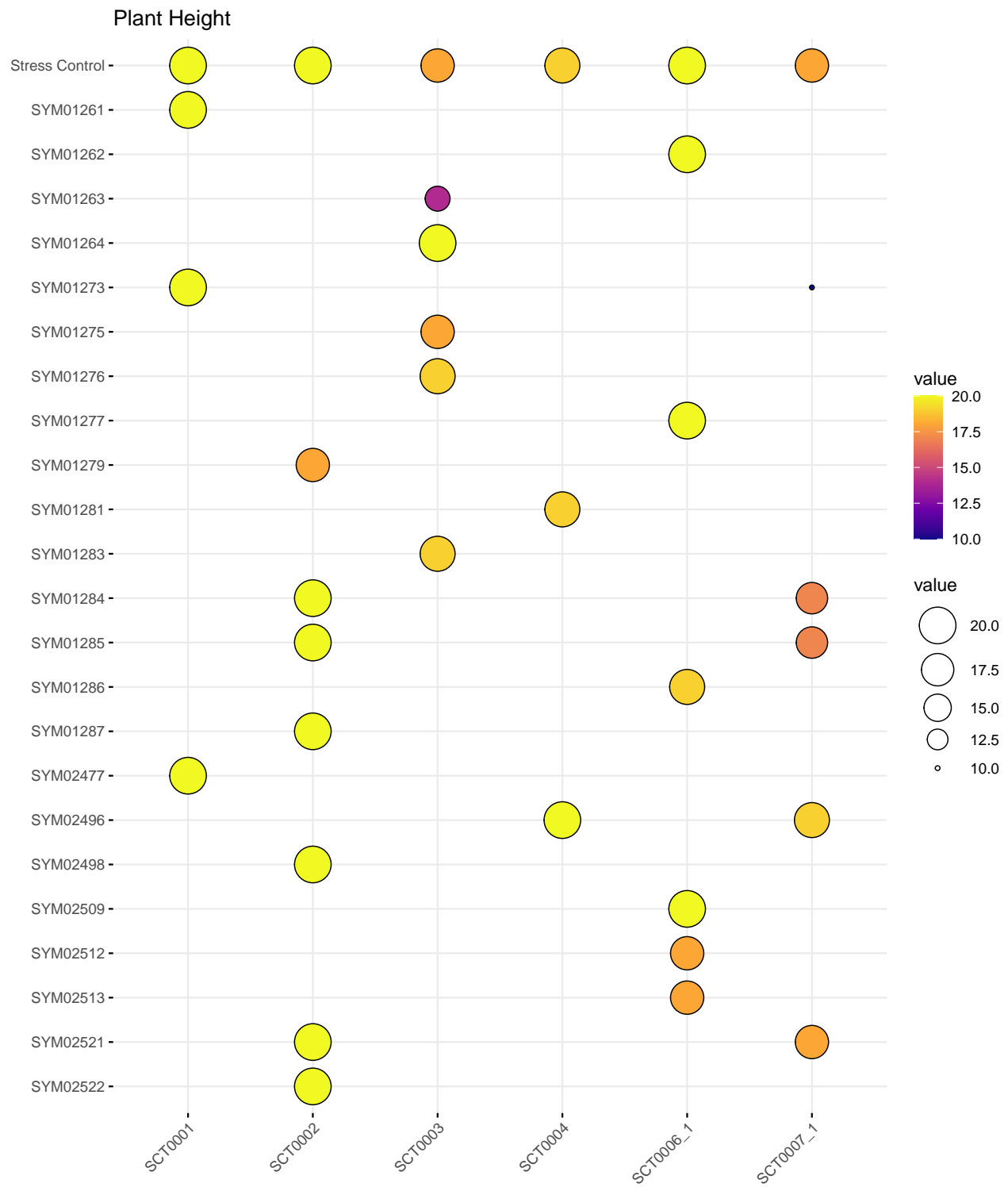
```
## Warning: Removed 110 rows containing missing values (geom_point).
```



```
##
```

```
## [[5]]
```

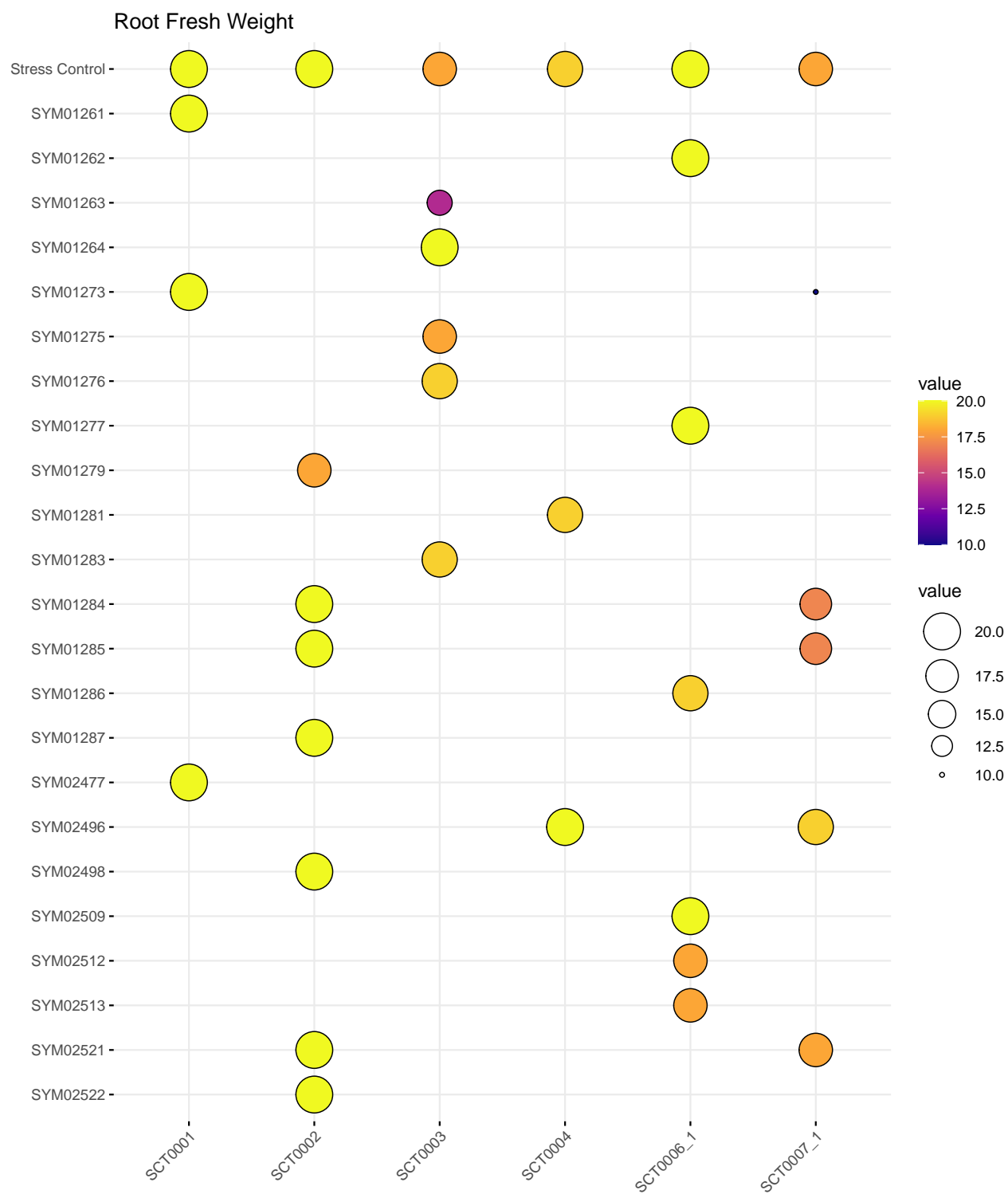
```
## Warning: Removed 110 rows containing missing values (geom_point).
```



```
##
```

```
## [[6]]
```

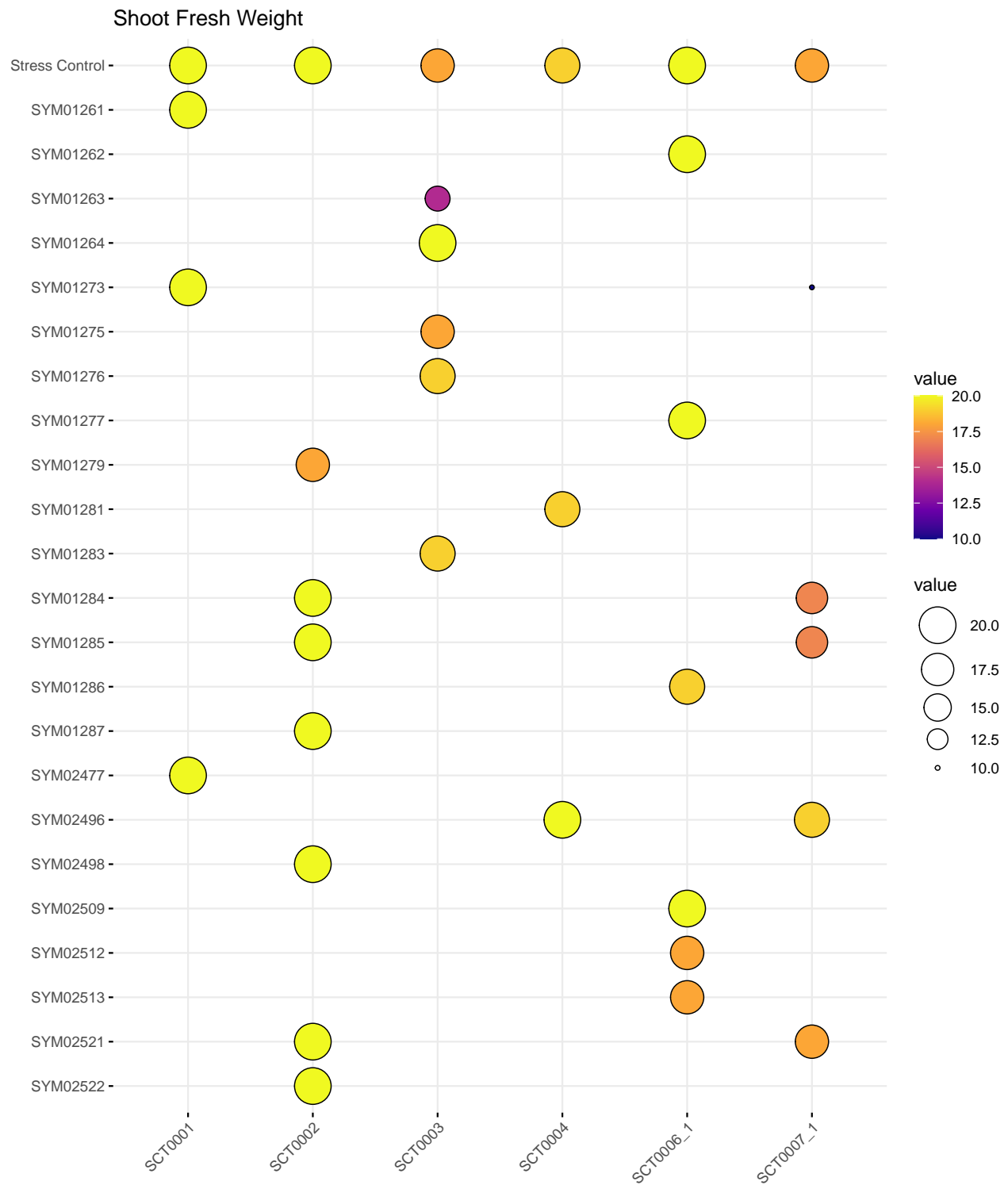
```
## Warning: Removed 110 rows containing missing values (geom_point).
```



```
##
```

```
## [[7]]
```

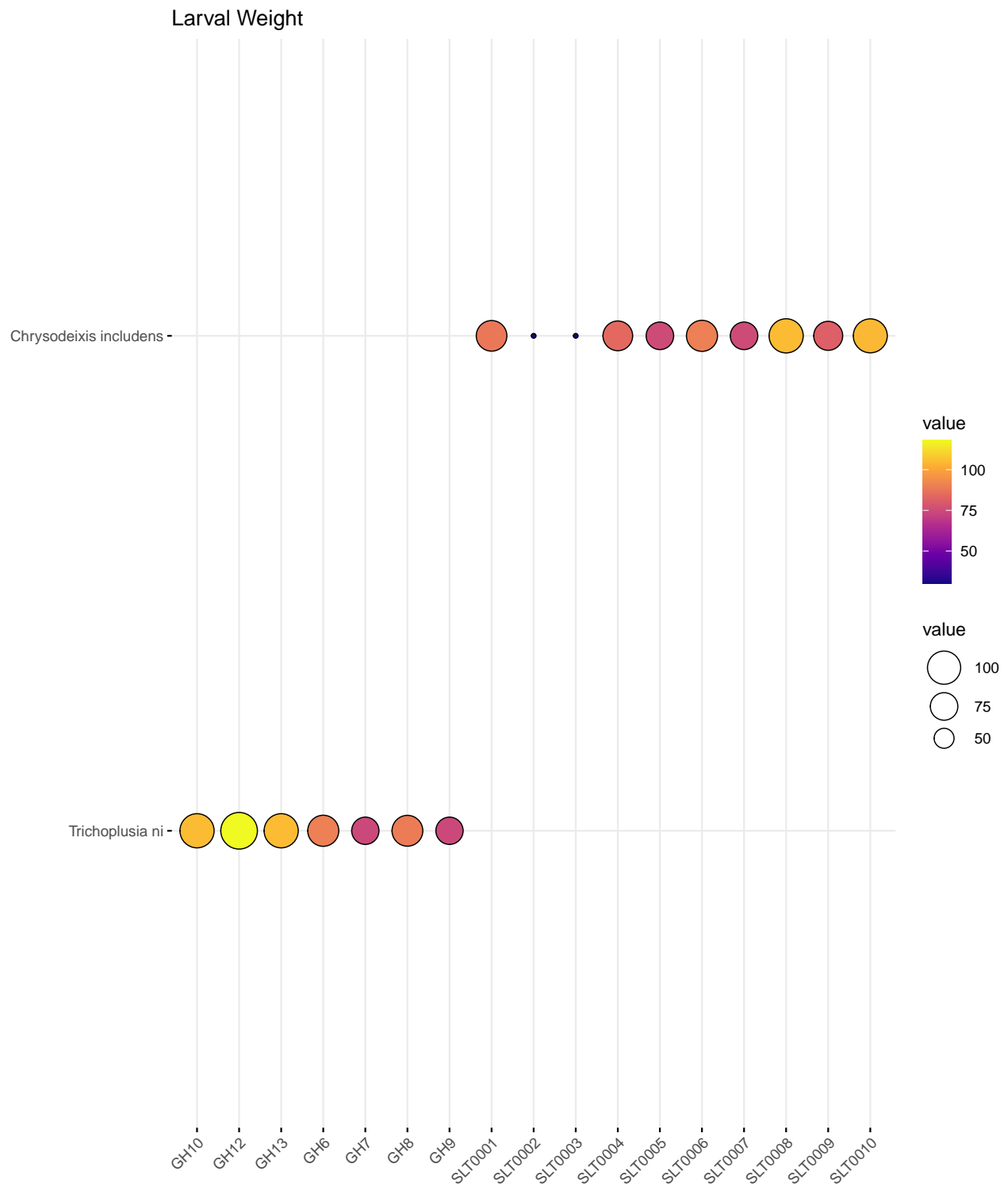
```
## Warning: Removed 110 rows containing missing values (geom_point).
```



```
print(fq.type.id)
```

```
## [[1]]
```

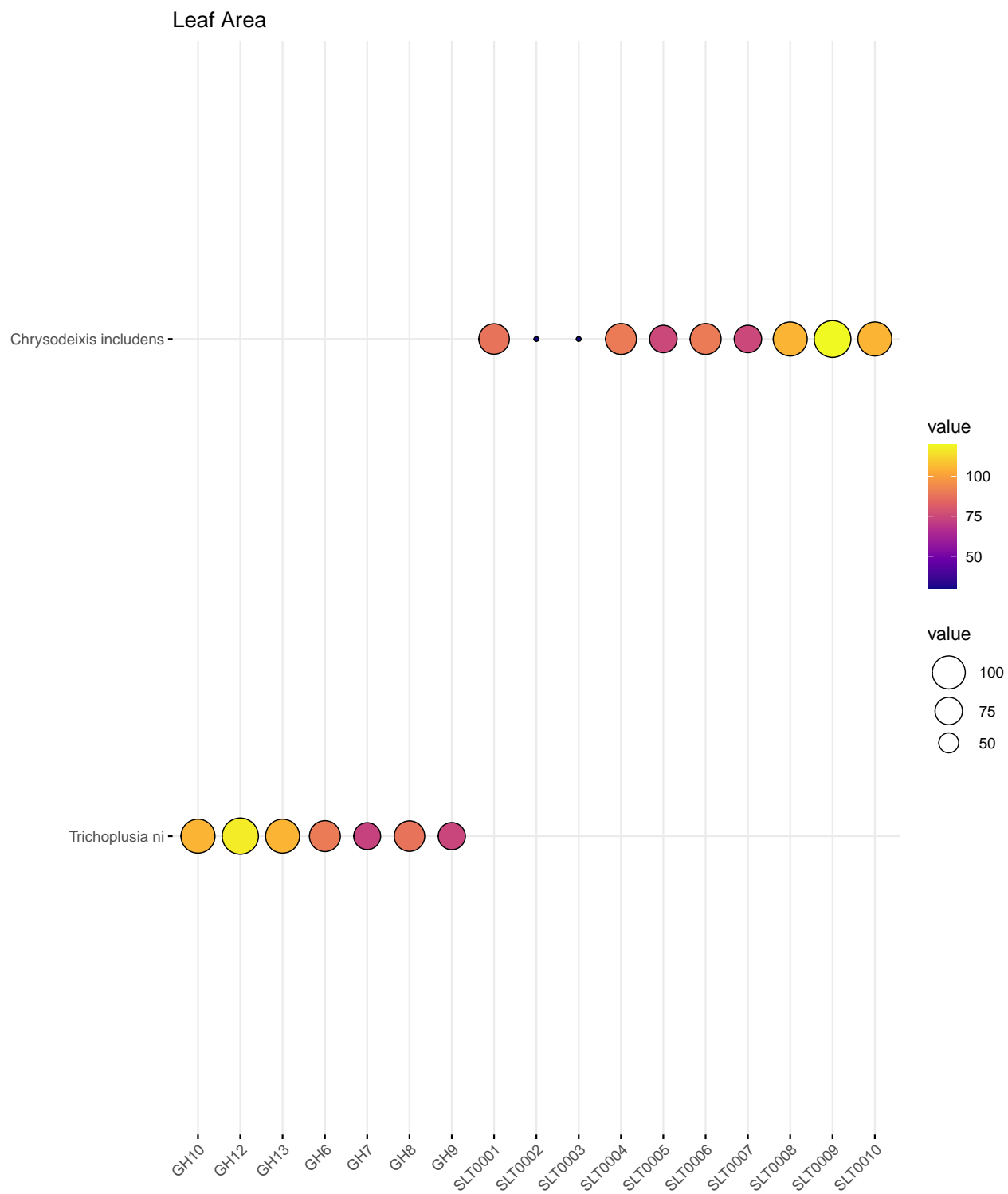
```
## Warning: Removed 17 rows containing missing values (geom_point).
```



##

[[2]]

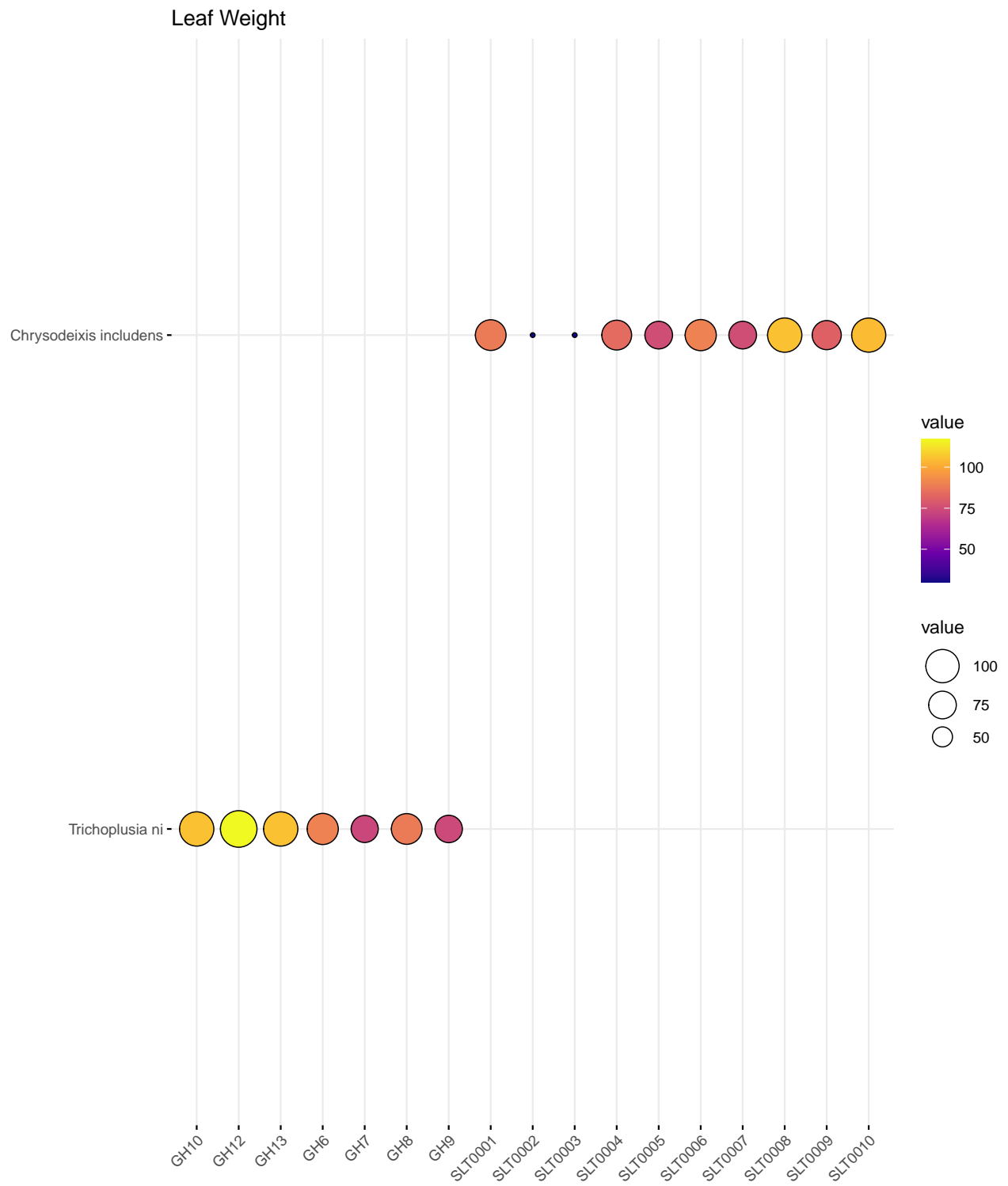
Warning: Removed 17 rows containing missing values (geom_point).



```
##
```

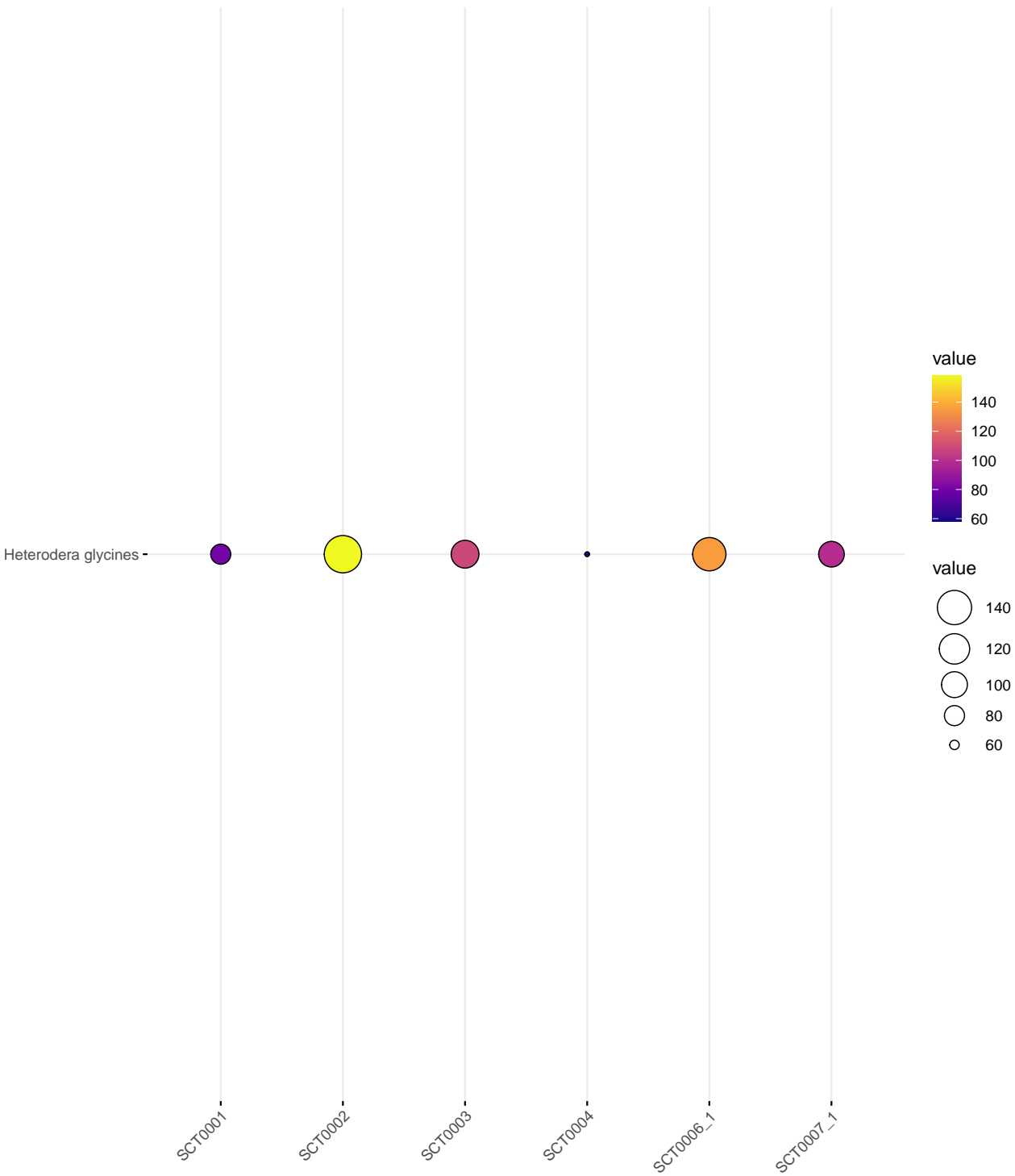
```
## [[3]]
```

```
## Warning: Removed 17 rows containing missing values (geom_point).
```

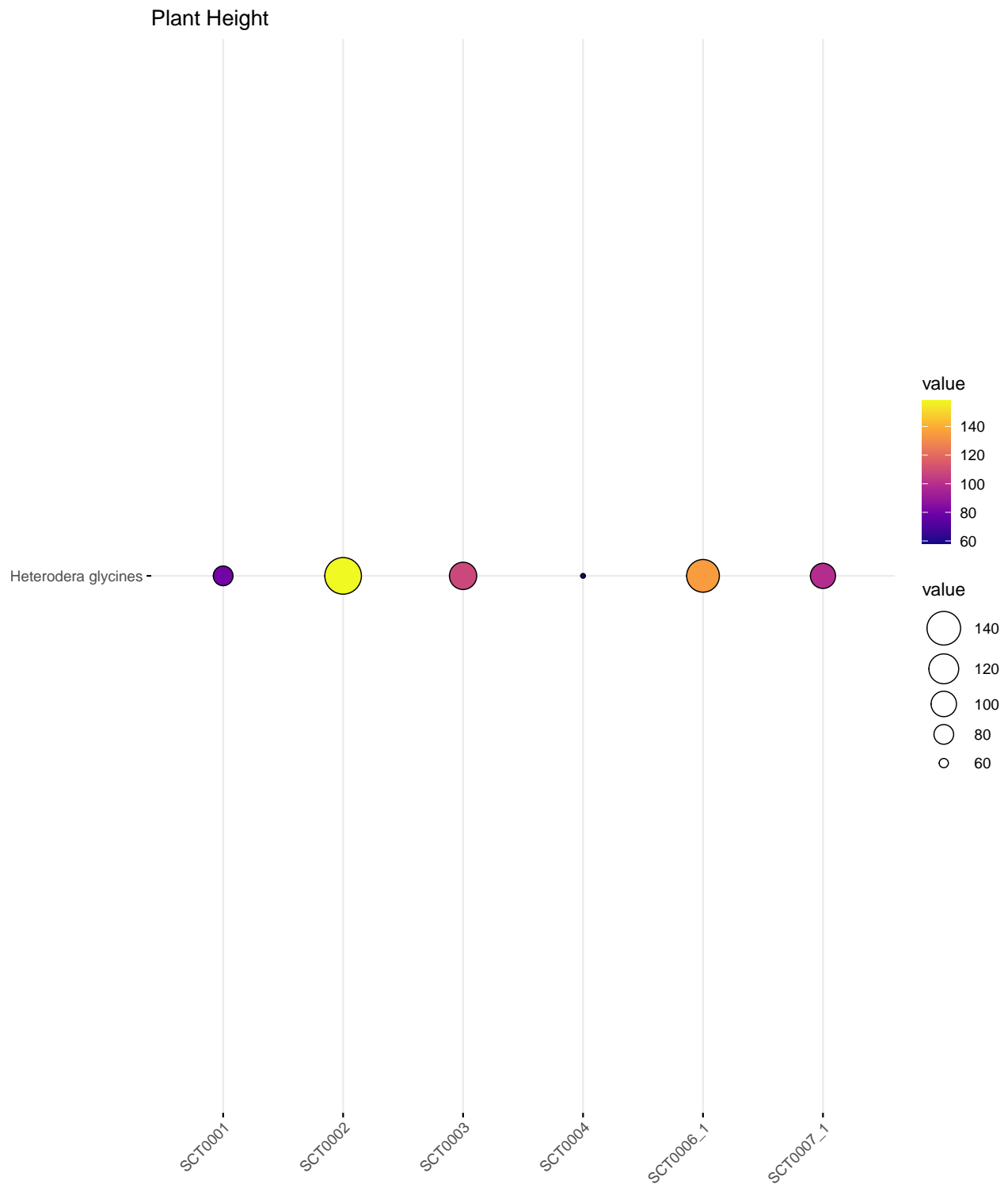



[[4]]

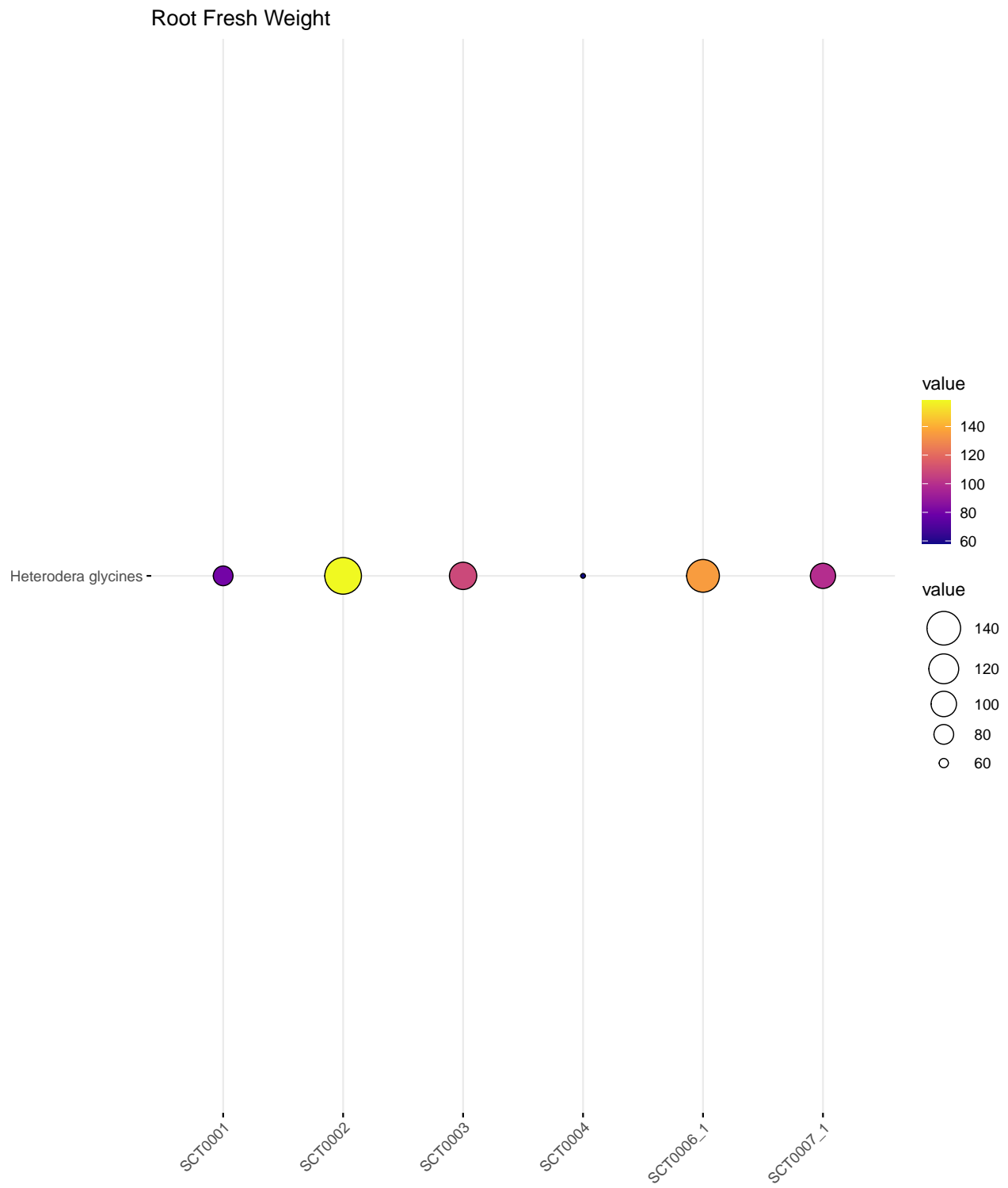
Cysts and Females



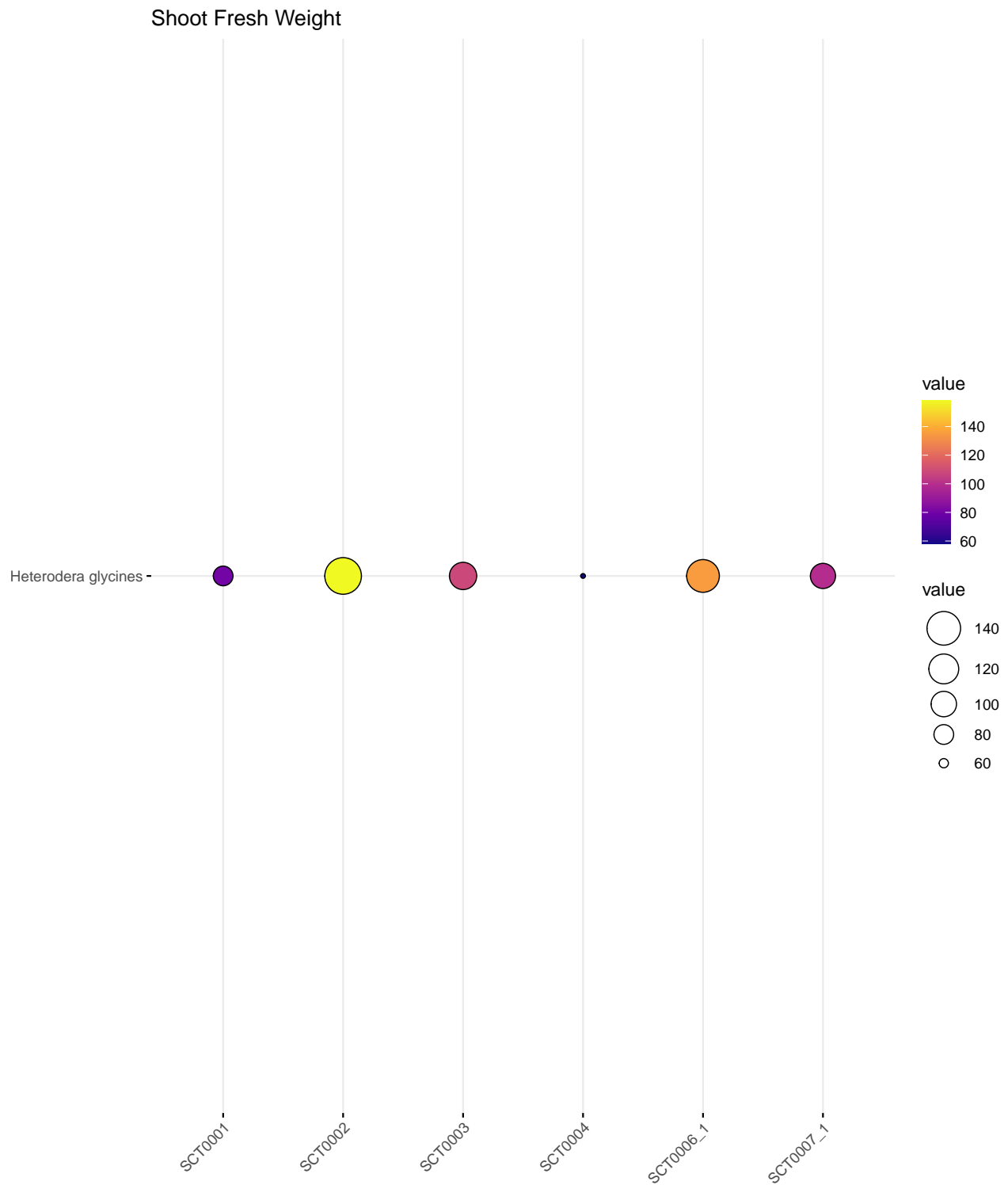
[[5]]



[[6]]



[[7]]



7.2 Technical details of linear mixed effect models

In this section we discuss the model mentioned in Section 4.1 in more details. Recall that in this project we apply linear mixed effect models to estimate the effect of treatments versus the control. In particular, we fit a model for each metric since different metrics have different practical meanings and the effect of a treatment

may be different for distinct metrics. For each metric, we use the measured values of the metric as responses and include treatments and greenhouse IDs as covariates. For those metrics with two different stressor types, we also use stressor types as covariates. We also include interaction terms between treatments and stressor types, allowing treatment effects to vary with stressor types.

We begin with multiple regression models where all covariates are treated as fixed effect covariates. The models can be written as

$$y = \beta_0 + \alpha w + \sum_{j=1}^J (\beta_j x_j + \gamma_j x_j w) + \sum_{k=1}^K u_k g_k + e, \quad \text{for metrics with stressors 1 and 2} \quad (3)$$

$$y = \beta_0 + \sum_{j=1}^J \beta_j x_j + \sum_{k=1}^K u_k g_k + e, \quad \text{for metrics with stressor 3,} \quad (4)$$

where y is the measured values of one of the seven metrics, x_j, w and g_k are dummy variables for the j th treatment, the stressor types, and the k th greenhouse, respectively, and $e \sim N(0, \sigma^2)$ is the error term. Note that the models include intercept terms β_0 so that β_j can be interpreted as the effect of the j th treatment versus the control. To distinguish from the models with random effects, we refer to these models as fixed effect models (FEMs).

One problem of (3) is that it suffers from multicollinearity, which means one of the covariates is a linear combination of others. Since one greenhouse is only assigned with only one of the two stressor types, there are two groups of greenhouses and each group is associated with one stressor type, which implies that there is collinearity between w and $\{g_k\}$. To see this, if we add all dummy variables of greenhouses corresponding to a same stressor type together, we will get the same dummy variable for that stressor type. Under this circumstance, the FEM is not able to estimate the greenhouse effects and the stressor type effects at the same time.

As a result, we instead treat the greenhouse effects as random effects by assuming that they are randomly drawn from a normally distributed population with zero mean and unknown variance. The models admit the same forms as (3) and (4), and they further assume that $u_1, \dots, u_K \stackrel{iid}{\sim} N(0, \tau^2)$ with unknown τ^2 and u_g and that e are independent for all g . In other words, we include a random intercept term for each greenhouse. We refer to these models as random effect models (REMs). R package `lme4` (Bates et al. 2015) was used to fit REMs.

By assuming that greenhouse effects are from a same population, we are able to estimate the stressor type and greenhouse effects at the same time. Other advantages of REMs over FEMs include (i) we can make prediction for both existing greenhouses and new greenhouses while generalization to other greenhouses is tricky in FEMs; (ii) we don't need to estimate redundant coefficients so that the model can be more robust.

Denote by θ_{jk} the effect of treatment j under stressor type k . In Model (4), the effect of the j th treatment (under stressor 3) is simply $\theta_{j3} = \beta_j$. In Model (3) with stressor types 1 and 2, let's define $w = 0$ when stressor 1 is applied and $w = 1$ when stressor 2 is applied. The effects of the j th treatment under different stressor types can be summarized in the following table:

Stressor	Effect of the j th treatment
1	$\theta_{j1} = \beta_j$
2	$\theta_{j2} = \beta_j + \gamma_j$

To derive the above table, let's assume the greenhouse effect is 0 for now. Under stressor 1, $w = 0$, and thus the expected value of the metric under the control and the j th treatment are $\mathbb{E}(y) = \beta_0$ and $\mathbb{E}(y) = \beta_0 + \beta_j$, respectively. The effect of the j th treatment under stressor 1 is therefore β_j , the difference between them. Under stressor 2, $w = 1$, and thus the expected response value under the control and the j th treatment become $\mathbb{E}(y) = \beta_0 + \alpha$ and $\mathbb{E}(y) = \beta_0 + \alpha + \beta_j + \gamma_j$, respectively. The effect of the j th treatment under stressor 2 is again their difference $\beta_j + \gamma_j$.

7.3 Comparison of the mixed effect model with the fixed effect model

The following code chunk is to obtain required objects for the linear fixed-effects models for different metrics. Note that `output.FEM` is a list containing `lm` objects for different metrics. Each element of the object `coef.FEM` is a data.frame consisting of three different columns: estimated coefficients of the fungal treatments (`point_est`), lower bounds of their 95% confidence intervals (`lower`), and upper bounds of their 95% confidence intervals (`upper`). However, their 95% confidence intervals are not useful since multiple testing is performed in this experiment. As you can see below, the code chunk gives warning messages. This is because of the fact that there is nested structure in our dataset. In such sense, it appears that the fixed-effects model is not appropriate for analyzing the dataset we have.

```
output.FEM <- list()
coef.FEM <- list()
emmobjsfEM <- list()
for(k in 1:n.metric) {
  if(metrics[k] == "Leaf Area")
  {
    temp = lm(log(value) ~ trt * type + id, data = prunedat.list[[k]])
    output.FEM[[k]] <- temp
    emmobjsfEM[[k]] <- emmeans(temp, specs = c("trt", "type"))

  } else if(n.type[k] == 1) {

    temp = lm(value ~ trt + id, data = prunedat.list[[k]])
    output.FEM[[k]] <- temp
    emmobjsfEM[[k]] <- emmeans(temp, specs = c("trt"))

  } else if(n.type[k] == 2) {

    temp = lm(value ~ trt * type + id, data = prunedat.list[[k]])
    output.FEM[[k]] <- temp
    emmobjsfEM[[k]] <- emmeans(temp, specs = c("trt", "type"))

  } else {
    stop("something wrong!")
  }

  temp.coef <- coef(output.FEM[[k]])
  ind <- which(substring(names(temp.coef), 1, 3) == "trt")
  temp.coef <- temp.coef[ind]
  temp.coef <- data.frame(treatment = substring(names(temp.coef), 4),
    point_est = as.numeric(temp.coef))

  temp.confint <- confint(output.FEM[[k]])
  ind <- which(substring(rownames(temp.confint), 1, 3) == "trt")
  temp.confint <- temp.confint[ind, ]
  temp.confint <- data.frame(treatment = substring(rownames(temp.confint), 4),
    lw = temp.confint[, 1],
    up = temp.confint[, 2])

  coef.FEM[[k]] <- full_join(temp.coef, temp.confint, by = "treatment")

  rownames(coef.FEM[[k]]) <- NULL
  colnames(coef.FEM[[k]]) <- c("treatment", "point_est", "lower", "upper")
}
```

```
} ; rm(k, ind, temp, temp.coef, temp.confint)
```

```
## NOTE: A nesting structure was detected in the fitted model:
##      id %in% type
## NOTE: A nesting structure was detected in the fitted model:
##      id %in% type
## NOTE: A nesting structure was detected in the fitted model:
##      id %in% type
```

```
names(output.FEM) <- metrics
names(coef.FEM) <- metrics
```

The object coef.FEM is presented below:

```
coef.FEM
```

```
## $`Larval Weight`
##      treatment    point_est      lower      upper
## 1      SYM01261    0.03183723 -3.00175920  3.0654337
## 2      SYM01262    1.13425846 -1.69041254  3.9589295
## 3      SYM01263    0.06229566 -2.16573181  2.2903231
## 4      SYM01264    0.76747825 -2.40950583  3.9444623
## 5      SYM01273   -2.39570949 -4.37845056 -0.4129684
## 6      SYM01275    0.32633495 -1.49764428  2.1503142
## 7      SYM01276   -0.62461603 -3.53631096  2.2870789
## 8      SYM01277   -0.19625801 -3.29725192  2.9047359
## 9      SYM01279   -1.28003836 -3.03426537  0.4741887
## 10     SYM01281   -4.06143862 -6.54242219 -1.5804550
## 11     SYM01283    0.08103178 -2.88580058  3.0478641
## 12     SYM01284    0.56417037 -1.68171687  2.8100576
## 13     SYM01285    0.65675336 -1.51464558  2.8281523
## 14     SYM01286    0.93000981 -1.46738434  3.3274040
## 15     SYM01287   -3.56980747 -5.82940028 -1.3102147
## 16     SYM02477    2.35861359  0.21003666  4.5071905
## 17     SYM02496    0.43970347 -1.71479659  2.5942035
## 18     SYM02498   -1.29853014 -3.40594324  0.8088830
## 19     SYM02509   -1.04228185 -2.85305116  0.7684875
## 20     SYM02512   -0.85340764 -3.00790771  1.3010924
## 21     SYM02513    2.78167951  0.69324461  4.8701144
## 22     SYM02521   -0.47430156 -3.44113392  2.4925308
## 23     SYM02522   -2.29940376 -4.01508770 -0.5837198
## 24 SYM01261:typeTrichoplusia ni  3.48253064 -0.78453965  7.7496009
## 25 SYM01262:typeTrichoplusia ni -1.58448101 -5.61448252  2.4455205
## 26 SYM01263:typeTrichoplusia ni  2.75239595 -0.38316316  5.8879551
## 27 SYM01264:typeTrichoplusia ni  5.21688961  0.84671692  9.5870623
## 28 SYM01273:typeTrichoplusia ni  1.52117206 -1.41769179  4.4600359
## 29 SYM01275:typeTrichoplusia ni  2.74985481  0.14189234  5.3578173
## 30 SYM01276:typeTrichoplusia ni  4.23368633  0.07379586  8.3935768
## 31 SYM01277:typeTrichoplusia ni  4.80729254  0.49204692  9.1225382
## 32 SYM01279:typeTrichoplusia ni  1.24433141 -1.28868320  3.7773460
## 33 SYM01281:typeTrichoplusia ni  0.52063057 -2.75978083  3.8010420
## 34 SYM01283:typeTrichoplusia ni -0.53131937 -4.79387337  3.7312346
## 35 SYM01284:typeTrichoplusia ni -3.70429588 -6.85784587 -0.5507459
## 36 SYM01285:typeTrichoplusia ni -4.10295745 -7.17226225 -1.0336527
## 37 SYM01286:typeTrichoplusia ni -0.23902421 -3.50220774  3.0241593
```



```

## 38 SYM01287:typeTrichoplusia ni 6.05982497 2.91073109 9.2089188
## 39 SYM02477:typeTrichoplusia ni -0.53556785 -4.27504043 3.2039047
## 40 SYM02496:typeTrichoplusia ni 6.47614925 2.90306486 10.0492336
## 41 SYM02498:typeTrichoplusia ni 0.90949586 -2.11809895 3.9370907
## 42 SYM02509:typeTrichoplusia ni -1.15058891 -3.97628247 1.6751046
## 43 SYM02512:typeTrichoplusia ni 1.77926036 -1.79382402 5.3523448
## 44 SYM02513:typeTrichoplusia ni 6.60183523 2.97026784 10.2334026
## 45 SYM02521:typeTrichoplusia ni -1.51043048 -5.77298448 2.7521235
## 46 SYM02522:typeTrichoplusia ni 2.79499663 0.09242234 5.4975709
##
## $`Leaf Area`
##          treatment    point_est      lower      upper
## 1          SYM01261  0.013482238 -0.15997226 0.186936738
## 2          SYM01262  0.013762182 -0.14924438 0.176768745
## 3          SYM01263 -0.002406065 -0.12907895 0.124266815
## 4          SYM01264  0.276315044  0.10286054 0.449769544
## 5          SYM01273 -0.055472749 -0.15884092 0.047895422
## 6          SYM01275  0.016749494 -0.08802320 0.121522185
## 7          SYM01276 -0.016756272 -0.18372847 0.150215927
## 8          SYM01277  0.130625313 -0.04282919 0.304079813
## 9          SYM01279 -0.111522849 -0.21255267 -0.010493028
## 10         SYM01281 -0.098735921 -0.21857587 0.021104029
## 11         SYM01283  0.088646520 -0.08171575 0.259008791
## 12         SYM01284  0.017550353 -0.10597703 0.141077732
## 13         SYM01285 -0.035721930 -0.15737578 0.085931919
## 14         SYM01286  0.025443514 -0.09808386 0.148970893
## 15         SYM01287 -0.006101062 -0.12775491 0.115552787
## 16         SYM02477 -0.052104970 -0.17602388 0.071813944
## 17         SYM02496 -0.017456891 -0.14236729 0.107453511
## 18         SYM02498 -0.056708154 -0.17713758 0.063721269
## 19         SYM02509 -0.048379019 -0.15250103 0.055742994
## 20         SYM02512 -0.040530670 -0.16544107 0.084379733
## 21         SYM02513 -0.001762430 -0.12217137 0.118646507
## 22         SYM02521 -0.179392984 -0.34975525 -0.009030713
## 23         SYM02522 -0.068743228 -0.16779143 0.030304971
## 24 SYM01261:typeTrichoplusia ni -0.183724105 -0.42958495 0.062136739
## 25 SYM01262:typeTrichoplusia ni  0.120670296 -0.11254387 0.353884466
## 26 SYM01263:typeTrichoplusia ni -0.149769233 -0.33020679 0.030668325
## 27 SYM01264:typeTrichoplusia ni -0.461354253 -0.70721510 -0.215493408
## 28 SYM01273:typeTrichoplusia ni  0.236992423  0.07410012 0.399884731
## 29 SYM01275:typeTrichoplusia ni -0.244019307 -0.39491086 -0.093127752
## 30 SYM01276:typeTrichoplusia ni -0.156533202 -0.39654360 0.083477193
## 31 SYM01277:typeTrichoplusia ni -0.195015402 -0.44087625 0.050845442
## 32 SYM01279:typeTrichoplusia ni -0.202106961 -0.34881301 -0.055400909
## 33 SYM01281:typeTrichoplusia ni  0.029297278 -0.14354863 0.202143188
## 34 SYM01283:typeTrichoplusia ni -0.095492514 -0.34169410 0.150709072
## 35 SYM01284:typeTrichoplusia ni -0.108689534 -0.28690707 0.069528003
## 36 SYM01285:typeTrichoplusia ni  0.180067020  0.00499965 0.355134391
## 37 SYM01286:typeTrichoplusia ni  0.024903923 -0.15449123 0.204299071
## 38 SYM01287:typeTrichoplusia ni  0.056673937 -0.11940324 0.232751119
## 39 SYM02477:typeTrichoplusia ni  0.054869359 -0.16180509 0.271543804
## 40 SYM02496:typeTrichoplusia ni -0.264235032 -0.47159404 -0.056876028
## 41 SYM02498:typeTrichoplusia ni -0.214084734 -0.38881060 -0.039358866
## 42 SYM02509:typeTrichoplusia ni  0.081886547 -0.08148517 0.245258267

```

```

## 43 SYM02512:typeTrichoplusia ni -0.210990954 -0.41834996 -0.003631950
## 44 SYM02513:typeTrichoplusia ni -0.296670929 -0.50696498 -0.086376880
## 45 SYM02521:typeTrichoplusia ni 0.074838589 -0.17417333 0.323850510
## 46 SYM02522:typeTrichoplusia ni -0.068983705 -0.22553120 0.087563789
##
## $`Leaf Weight`
##      treatment      point_est      lower      upper
## 1      SYM01261 0.0275433330 -0.37398142 0.42906808
## 2      SYM01262 0.0548922889 -0.31897924 0.42876381
## 3      SYM01263 0.0418852501 -0.25301494 0.33678544
## 4      SYM01264 0.0123275066 -0.40817594 0.43283095
## 5      SYM01273 0.0455645619 -0.21686969 0.30799882
## 6      SYM01275 0.0403813914 -0.20103925 0.28180204
## 7      SYM01276 0.0795500034 -0.30583995 0.46493995
## 8      SYM01277 -0.0006965717 -0.41114201 0.40974886
## 9      SYM01279 0.0338544924 -0.19833380 0.26604278
## 10     SYM01281 0.0730679067 -0.25531338 0.40144920
## 11     SYM01283 -0.2452769158 -0.63796482 0.14741099
## 12     SYM01284 -0.1395280757 -0.43679218 0.15773602
## 13     SYM01285 0.0408930453 -0.24651183 0.32829792
## 14     SYM01286 0.0200655107 -0.29725194 0.33738296
## 15     SYM01287 -0.1509631190 -0.45004128 0.14811504
## 16     SYM02477 0.6015709070 0.31718673 0.88595508
## 17     SYM02496 0.0588298979 -0.22633826 0.34399805
## 18     SYM02498 -0.0156285649 -0.29456432 0.26330719
## 19     SYM02509 0.0533491909 -0.18632300 0.29302138
## 20     SYM02512 0.0002567955 -0.28491136 0.28542495
## 21     SYM02513 0.2615898546 -0.01483396 0.53801367
## 22     SYM02521 -0.0351756768 -0.42786358 0.35751223
## 23     SYM02522 0.0362633759 -0.19082338 0.26335013
## 24 SYM01261:typeTrichoplusia ni -0.0716803742 -0.63669335 0.49333260
## 25 SYM01262:typeTrichoplusia ni -0.2913476261 -0.82478943 0.24209417
## 26 SYM01263:typeTrichoplusia ni 0.0691083873 -0.34670767 0.48492445
## 27 SYM01264:typeTrichoplusia ni -0.0526508114 -0.63130501 0.52600339
## 28 SYM01273:typeTrichoplusia ni -0.4340812458 -0.82313029 -0.04503220
## 29 SYM01275:typeTrichoplusia ni 0.1153389340 -0.23056735 0.46124522
## 30 SYM01276:typeTrichoplusia ni -0.4338832661 -0.98454993 0.11678340
## 31 SYM01277:typeTrichoplusia ni -0.1680741048 -0.73946101 0.40331280
## 32 SYM01279:typeTrichoplusia ni 0.1180042287 -0.21786012 0.45386858
## 33 SYM01281:typeTrichoplusia ni 0.0152126584 -0.41904422 0.44946953
## 34 SYM01283:typeTrichoplusia ni -0.0323610258 -0.59683184 0.53210979
## 35 SYM01284:typeTrichoplusia ni 0.1331316134 -0.28430682 0.55057005
## 36 SYM01285:typeTrichoplusia ni -0.3224566988 -0.72876814 0.08385474
## 37 SYM01286:typeTrichoplusia ni -0.1357408438 -0.57021878 0.29873709
## 38 SYM01287:typeTrichoplusia ni 0.0593057002 -0.35756439 0.47617579
## 39 SYM02477:typeTrichoplusia ni -1.0287129043 -1.52398845 -0.53343736
## 40 SYM02496:typeTrichoplusia ni 0.1527736467 -0.32040903 0.62595633
## 41 SYM02498:typeTrichoplusia ni 0.2278318733 -0.17368223 0.62934597
## 42 SYM02509:typeTrichoplusia ni 0.2854030835 -0.08866934 0.65947551
## 43 SYM02512:typeTrichoplusia ni 0.1808850965 -0.29229758 0.65406778
## 44 SYM02513:typeTrichoplusia ni -0.3516724263 -0.83242027 0.12907542
## 45 SYM02521:typeTrichoplusia ni -0.0771044712 -0.64795527 0.49374632
## 46 SYM02522:typeTrichoplusia ni 0.0428393581 -0.31501295 0.40069166
##

```

```

## $`Cysts and Females`
##      treatment point_est      lower      upper
## 1  SYM01261  23.265168   4.697777  41.8325585
## 2  SYM01262  -8.650000 -28.329033  11.0290333
## 3  SYM01263 -38.984127 -61.159885 -16.8083686
## 4  SYM01264 -33.655556 -53.873840 -13.4372708
## 5  SYM01273  16.780335   2.042664  31.5180067
## 6  SYM01275 -25.888889 -46.632411  -5.1453664
## 7  SYM01276  26.812865   6.344104  47.2816272
## 8  SYM01277   7.500000 -12.179033  27.1790333
## 9  SYM01279 -16.194196 -34.305294   1.9169022
## 10 SYM01281 -37.249728 -55.941604 -18.5578524
## 11 SYM01283  17.444444  -3.024317  37.9132062
## 12 SYM01284 -17.788356 -31.382362  -4.1943507
## 13 SYM01285 -16.599167 -30.193173  -3.0051615
## 14 SYM01286  -9.128947 -29.065234  10.8073392
## 15 SYM01287 -17.077529 -34.584590   0.4295319
## 16 SYM02477  68.165168  49.597777  86.7325585
## 17 SYM02496 -51.455391 -64.718878 -38.1919038
## 18 SYM02498 -16.527529 -34.034590   0.9795319
## 19 SYM02509 -21.900000 -41.579033  -2.2209667
## 20 SYM02512 -13.716667 -33.934951   6.5016181
## 21 SYM02513 -13.383333 -33.601618   6.8349514
## 22 SYM02521 -25.172593 -38.651667 -11.6935181
## 23 SYM02522  -5.877529 -23.384590  11.6295319
##
## $`Plant Height`
##      treatment point_est      lower      upper
## 1  SYM01261   1.1572831 -0.209742670  2.5243089
## 2  SYM01262   0.3250000 -1.123870531  1.7738705
## 3  SYM01263 -2.9174603 -4.550152443 -1.2847682
## 4  SYM01264 -0.7888889 -2.277461854  0.6996841
## 5  SYM01273 -0.6354338 -1.720496159  0.4496285
## 6  SYM01275 -0.6555556 -2.182799193  0.8716881
## 7  SYM01276 -2.3152047 -3.822219030 -0.8081903
## 8  SYM01277 -0.1850000 -1.633870531  1.2638705
## 9  SYM01279 -1.0270326 -2.360463761  0.3063985
## 10 SYM01281   0.5841840 -0.792006938  1.9603750
## 11 SYM01283   0.1847953 -1.322219030  1.6918097
## 12 SYM01284   1.2150192  0.214159321  2.2158790
## 13 SYM01285 -0.1957916 -1.196651490  0.8050682
## 14 SYM01286   1.1434211 -0.324389766  2.6112319
## 15 SYM01287 -1.7664771 -3.055435928 -0.4775182
## 16 SYM02477   1.7072831  0.340257330  3.0743089
## 17 SYM02496   0.9781062  0.001580838  1.9546316
## 18 SYM02498 -2.0464771 -3.335435928 -0.7575182
## 19 SYM02509   0.2600000 -1.188870531  1.7088705
## 20 SYM02512   0.1916667 -1.296906298  1.6802396
## 21 SYM02513 -0.4472222 -1.935795187  1.0413507
## 22 SYM02521   0.5698643 -0.422533766  1.5622623
## 23 SYM02522   2.1235229  0.834564072  3.4124818
##
## $`Root Fresh Weight`
##      treatment point_est      lower      upper

```

```

## 1  SYM01261  0.05358693 -0.06076686  1.679407e-01
## 2  SYM01262 -0.17000000 -0.29120023 -4.879977e-02
## 3  SYM01263  0.01039683 -0.12618036  1.469740e-01
## 4  SYM01264  0.07911111 -0.04541029  2.036325e-01
## 5  SYM01273  0.18617385  0.09540673  2.769410e-01
## 6  SYM01275 -0.12777778 -0.25553404 -2.151893e-05
## 7  SYM01276 -0.27546784 -0.40153188 -1.494038e-01
## 8  SYM01277 -0.14900000 -0.27020023 -2.779977e-02
## 9  SYM01279 -0.01423255 -0.12577610  9.731100e-02
## 10 SYM01281  0.01440868 -0.10071179  1.295292e-01
## 11 SYM01283 -0.24757310 -0.37363715 -1.215091e-01
## 12 SYM01284 -0.02672571 -0.11044916  5.699775e-02
## 13 SYM01285  0.04813916 -0.03558429  1.318626e-01
## 14 SYM01286 -0.17047368 -0.29325830 -4.768907e-02
## 15 SYM01287  0.20721189  0.09938852  3.150353e-01
## 16 SYM02477 -0.05841307 -0.17276686  5.594072e-02
## 17 SYM02496  0.03999166 -0.04169618  1.216795e-01
## 18 SYM02498  0.20221189  0.09438852  3.100353e-01
## 19 SYM02509 -0.25450000 -0.37570023 -1.332998e-01
## 20 SYM02512 -0.06877778 -0.19329918  5.574362e-02
## 21 SYM02513 -0.22044444 -0.34496584 -9.592305e-02
## 22 SYM02521 -0.01356588 -0.09658149  6.944973e-02
## 23 SYM02522  0.04221189 -0.06561148  1.500353e-01
##
## $`Shoot Fresh Weight`
##      treatment      point_est      lower      upper
## 1  SYM01261 -0.0119736056 -0.113294752  0.08934754
## 2  SYM01262  0.1625000000  0.055112687  0.26988731
## 3  SYM01263 -0.1712698413 -0.292281634 -0.05025805
## 4  SYM01264  0.0464444444 -0.063885532  0.15677442
## 5  SYM01273  0.0390527887 -0.041369808  0.11947539
## 6  SYM01275  0.0838888889 -0.029307278  0.19708506
## 7  SYM01276 -0.0437134503 -0.155410264  0.06798336
## 8  SYM01277  0.1305000000  0.023112687  0.23788731
## 9  SYM01279 -0.0021009880 -0.100932171  0.09673019
## 10 SYM01281 -0.0446296883 -0.146630142  0.05737076
## 11 SYM01283  0.0104970760 -0.101199738  0.12219389
## 12 SYM01284  0.0102251517 -0.063956528  0.08440683
## 13 SYM01285  0.0645494760 -0.009632204  0.13873116
## 14 SYM01286  0.1258421053  0.017050977  0.23463323
## 15 SYM01287 -0.0003232102 -0.095858199  0.09521178
## 16 SYM02477 -0.0639736056 -0.165294752  0.03734754
## 17 SYM02496 -0.0215278921 -0.093905952  0.05085017
## 18 SYM02498  0.0201767898 -0.075358199  0.11571178
## 19 SYM02509  0.1760000000  0.068612687  0.28338731
## 20 SYM02512  0.2084444444  0.098114468  0.31877442
## 21 SYM02513  0.0367777778 -0.073552198  0.14710775
## 22 SYM02521  0.0249325313 -0.048621975  0.09848704
## 23 SYM02522  0.0221767898 -0.073358199  0.11771178

```

The following code chunk is to obtain required objects for the linear mixed-effects models for different metrics. Note that `output.REM` is a list containing `lmer` objects for different metrics. Each element of the object `coef.REM` is a data.frame consisting of three different columns: estimated coefficients of the fungal treatments (`point_est`), lower bounds of their 95% confidence interval (`lower`), and upper bounds of their

95% confidence interval (upper). Again, their 95% confidence intervals are also not useful for the same reason.

```
output.REM      <- list()
coef.REM        <- list()
emmobjsREM      <- list()
for(k in 1:n.metric) {
  if(metrics[k] == "Leaf Area") {

    temp = lmer(log(value) ~ trt * type + (1|id), data = prunedat.list[[k]])
    output.REM[[k]] <- temp
    emmobjsREM[[k]] <- emmeans(temp, specs = c("trt", "type"))

  } else if(n.type[k] == 1) {

    temp = lmer(value ~ trt + (1|id), data = prunedat.list[[k]])
    output.REM[[k]] <- temp
    emmobjsREM[[k]] <- emmeans(temp, specs = c("trt"))

  } else if(n.type[k] == 2) {

    temp = lmer(value ~ trt * type + (1|id), data = prunedat.list[[k]])
    output.REM[[k]] <- temp
    emmobjsREM[[k]] <- emmeans(temp, specs = c("trt", "type"))

  } else {
    stop("something wrong!")
  }

  temp.coef      <- coef(output.REM[[k]])$id
  ind            <- which(substring(colnames(temp.coef), 1, 3) == "trt")
  temp.coef      <- temp.coef[1, ind]
  temp.coef      <- data.frame(treatment = substring(colnames(temp.coef), 4),
                               point_est = as.numeric(temp.coef))

  temp.confint   <- confint(output.REM[[k]])
  ind            <- which(substring(rownames(temp.confint), 1, 3) == "trt")
  temp.confint   <- temp.confint[ind, ]
  temp.confint   <- data.frame(treatment = substring(rownames(temp.confint), 4),
                               lw = as.numeric(temp.confint[, 1]),
                               up = as.numeric(temp.confint[, 2]))

  coef.REM[[k]] <- full_join(temp.coef, temp.confint, by = "treatment")

  rownames(coef.REM[[k]]) <- NULL
  colnames(coef.REM[[k]]) <- c("treatment", "point_est", "lower", "upper")
} ; rm(k, ind, temp, temp.coef, temp.confint)

names(output.REM) <- metrics
names(coef.REM) <- metrics
```

The object coef.REM is presented below:

```
coef.REM

## $`Larval Weight`
##           treatment point_est      lower      upper
```

```

## 1          SYM01261 -0.11958487 -3.11404232  2.8437071
## 2          SYM01262  1.22700166 -1.53904312  4.0122968
## 3          SYM01263 -0.06654235 -2.26824627  2.1085989
## 4          SYM01264  0.61605616 -2.51957786  3.7205050
## 5          SYM01273 -2.32848202 -4.26929207 -0.3737670
## 6          SYM01275  0.22624249 -1.57591849  2.0077440
## 7          SYM01276 -0.59827751 -3.45517933  2.2640931
## 8          SYM01277 -0.34768011 -3.40849799  2.6819620
## 9          SYM01279 -1.32087728 -3.04857313  0.3983751
## 10         SYM01281 -4.03182157 -6.46590462 -1.5916092
## 11         SYM01283  0.09524198 -2.81571956  3.0090442
## 12         SYM01284  0.58959943 -1.61243052  2.7967929
## 13         SYM01285  0.72475450 -1.40104909  2.8646049
## 14         SYM01286  0.95299999 -1.39811518  3.3087750
## 15         SYM01287 -3.49838051 -5.71068336 -1.2713083
## 16         SYM02477  2.38967602  0.28316960  4.5025395
## 17         SYM02496  0.46889753 -1.64290341  2.5867118
## 18         SYM02498 -1.37410716 -3.45278361  0.6889192
## 19         SYM02509 -0.98158651 -2.75367466  0.8030228
## 20         SYM02512 -0.89326994 -3.01227067  1.2175346
## 21         SYM02513  2.81940796  0.77172926  4.8748944
## 22         SYM02521 -0.46009135 -3.37105289  2.4537109
## 23         SYM02522 -2.26581515 -3.94840523 -0.5762570
## 24 SYM01261:typeTrichoplusia ni  3.55533649 -0.62544139  7.7511282
## 25 SYM01262:typeTrichoplusia ni -1.51250687 -5.46424240  2.4541864
## 26 SYM01263:typeTrichoplusia ni  2.78850817 -0.28526258  5.8697166
## 27 SYM01264:typeTrichoplusia ni  5.28969546  1.00736998  9.5870409
## 28 SYM01273:typeTrichoplusia ni  1.57156264 -1.30952237  4.4630742
## 29 SYM01275:typeTrichoplusia ni  2.77632813  0.21896987  5.3391565
## 30 SYM01276:typeTrichoplusia ni  4.16586471  0.07332293  8.2443461
## 31 SYM01277:typeTrichoplusia ni  4.88009839  0.65187066  9.1233429
## 32 SYM01279:typeTrichoplusia ni  1.22347986 -1.26692642  3.7095649
## 33 SYM01281:typeTrichoplusia ni  0.50360030 -2.72070120  3.7243318
## 34 SYM01283:typeTrichoplusia ni -0.51648916 -4.69856802  3.6686059
## 35 SYM01284:typeTrichoplusia ni -3.67994534 -6.77283820 -0.5820544
## 36 SYM01285:typeTrichoplusia ni -4.05334054 -7.06246848 -1.0339374
## 37 SYM01286:typeTrichoplusia ni -0.21223479 -3.41260258  2.9936366
## 38 SYM01287:typeTrichoplusia ni  6.10764017  3.01980489  9.2053777
## 39 SYM02477:typeTrichoplusia ni -0.53758987 -4.20807398  3.1324064
## 40 SYM02496:typeTrichoplusia ni  6.41154938  2.89525111  9.9145324
## 41 SYM02498:typeTrichoplusia ni  0.91518384 -2.05802097  3.8895768
## 42 SYM02509:typeTrichoplusia ni -1.09366619 -3.86271785  1.6871744
## 43 SYM02512:typeTrichoplusia ni  1.78371685 -1.72513042  5.2935023
## 44 SYM02513:typeTrichoplusia ni  6.52262368  2.94743705 10.0814117
## 45 SYM02521:typeTrichoplusia ni -1.49560028 -5.67767913  2.6894948
## 46 SYM02522:typeTrichoplusia ni  2.82606378  0.17344605  5.4851859
##
## $`Leaf Area`
##          treatment    point_est      lower      upper
## 1          SYM01261  0.013856166 -0.15642217  0.1842127079
## 2          SYM01262  0.015260399 -0.14479889  0.1756334046
## 3          SYM01263 -0.003042264 -0.12748023  0.1212634189
## 4          SYM01264  0.276688972  0.10641064  0.4470455136
## 5          SYM01273 -0.054455377 -0.15589133  0.0471937092

```

```

## 6          SYM01275  0.016456619 -0.08647275  0.1193248338
## 7          SYM01276 -0.017349585 -0.18149493  0.1466722053
## 8          SYM01277  0.130999241 -0.03927909  0.3013557828
## 9          SYM01279 -0.112138138 -0.21150410 -0.0129008773
## 10         SYM01281 -0.098876157 -0.21666519  0.0188844429
## 11         SYM01283  0.084463526 -0.08333492  0.2513919988
## 12         SYM01284  0.015615277 -0.10591838  0.1367474798
## 13         SYM01285 -0.034816401 -0.15424726  0.0848043540
## 14         SYM01286  0.023508438 -0.09802522  0.1446406409
## 15         SYM01287 -0.005195532 -0.12462639  0.1144252226
## 16         SYM02477 -0.053669456 -0.17556970  0.0679062024
## 17         SYM02496 -0.015919575 -0.13841938  0.1068974275
## 18         SYM02498 -0.057334431 -0.17575521  0.0609551822
## 19         SYM02509 -0.047366730 -0.14954518  0.0550238013
## 20         SYM02512 -0.040372805 -0.16300972  0.0822966753
## 21         SYM02513 -0.001438558 -0.11973822  0.1169295471
## 22         SYM02521 -0.183575978 -0.35137443 -0.0166475053
## 23         SYM02522 -0.067698879 -0.16496975  0.0297910333
## 24 SYM01261:typeTrichoplusia ni -0.181370469 -0.42256796  0.0603044874
## 25 SYM01262:typeTrichoplusia ni  0.112428256 -0.11772163  0.3408577738
## 26 SYM01263:typeTrichoplusia ni -0.144776848 -0.32147198  0.0329465062
## 27 SYM01264:typeTrichoplusia ni -0.459000617 -0.70019811 -0.2173256601
## 28 SYM01273:typeTrichoplusia ni  0.231922842  0.07132806  0.3914664350
## 29 SYM01275:typeTrichoplusia ni -0.238517419 -0.38619294 -0.0897041278
## 30 SYM01276:typeTrichoplusia ni -0.156548303 -0.39237409  0.0792721300
## 31 SYM01277:typeTrichoplusia ni -0.192661767 -0.43385926  0.0490131901
## 32 SYM01279:typeTrichoplusia ni -0.197287710 -0.34101221 -0.0525612291
## 33 SYM01281:typeTrichoplusia ni  0.028465977 -0.14149603  0.1982580051
## 34 SYM01283:typeTrichoplusia ni -0.098290113 -0.34034046  0.1431900821
## 35 SYM01284:typeTrichoplusia ni -0.110925051 -0.28617395  0.0638695039
## 36 SYM01285:typeTrichoplusia ni  0.175109282  0.00255698  0.3466335949
## 37 SYM01286:typeTrichoplusia ni  0.022571508 -0.15384440  0.1985129447
## 38 SYM01287:typeTrichoplusia ni  0.051623384 -0.12193421  0.2241334155
## 39 SYM02477:typeTrichoplusia ni  0.049453253 -0.16389555  0.2616871398
## 40 SYM02496:typeTrichoplusia ni -0.258857680 -0.46208375 -0.0545117246
## 41 SYM02498:typeTrichoplusia ni -0.206992687 -0.37803211 -0.0344777553
## 42 SYM02509:typeTrichoplusia ni  0.076822049 -0.08424384  0.2368377998
## 43 SYM02512:typeTrichoplusia ni -0.204234150 -0.40733971  0.0002774584
## 44 SYM02513:typeTrichoplusia ni -0.297603217 -0.50432383 -0.0910797785
## 45 SYM02521:typeTrichoplusia ni  0.072040991 -0.17277899  0.3162907035
## 46 SYM02522:typeTrichoplusia ni -0.069942632 -0.22395564  0.0838684920
##
## $`Leaf Weight`
##          treatment    point_est      lower      upper
## 1          SYM01261 -0.018296614 -0.415120901  0.36709705
## 2          SYM01262  0.073341773 -0.289975293  0.44140946
## 3          SYM01263  0.003362323 -0.289133793  0.28617542
## 4          SYM01264 -0.033512440 -0.449195428  0.37069530
## 5          SYM01273  0.057811642 -0.196831041  0.31546549
## 6          SYM01275  0.009150749 -0.230664712  0.24104817
## 7          SYM01276  0.086325740 -0.288828391  0.46329310
## 8          SYM01277 -0.046536519 -0.452227486  0.34770211
## 9          SYM01279  0.020162412 -0.208711734  0.24553861
## 10         SYM01281  0.081658014 -0.238132737  0.40366496

```

```

## 11          SYM01283 -0.208140054 -0.586449789 0.17961081
## 12          SYM01284 -0.112659500 -0.399090887 0.18049985
## 13          SYM01285 0.057292120 -0.221133096 0.33980543
## 14          SYM01286 0.049166322 -0.256652808 0.36231200
## 15          SYM01287 -0.134280141 -0.424227704 0.15985140
## 16          SYM02477 0.623467809 0.348687906 0.90373129
## 17          SYM02496 0.058466682 -0.218811265 0.33568245
## 18          SYM02498 -0.039822407 -0.316079159 0.23018962
## 19          SYM02509 0.066194595 -0.165829981 0.30134424
## 20          SYM02512 -0.012262355 -0.291216677 0.26358053
## 21          SYM02513 0.267761910 -0.001539879 0.53858309
## 22          SYM02521 0.001961185 -0.376348550 0.38971205
## 23          SYM02522 0.038883238 -0.183208635 0.26157362
## 24 SYM01261:typeTrichoplusia ni -0.071699273 -0.620616569 0.47735269
## 25 SYM01262:typeTrichoplusia ni -0.259584287 -0.777336844 0.26658339
## 26 SYM01263:typeTrichoplusia ni 0.060073555 -0.345066494 0.46300639
## 27 SYM01264:typeTrichoplusia ni -0.052669711 -0.615160806 0.50995639
## 28 SYM01273:typeTrichoplusia ni -0.407945436 -0.784575046 -0.02456598
## 29 SYM01275:typeTrichoplusia ni 0.105083546 -0.232719484 0.44035634
## 30 SYM01276:typeTrichoplusia ni -0.435450664 -0.972741526 0.10145829
## 31 SYM01277:typeTrichoplusia ni -0.168093004 -0.723353672 0.38730249
## 32 SYM01279:typeTrichoplusia ni 0.106558311 -0.223182138 0.43337518
## 33 SYM01281:typeTrichoplusia ni 0.022135189 -0.401500909 0.44742659
## 34 SYM01283:typeTrichoplusia ni -0.027497680 -0.575564212 0.52147322
## 35 SYM01284:typeTrichoplusia ni 0.140539620 -0.264565679 0.54727558
## 36 SYM01285:typeTrichoplusia ni -0.300472884 -0.694224390 0.09893213
## 37 SYM01286:typeTrichoplusia ni -0.130298742 -0.552302852 0.29282132
## 38 SYM01287:typeTrichoplusia ni 0.081413541 -0.322772904 0.49128979
## 39 SYM02477:typeTrichoplusia ni -1.008609599 -1.487733568 -0.52464109
## 40 SYM02496:typeTrichoplusia ni 0.123794291 -0.342328732 0.58248600
## 41 SYM02498:typeTrichoplusia ni 0.213069440 -0.181069335 0.60344131
## 42 SYM02509:typeTrichoplusia ni 0.310940570 -0.050906327 0.67938877
## 43 SYM02512:typeTrichoplusia ni 0.164061675 -0.300173170 0.62397384
## 44 SYM02513:typeTrichoplusia ni -0.352636142 -0.821713547 0.11636023
## 45 SYM02521:typeTrichoplusia ni -0.072241126 -0.626655976 0.48307903
## 46 SYM02522:typeTrichoplusia ni 0.050654621 -0.298829841 0.40237656
##
## $`Cysts and Females`
##      treatment point_est      lower      upper
## 1  SYM01261  22.482344  4.2320230 40.4406765
## 2  SYM01262  -9.694155 -28.9935060 9.2338787
## 3  SYM01263 -37.090701 -58.3802168 -15.1135702
## 4  SYM01264 -31.762129 -51.1228141 -11.7231134
## 5  SYM01273  16.378664  1.9222692 30.6865807
## 6  SYM01275 -23.995462 -43.8738123 -3.4360283
## 7  SYM01276  28.706292  9.0987305 48.9935240
## 8  SYM01277  6.455845 -12.8435060 25.3838787
## 9  SYM01279 -16.769145 -34.5868814 0.8249293
## 10 SYM01281 -36.856808 -55.0006236 -18.5643589
## 11 SYM01283  19.337871 -0.2696906 39.6251029
## 12 SYM01284 -17.933444 -31.2215926 -4.6982981
## 13 SYM01285 -16.744254 -30.0324034 -3.5091089
## 14 SYM01286 -10.173103 -29.7278812 9.0094788
## 15 SYM01287 -17.652479 -34.8749513 -0.6531645

```



```
## 16 SYM02477 67.382344 49.1320230 85.3406765
## 17 SYM02496 -51.078200 -63.9524248 -38.0563647
## 18 SYM02498 -17.102479 -34.3249513 -0.1031645
## 19 SYM02509 -22.944155 -42.2435060 -4.0161213
## 20 SYM02512 -14.760822 -34.5955034 4.7007372
## 21 SYM02513 -14.427489 -34.2621700 5.0340706
## 22 SYM02521 -25.304371 -38.4768039 -12.1797322
## 23 SYM02522 -6.452479 -23.6749513 10.5468355
```

```
##
```

```
## $`Plant Height`
```

```
##      treatment point_est      lower      upper
## 1 SYM01261 1.0960077 -0.25469187 2.4253674
## 2 SYM01262 0.3593743 -1.05071414 1.7810777
## 3 SYM01263 -2.9462750 -4.54651789 -1.3557489
## 4 SYM01264 -0.8177035 -2.27585373 0.6308044
## 5 SYM01273 -0.6676424 -1.73645572 0.3899596
## 6 SYM01275 -0.6843702 -2.18066028 0.8022552
## 7 SYM01276 -2.3440193 -3.82035907 -0.8773326
## 8 SYM01277 -0.1506257 -1.56071414 1.2710777
## 9 SYM01279 -0.9680099 -2.26619460 0.3509766
## 10 SYM01281 0.5531093 -0.79983207 1.8952464
## 11 SYM01283 0.1559807 -1.32035907 1.6226674
## 12 SYM01284 1.2588348 0.28479378 2.2482484
## 13 SYM01285 -0.1519760 -1.12601703 0.8374376
## 14 SYM01286 1.1777954 -0.25094648 2.6181633
## 15 SYM01287 -1.7074543 -2.96201145 -0.4321011
## 16 SYM02477 1.6460077 0.29530813 2.9753674
## 17 SYM02496 0.9748006 0.01806665 1.9303690
## 18 SYM02498 -1.9874543 -3.24201145 -0.7121011
## 19 SYM02509 0.2943743 -1.11571414 1.7160777
## 20 SYM02512 0.2260410 -1.22314658 1.6868665
## 21 SYM02513 -0.4128479 -1.86203547 1.0479776
## 22 SYM02521 0.6132091 -0.35258797 1.5942098
## 23 SYM02522 2.1825457 0.92798855 3.4578989
```

```
##
```

```
## $`Root Fresh Weight`
```

```
##      treatment point_est      lower      upper
## 1 SYM01261 0.04427251 -0.06974469 0.154846464
## 2 SYM01262 -0.16977589 -0.28764239 -0.051829731
## 3 SYM01263 0.01769967 -0.11426775 0.152217687
## 4 SYM01264 0.08641396 -0.03366296 0.209012069
## 5 SYM01273 0.18057492 0.09054407 0.268554538
## 6 SYM01275 -0.12047493 -0.24374336 0.005323408
## 7 SYM01276 -0.26816499 -0.38976398 -0.144040562
## 8 SYM01277 -0.14877589 -0.26664239 -0.030829731
## 9 SYM01279 -0.01540900 -0.12474215 0.093493319
## 10 SYM01281 0.01656170 -0.09550136 0.129405546
## 11 SYM01283 -0.24027025 -0.36186925 -0.116145825
## 12 SYM01284 -0.02651988 -0.10830229 0.055348520
## 13 SYM01285 0.04834499 -0.03343743 0.130213385
## 14 SYM01286 -0.17024958 -0.28968382 -0.050735541
## 15 SYM01287 0.20603544 0.10036464 0.311276200
## 16 SYM02477 -0.06772749 -0.18174469 0.042846464
## 17 SYM02496 0.04198831 -0.03752090 0.122238663
```

```
## 18 SYM02498 0.20103544 0.09536464 0.306276200
## 19 SYM02509 -0.25427589 -0.37214239 -0.136329731
## 20 SYM02512 -0.06855367 -0.18970609 0.052678729
## 21 SYM02513 -0.22022034 -0.34137275 -0.098987937
## 22 SYM02521 -0.01331726 -0.09439701 0.067864361
## 23 SYM02522 0.04103544 -0.06463536 0.146276200
##
## `$Shoot Fresh Weight`
##      treatment    point_est      lower      upper
## 1  SYM01261 -0.015073295 -0.114983070 0.08379504
## 2  SYM01262 0.160435869 0.054881387 0.26530555
## 3  SYM01263 -0.171827488 -0.290448986 -0.05339049
## 4  SYM01264 0.045886797 -0.062233439 0.15382313
## 5  SYM01273 0.037609465 -0.041497617 0.11623179
## 6  SYM01275 0.083331242 -0.027607117 0.19408552
## 7  SYM01276 -0.044271097 -0.153735286 0.06500910
## 8  SYM01277 0.128435869 0.022881387 0.23330555
## 9  SYM01279 0.001052872 -0.095414023 0.09858370
## 10 SYM01281 -0.043756660 -0.143599128 0.05637643
## 11 SYM01283 0.009939429 -0.099524760 0.11921963
## 12 SYM01284 0.012788857 -0.059584124 0.08602579
## 13 SYM01285 0.067113182 -0.005259799 0.14035011
## 14 SYM01286 0.123777974 0.016843938 0.23002696
## 15 SYM01287 0.002830650 -0.090402972 0.09712815
## 16 SYM02477 -0.067073295 -0.166983070 0.03179504
## 17 SYM02496 -0.020169449 -0.090921656 0.05103750
## 18 SYM02498 0.023330650 -0.069902972 0.11762815
## 19 SYM02509 0.173935869 0.068381387 0.27880555
## 20 SYM02512 0.206380313 0.097934089 0.31414122
## 21 SYM02513 0.034713646 -0.073732578 0.14247455
## 22 SYM02521 0.027477966 -0.044282202 0.10009586
## 23 SYM02522 0.025330650 -0.067902972 0.11962815
```

As we mentioned in the beginning of this section, fixed-effect coefficients of fungal treatments for the linear mixed-effects models are close to those for the linear fixed-effects models. To show this, we draw the following plots which depict the fixed-effect coefficient values for both fitted models. From the plots, we can easily see that the differences in the coefficients are very slight.

```
p <- list()
for(k in 1:n.metric) {

  temp.FEM <- coef.FEM[[k]]
  temp.FEM$model <- "Fixed Effects Model"

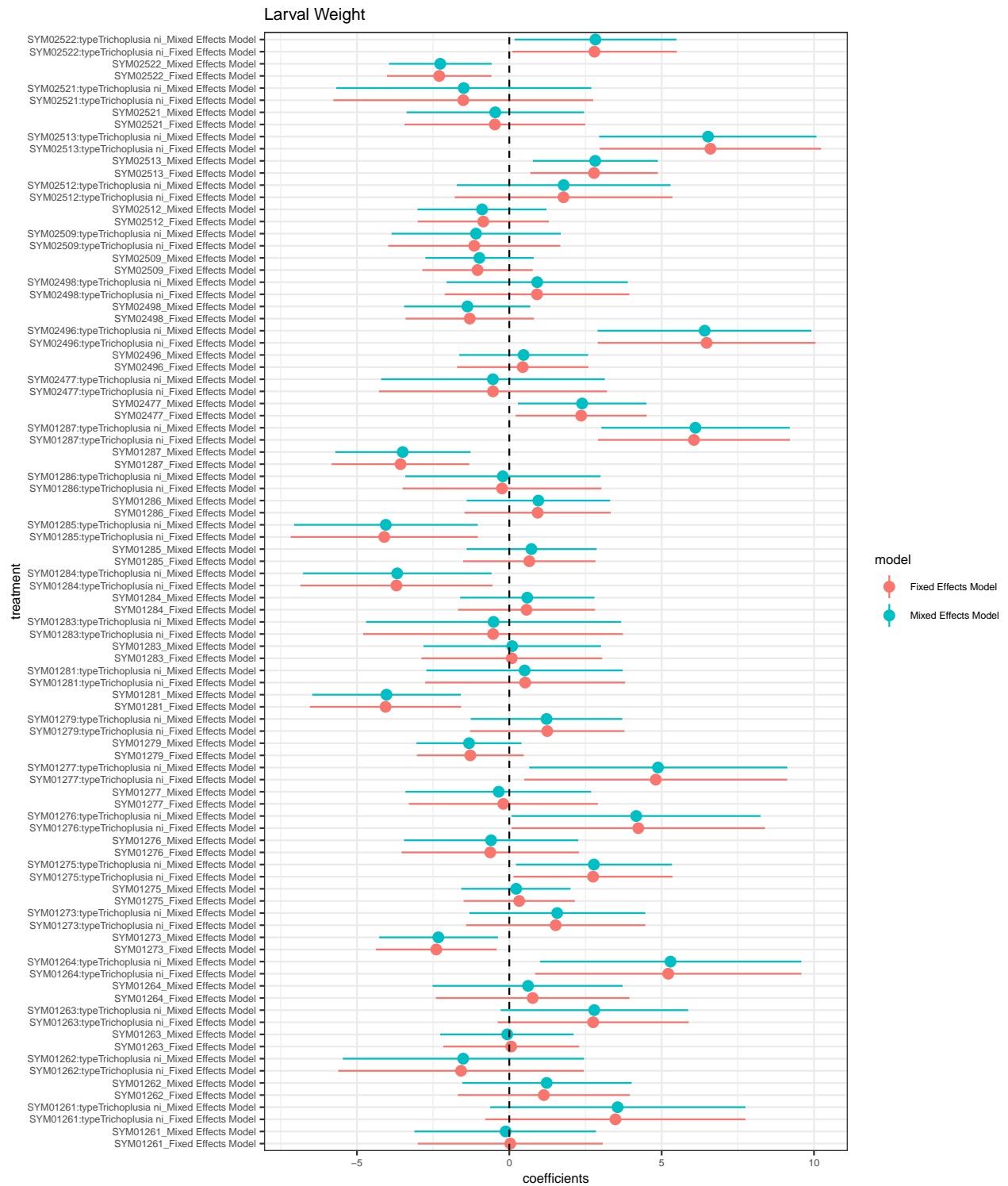
  temp.REM <- coef.REM[[k]]
  temp.REM$model <- "Mixed Effects Model"

  vis.dat <- rbind(temp.FEM, temp.REM) %>% mutate(category = paste0(treatment, "_", model))

  p[[k]] <- vis.dat %>% ggplot(aes(x = category, y = point_est, ymin = lower,
                                   ymax = upper, color = model)) +
    geom_pointrange() + geom_hline(yintercept = 0, lty = 2) +
    theme_bw() + ggtitle(metrics[k]) + coord_flip() +
    ylab("coefficients") + xlab("treatment") + theme(text = element_text(size=8))
} ; rm(k, temp.FEM, temp.REM, vis.dat)
```

```
print(p)
```

```
## [[1]]
```



```
##
```

```
## [[2]]
```

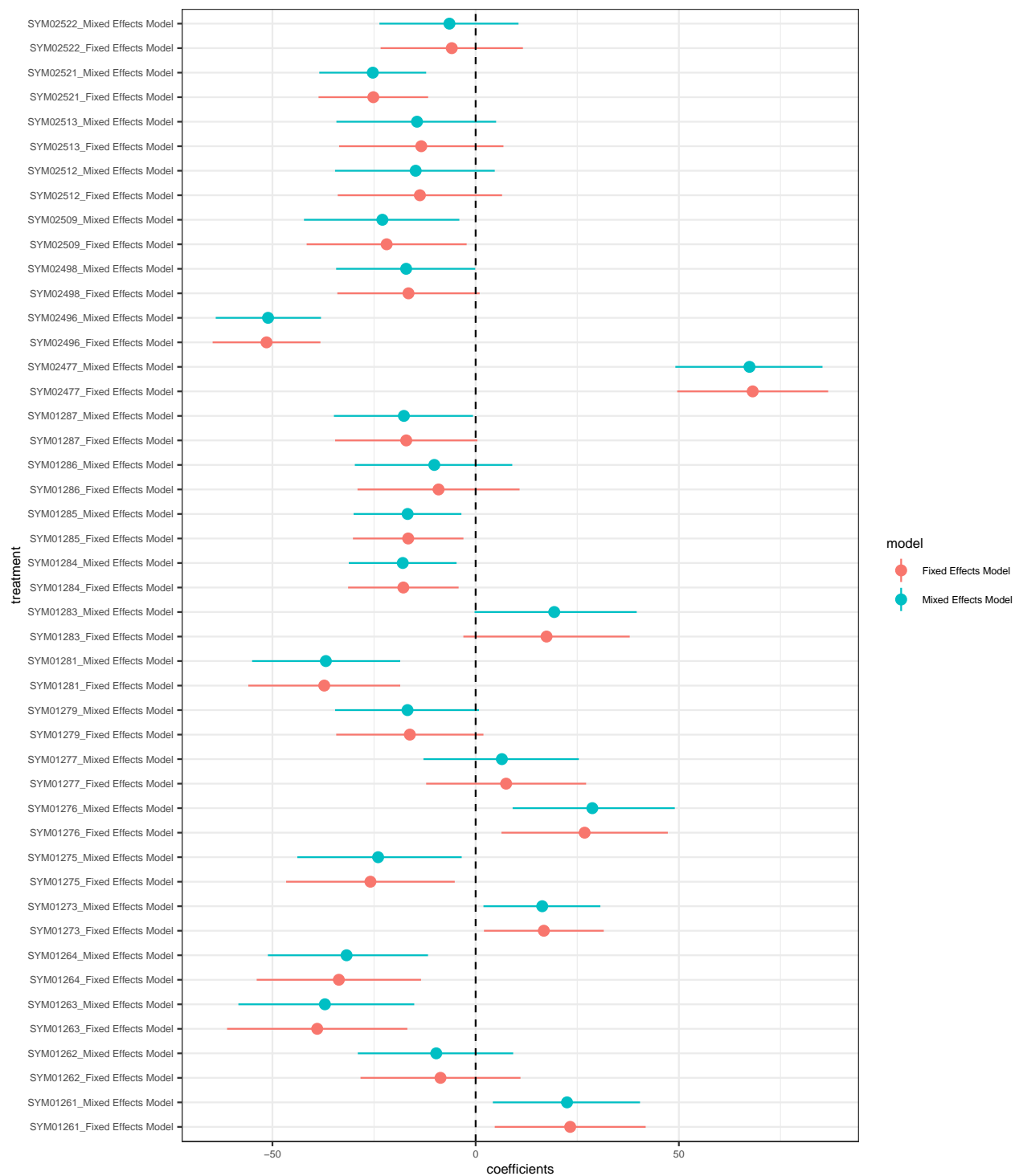
The forest plot displays 20 models, each with two coefficient estimates. The x-axis represents the coefficient value, ranging from -0.75 to 0.50. A vertical dashed line at 0.00 indicates the null hypothesis. The red dots represent one set of estimates, and the teal dots represent another. Horizontal lines indicate the confidence intervals for each estimate. The models are ordered by the red dot estimate, from most negative to most positive.

Model	Red Dot Estimate	Teal Dot Estimate
1	-0.05	0.00
2	-0.05	0.00
3	-0.05	0.00
4	-0.05	0.00
5	-0.05	0.00
6	-0.05	0.00
7	-0.05	0.00
8	-0.05	0.00
9	-0.05	0.00
10	-0.05	0.00
11	-0.05	0.00
12	-0.05	0.00
13	-0.05	0.00
14	-0.05	0.00
15	-0.05	0.00
16	-0.05	0.00
17	-0.05	0.00
18	-0.05	0.00
19	-0.05	0.00
20	-0.05	0.00

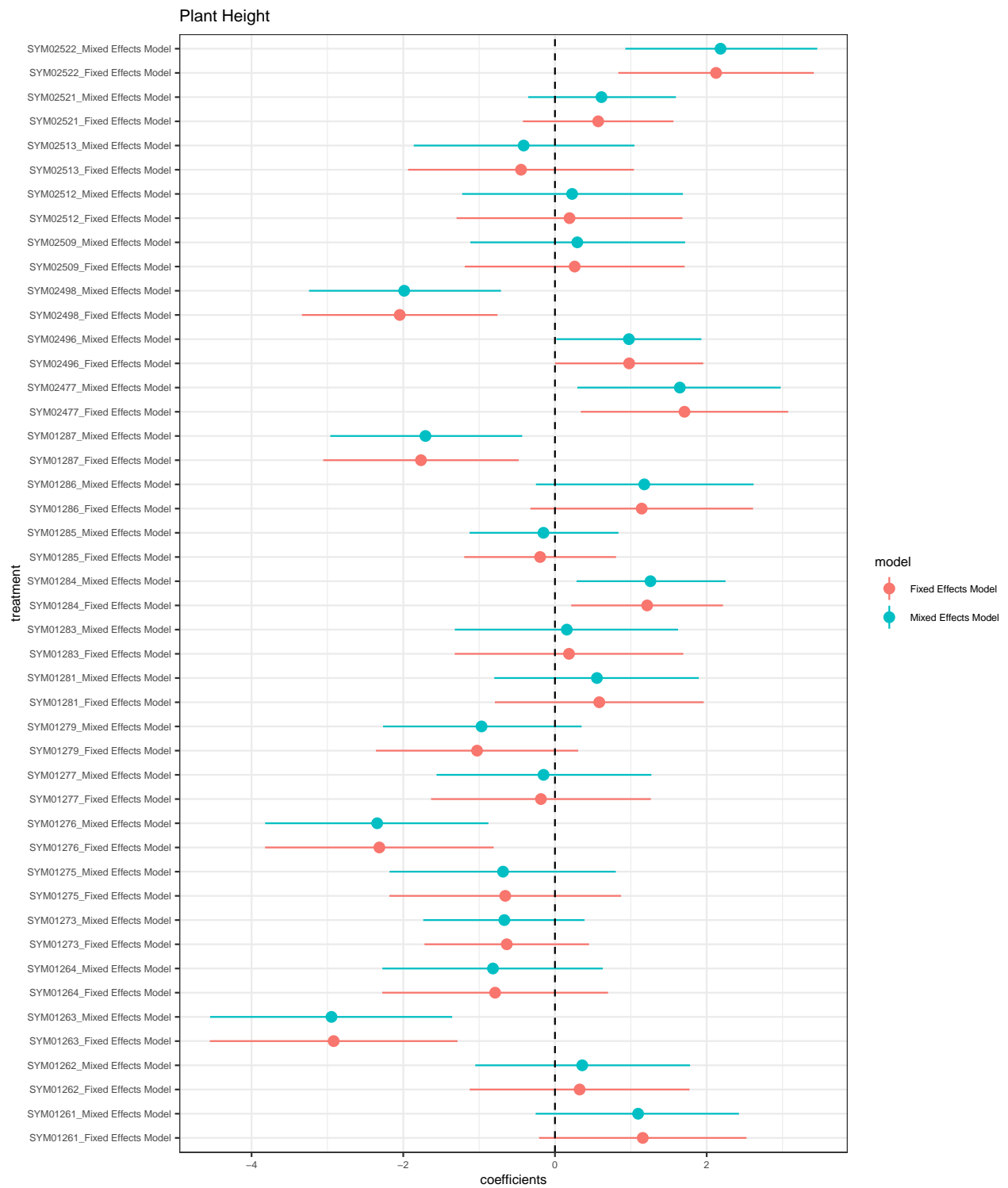
52

53

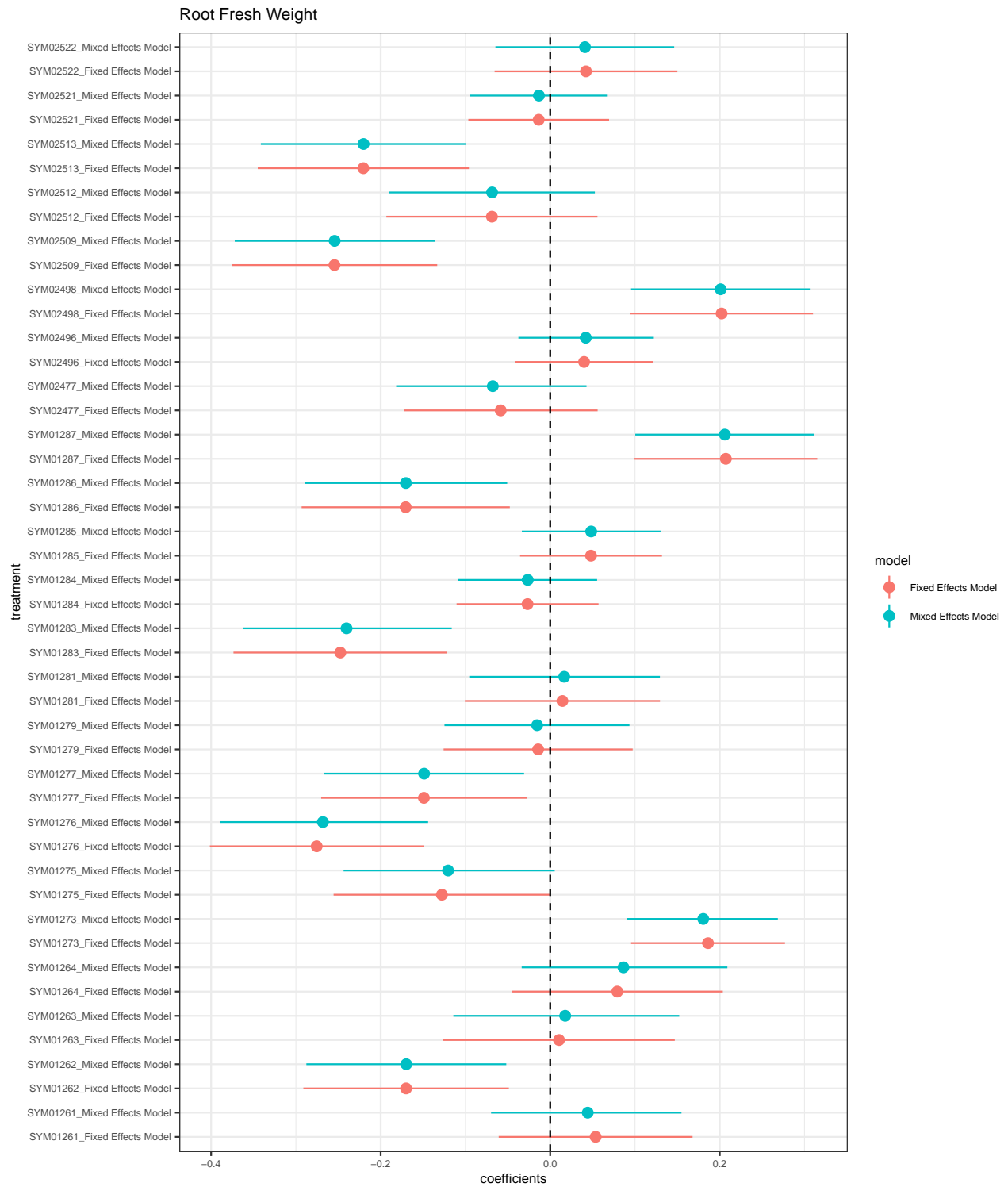
Cysts and Females



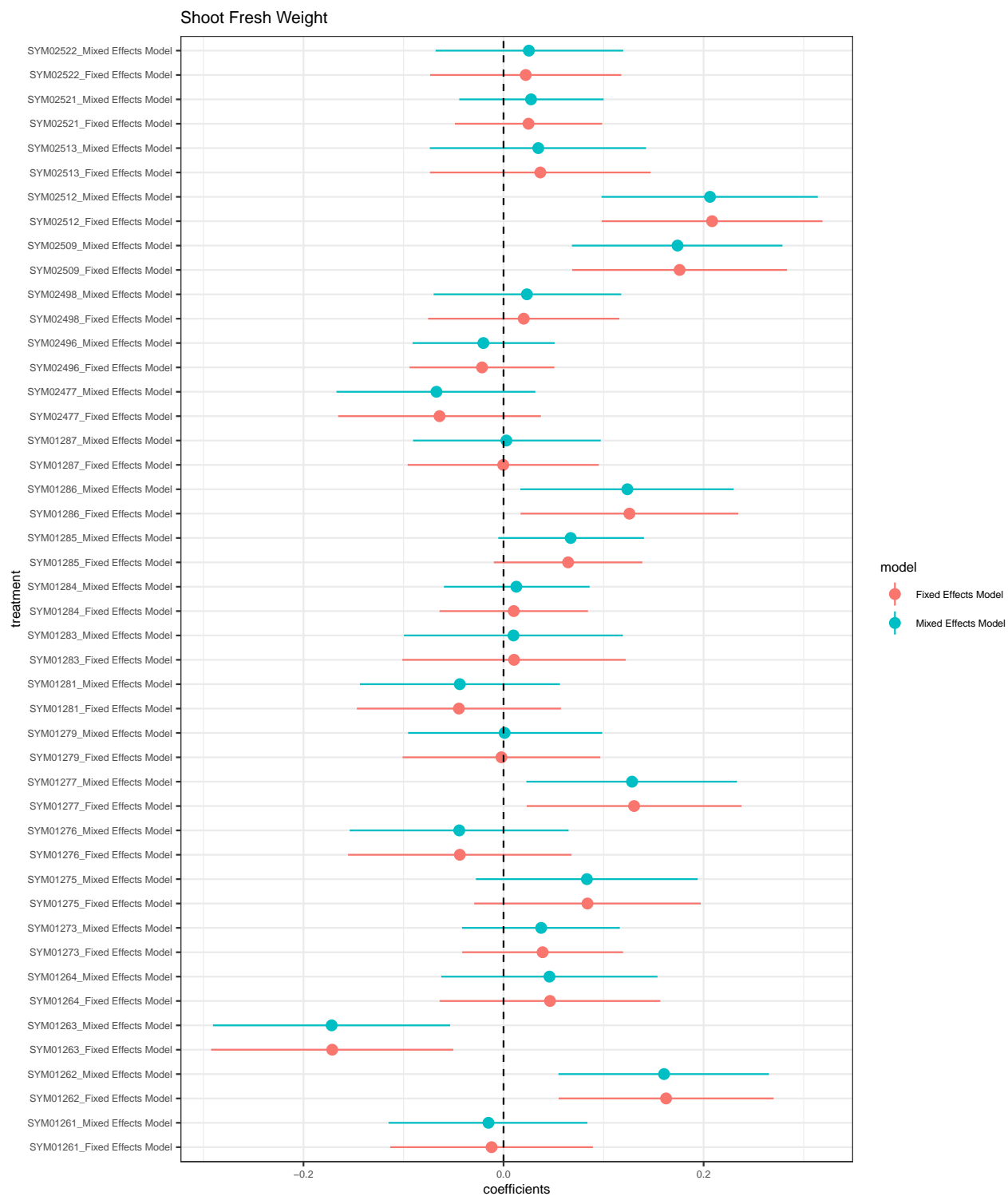
[[5]]



[[6]]



[[7]]



7.4 Diagnostic plots for REMs

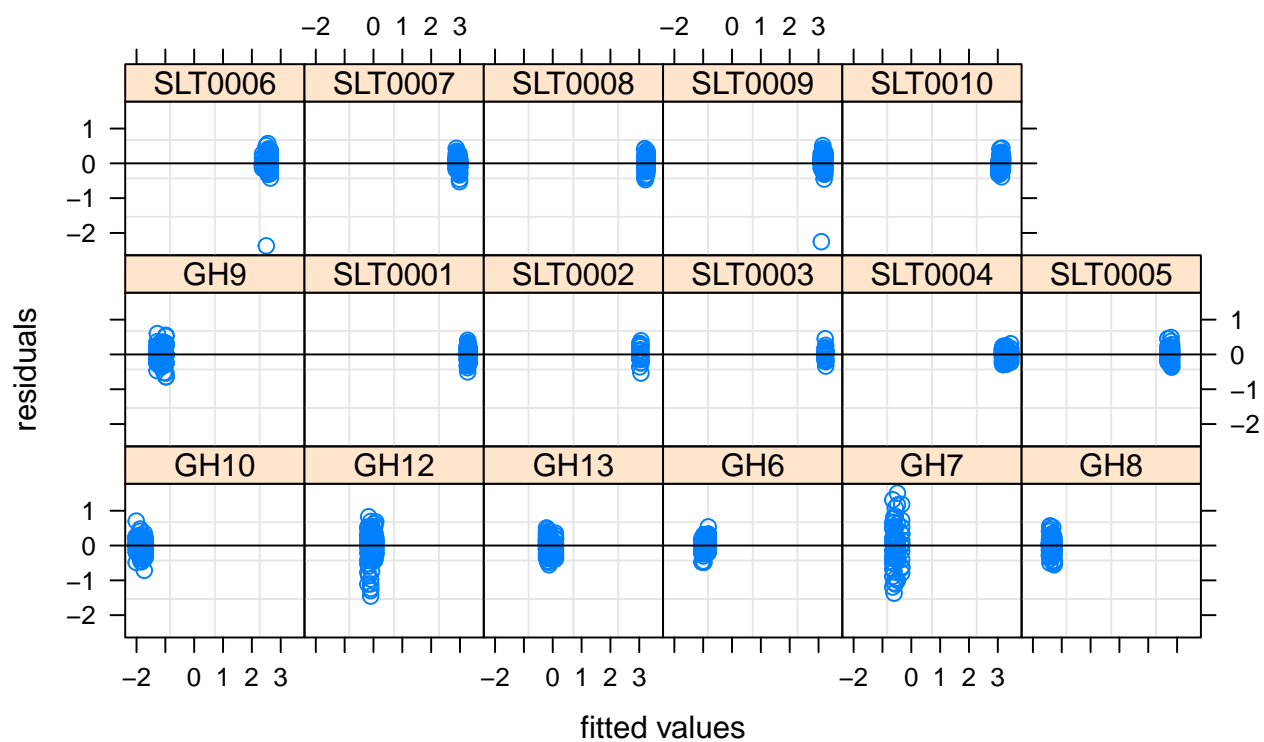
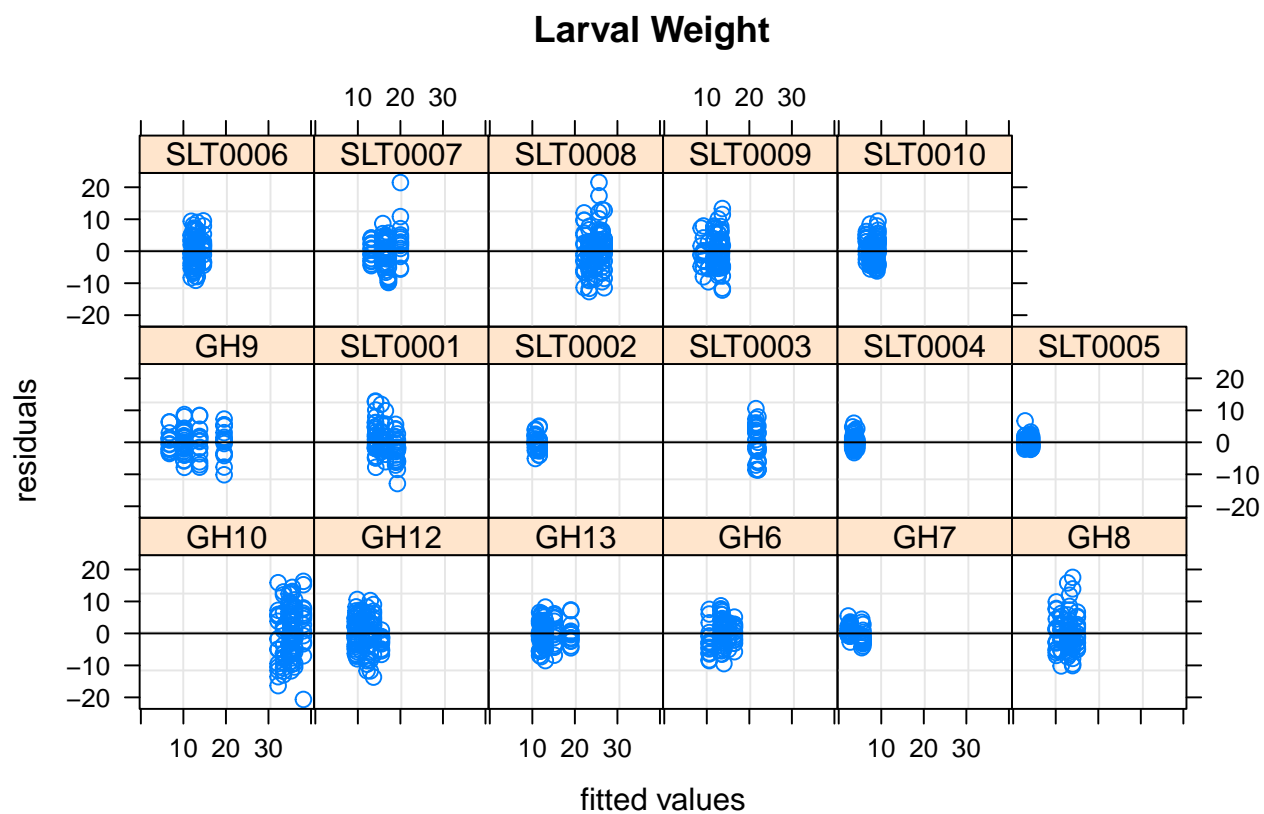
We first plot residuals $y - \hat{y}$ against fitted values \hat{y} from the REMs, grouped by each greenhouse ("id"). The ideal patterns should have zero mean, no special trends, and equal variances across different greenhouses.

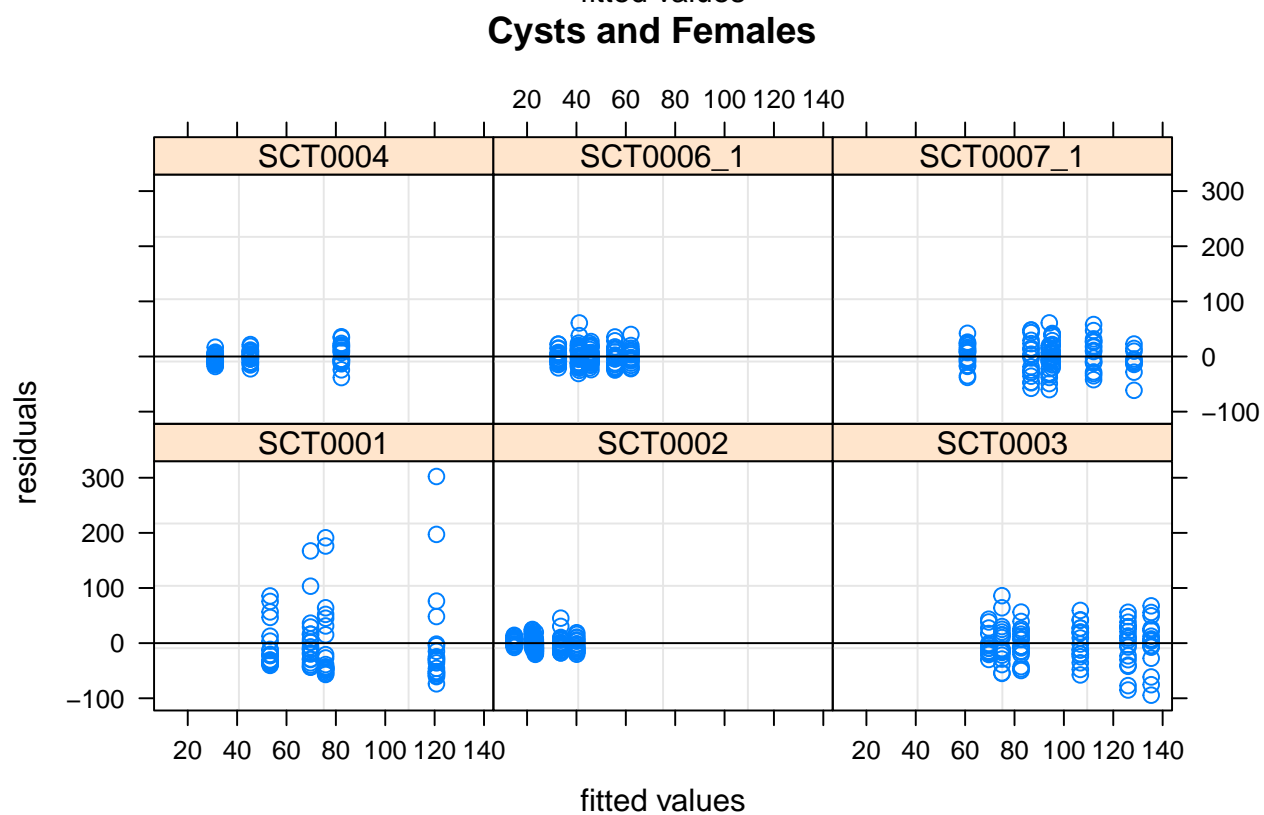
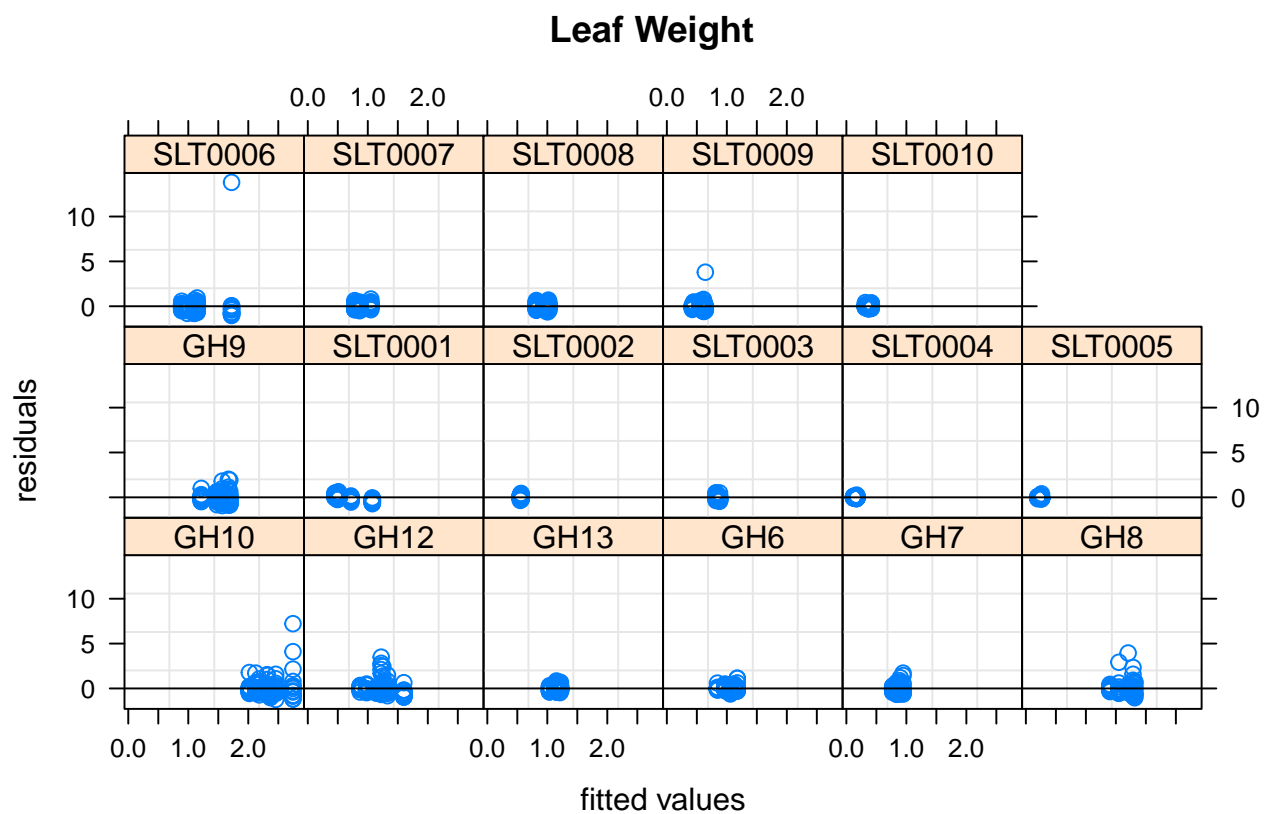
```

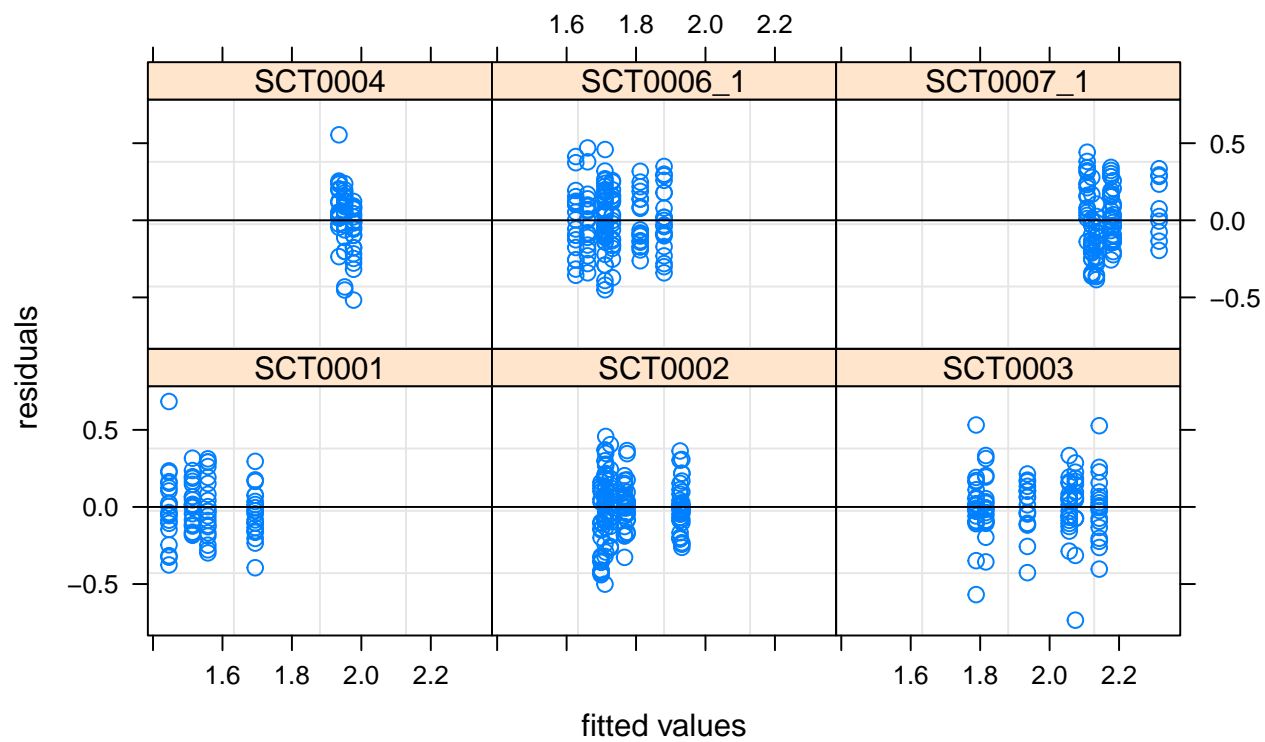
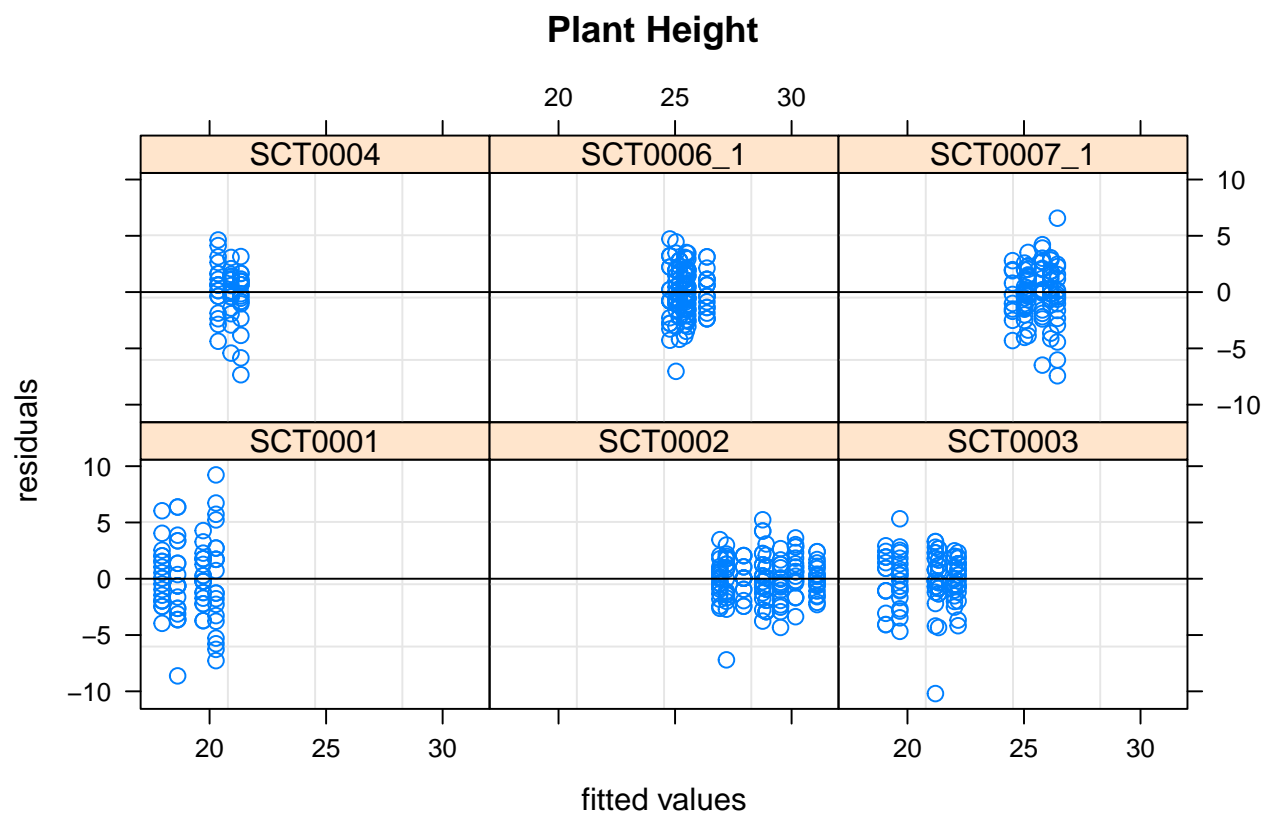
diagnostics <- list()
for(k in 1:n.metric) {
  diagnostics[[k]] <- plot(output.REM[[k]], resid(.) ~ fitted(.)|id,
                           abline = 0, xlab = 'fitted values',
                           ylab = 'residuals', main = paste(metrics[k]))
} ; rm(k)

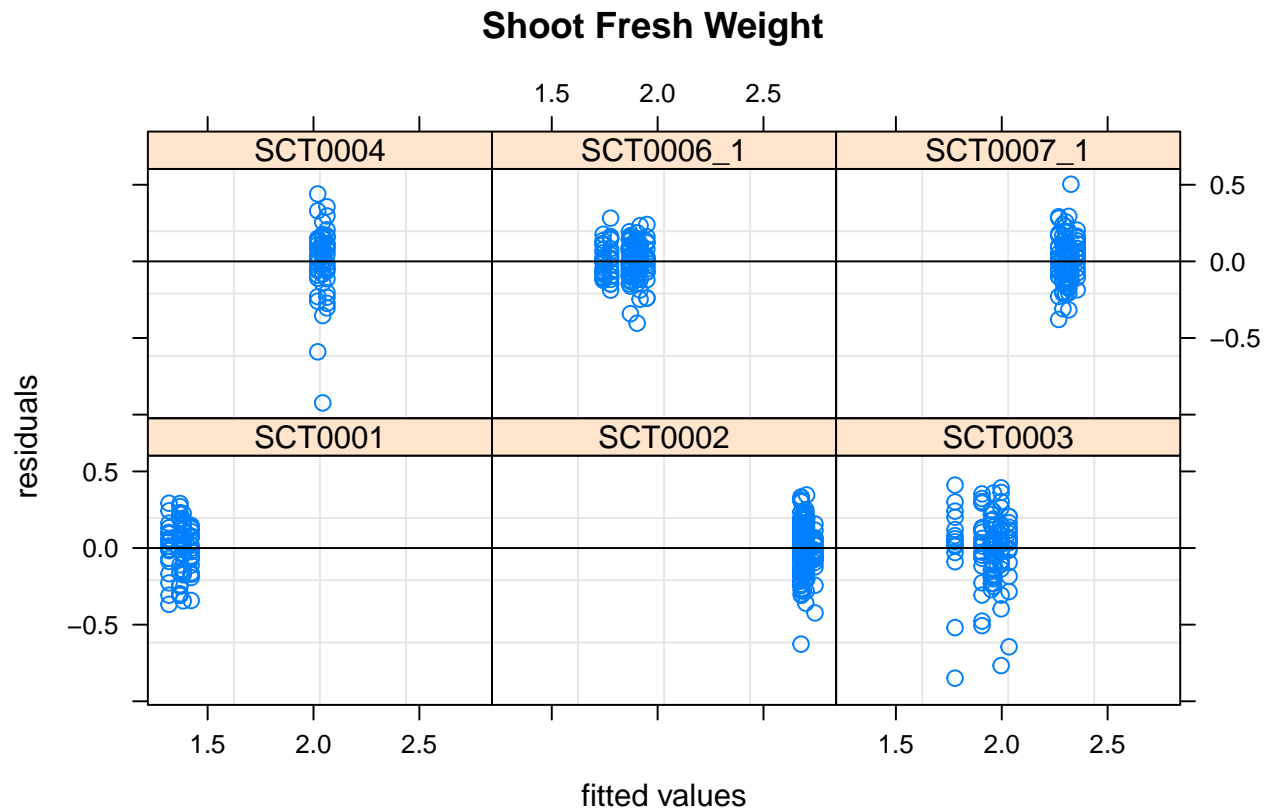
for(k in 1:n.metric) print(diagnostics[[k]])

```





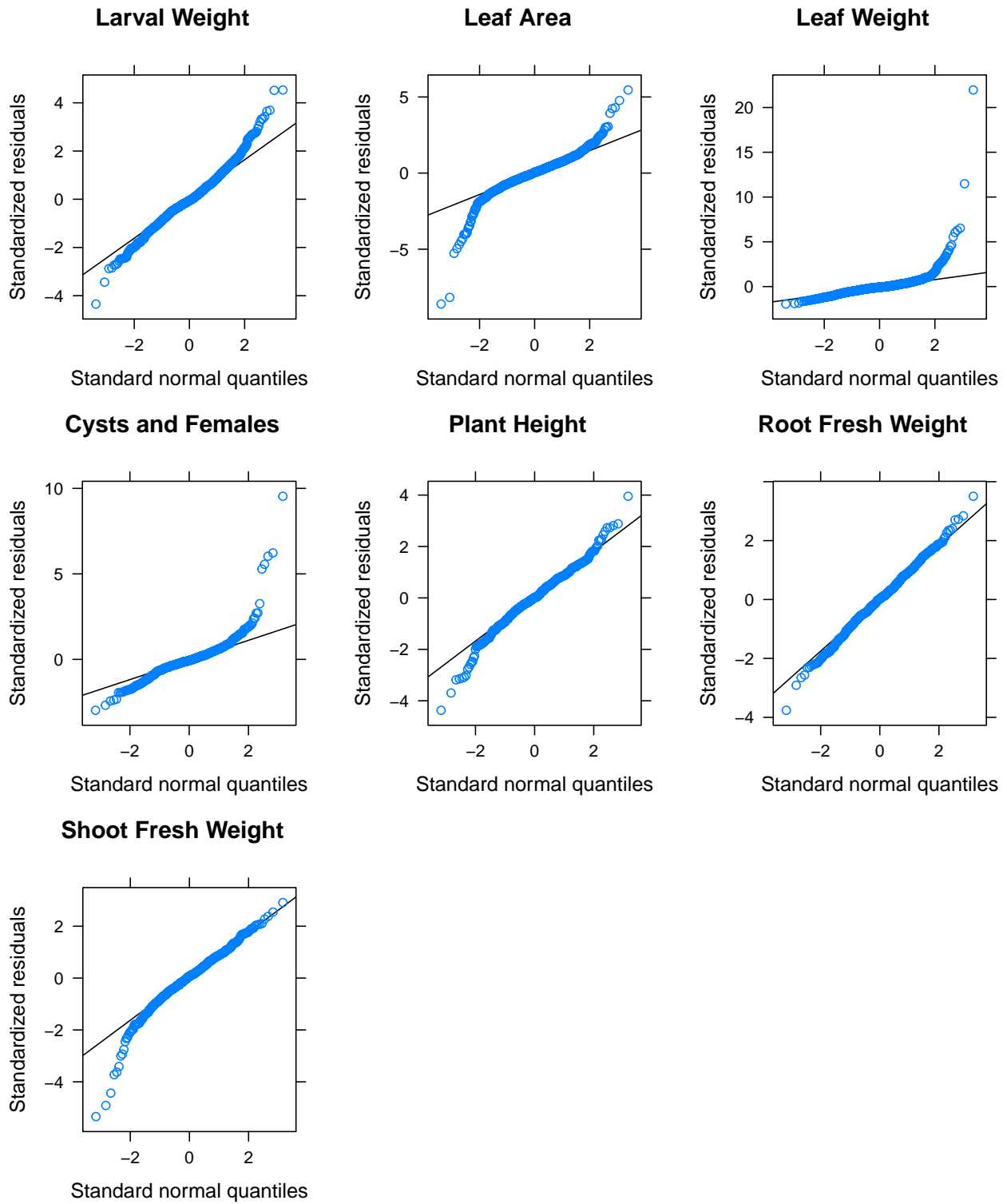




Next, we show Q-Q plots for residuals from each REM. Ideally the residuals should approximate normal distributions and the points should be on the 45 degree line.

```
p_qq <- list()
for(k in 1:n.metric) {
  p_qq[[k]] <- qqmath(output.REM[[k]], main = paste(metrics[k]))
} ; rm(k)
```

```
grid.arrange(p_qq[[1]], p_qq[[2]], p_qq[[3]],
              p_qq[[4]], p_qq[[5]], p_qq[[6]],
              p_qq[[7]],
              ncol=3)
```



The plots seem to imply that conditions for regression are met. There are some outliers, but that's all there is to note.

7.5 R code for rankings and ranking results for each treatment

```
sig.level <- 0.05

rankingbysig <- list()
for(j in 1:length(n.type)) {

  if(n.type[j] == 1) {

    emmoutput      <- summary(contrast(emmobjsREM[[j]], method = "trt.vs.ctrl", adjust = "none"))
    emmoutputpvals <- pull(emmoutput['p.value'], 'p.value')

    adjpvals       <- p.adjust(emmoutputpvals, method = "BY")
    labels         <- as.character(emmoutput$contrast)
    sigcols        <- which(adjpvals < sig.level)

    rankings       <- rep(0, times = 23)
    for(k in sigcols) rankings[k] <- sign(emmoutput$estimate)[k]

    names(rankings) <- labels
    rankingbysig[[j]] <- rankings
  }

  if(n.type[j] == 2) {

    rankings1      <- rep(0, times = 23)
    rankings2      <- rep(0, times = 23)

    emmoutput1     <- summary(contrast(emmobjsREM[[j]], method = "trt.vs.ctrl", adjust = "none"))
    emmoutputpvals1 <- pull(emmoutput1['p.value'], 'p.value')
    emmoutput2     <- summary(contrast(emmobjsREM[[j]], method = "trt.vs.ctrlk", adjust = "none",
                                     ref = 25))
    emmoutputpvals2 <- pull(emmoutput2['p.value'], 'p.value')
    emmoutputpvals <- c(emmoutputpvals1[1:23], emmoutputpvals2[25:47])

    adjpvals1      <- p.adjust(emmoutputpvals[1:23], method = "BY")
    adjpvals2      <- p.adjust(emmoutputpvals[24:46], method = "BY")
    labels         <- c(as.character(emmoutput1$contrast[1:23]),
                       as.character(emmoutput2$contrast[25:47]))

    sigcols        <- which(adjpvals1 < sig.level)
    if(length(sigcols) > 0) {
      for(k in sigcols) {
        rankings1[k] <- sign(emmoutput1$estimate)[k]
      }
    }
    ; names(rankings1) <- labels[1:23]

    sigcols        <- which(adjpvals2 < sig.level)
    if(length(sigcols) > 0) {
      for(k in sigcols) {
        rankings2[k] <- sign(emmoutput2$estimate)[k]
      }
    }
    ; names(rankings2) <- labels[24:46]
  }
}
```



```

    rankingbysig[[j]] <- cbind(rankings1,rankings2)
    rownames(rankingbysig[[j]]) <- paste(substring(labels[1:23], 1, 8), '- Stress Control')
  }
} ; names(rankingbysig) <- as.character(metrics)

posneg <- data.frame(metric = metrics, sgn = c(-1, -1, -1, -1, +1, +1, +1))

for(i in length(metrics)) {
  rankingbysig[[metrics[i]]] <- rankingbysig[[metrics[i]]] * posneg[i, 2]
} ; rm(i, j, k)
rankingbysig

```

```

## $`Larval Weight`
##
## rankings1 rankings2
## SYM01261 - Stress Control      0      0
## SYM01262 - Stress Control      0      0
## SYM01263 - Stress Control      0      0
## SYM01264 - Stress Control      0     -1
## SYM01273 - Stress Control      0      0
## SYM01275 - Stress Control      0     -1
## SYM01276 - Stress Control      0      0
## SYM01277 - Stress Control      0     -1
## SYM01279 - Stress Control      0      0
## SYM01281 - Stress Control      0     -1
## SYM01283 - Stress Control      0      0
## SYM01284 - Stress Control      0      0
## SYM01285 - Stress Control      0      1
## SYM01286 - Stress Control      0      0
## SYM01287 - Stress Control      0      0
## SYM02477 - Stress Control      0      0
## SYM02496 - Stress Control      0      1
## SYM02498 - Stress Control      0      0
## SYM02509 - Stress Control      0      0
## SYM02512 - Stress Control      0      0
## SYM02513 - Stress Control      0     -1
## SYM02521 - Stress Control      0      0
## SYM02522 - Stress Control      0      0
##
## $`Leaf Area`
##
## rankings1 rankings2
## SYM01261 - Stress Control      0      0
## SYM01262 - Stress Control      0      0
## SYM01263 - Stress Control      0      0
## SYM01264 - Stress Control      0      0
## SYM01273 - Stress Control      0      0
## SYM01275 - Stress Control      0      1
## SYM01276 - Stress Control      0      0
## SYM01277 - Stress Control      0      0
## SYM01279 - Stress Control      0      1
## SYM01281 - Stress Control      0      0
## SYM01283 - Stress Control      0      0
## SYM01284 - Stress Control      0      0
## SYM01285 - Stress Control      0      0

```

```

## SYM01286 - Stress Control      0      0
## SYM01287 - Stress Control      0      0
## SYM02477 - Stress Control      0      0
## SYM02496 - Stress Control      0      1
## SYM02498 - Stress Control      0      1
## SYM02509 - Stress Control      0      0
## SYM02512 - Stress Control      0      0
## SYM02513 - Stress Control      0      1
## SYM02521 - Stress Control      0      0
## SYM02522 - Stress Control      0      0
##
## $`Leaf Weight`
##                      rankings1 rankings2
## SYM01261 - Stress Control      0      0
## SYM01262 - Stress Control      0      0
## SYM01263 - Stress Control      0      0
## SYM01264 - Stress Control      0      0
## SYM01273 - Stress Control      0      0
## SYM01275 - Stress Control      0      0
## SYM01276 - Stress Control      0      0
## SYM01277 - Stress Control      0      0
## SYM01279 - Stress Control      0      0
## SYM01281 - Stress Control      0      0
## SYM01283 - Stress Control      0      0
## SYM01284 - Stress Control      0      0
## SYM01285 - Stress Control      0      0
## SYM01286 - Stress Control      0      0
## SYM01287 - Stress Control      0      0
## SYM02477 - Stress Control      1      0
## SYM02496 - Stress Control      0      0
## SYM02498 - Stress Control      0      0
## SYM02509 - Stress Control      0      0
## SYM02512 - Stress Control      0      0
## SYM02513 - Stress Control      0      0
## SYM02521 - Stress Control      0      0
## SYM02522 - Stress Control      0      0
##
## $`Cysts and Females`
## SYM01261 - Stress Control SYM01262 - Stress Control SYM01263 - Stress Control
##                      0                      0                      -1
## SYM01264 - Stress Control SYM01273 - Stress Control SYM01275 - Stress Control
##                      -1                      0                      0
## SYM01276 - Stress Control SYM01277 - Stress Control SYM01279 - Stress Control
##                      0                      0                      0
## SYM01281 - Stress Control SYM01283 - Stress Control SYM01284 - Stress Control
##                      -1                      0                      0
## SYM01285 - Stress Control SYM01286 - Stress Control SYM01287 - Stress Control
##                      0                      0                      0
## SYM02477 - Stress Control SYM02496 - Stress Control SYM02498 - Stress Control
##                      1                      -1                      0
## SYM02509 - Stress Control SYM02512 - Stress Control SYM02513 - Stress Control
##                      0                      0                      0
## SYM02521 - Stress Control SYM02522 - Stress Control
##                      -1                      0

```

```

##
## $`Plant Height`
## SYM01261 - Stress Control SYM01262 - Stress Control SYM01263 - Stress Control
##                                0                                0                                -1
## SYM01264 - Stress Control SYM01273 - Stress Control SYM01275 - Stress Control
##                                0                                0                                0
## SYM01276 - Stress Control SYM01277 - Stress Control SYM01279 - Stress Control
##                                0                                0                                0
## SYM01281 - Stress Control SYM01283 - Stress Control SYM01284 - Stress Control
##                                0                                0                                0
## SYM01285 - Stress Control SYM01286 - Stress Control SYM01287 - Stress Control
##                                0                                0                                0
## SYM02477 - Stress Control SYM02496 - Stress Control SYM02498 - Stress Control
##                                0                                0                                0
## SYM02509 - Stress Control SYM02512 - Stress Control SYM02513 - Stress Control
##                                0                                0                                0
## SYM02521 - Stress Control SYM02522 - Stress Control
##                                0                                1
##
## $`Root Fresh Weight`
## SYM01261 - Stress Control SYM01262 - Stress Control SYM01263 - Stress Control
##                                0                                0                                0
## SYM01264 - Stress Control SYM01273 - Stress Control SYM01275 - Stress Control
##                                0                                1                                0
## SYM01276 - Stress Control SYM01277 - Stress Control SYM01279 - Stress Control
##                                -1                                0                                0
## SYM01281 - Stress Control SYM01283 - Stress Control SYM01284 - Stress Control
##                                0                                -1                                0
## SYM01285 - Stress Control SYM01286 - Stress Control SYM01287 - Stress Control
##                                0                                0                                1
## SYM02477 - Stress Control SYM02496 - Stress Control SYM02498 - Stress Control
##                                0                                0                                1
## SYM02509 - Stress Control SYM02512 - Stress Control SYM02513 - Stress Control
##                                -1                                0                                -1
## SYM02521 - Stress Control SYM02522 - Stress Control
##                                0                                0
##
## $`Shoot Fresh Weight`
## SYM01261 - Stress Control SYM01262 - Stress Control SYM01263 - Stress Control
##                                0                                0                                0
## SYM01264 - Stress Control SYM01273 - Stress Control SYM01275 - Stress Control
##                                0                                0                                0
## SYM01276 - Stress Control SYM01277 - Stress Control SYM01279 - Stress Control
##                                0                                0                                0
## SYM01281 - Stress Control SYM01283 - Stress Control SYM01284 - Stress Control
##                                0                                0                                0
## SYM01285 - Stress Control SYM01286 - Stress Control SYM01287 - Stress Control
##                                0                                0                                0
## SYM02477 - Stress Control SYM02496 - Stress Control SYM02498 - Stress Control
##                                0                                0                                0
## SYM02509 - Stress Control SYM02512 - Stress Control SYM02513 - Stress Control
##                                0                                1                                0
## SYM02521 - Stress Control SYM02522 - Stress Control
##                                0                                0

```

We now give the full combined rankings as well.

```
for(j in which(n.type == 2)) rankingbysig[[j]] <- rankingbysig[[j]][,1] + rankingbysig[[j]][,2]

overall_rank1 <- sort( (2/6) * rankingbysig[[1]] +
                      (3/6) * rankingbysig[[2]] +
                      (1/6) * rankingbysig[[3]], decreasing = T)
names(overall_rank1) <- substring(names(overall_rank1), 1, 8)

overall_rank2 <- sort( (4/10) * rankingbysig[[4]] +
                      (1/10) * rankingbysig[[5]] +
                      (3/10) * rankingbysig[[6]] +
                      (2/10) * rankingbysig[[7]], decreasing = T)
names(overall_rank2) <- substring(names(overall_rank2), 1, 8)

temp1          <- data.frame(Treatment = as.character(names(overall_rank1)),
                             Rank1 = rank(-overall_rank1, ties.method = "min")) %>% tbl_df()
temp2          <- data.frame(Treatment = as.character(names(overall_rank2)),
                             Rank2 = rank(-overall_rank2, ties.method = "min")) %>% tbl_df()
overall_rank    <- full_join(temp1, temp2, by = 'Treatment')
overall_rank$Treatment <- as.character(overall_rank$Treatment) ; rm(temp1, temp2)

overall_rank <- overall_rank %>% mutate(Sum.rank = Rank1 + Rank2) %>%
  arrange(Sum.rank) %>% select(-Sum.rank) %>% as.data.frame()

overall_rank
```

##	Treatment	Rank1	Rank2
## 1	SYM02498	2	2
## 2	SYM02477	7	1
## 3	SYM01279	2	7
## 4	SYM01273	8	2
## 5	SYM01287	8	2
## 6	SYM01285	4	7
## 7	SYM01275	5	7
## 8	SYM02512	8	5
## 9	SYM02522	8	6
## 10	SYM01261	8	7
## 11	SYM01262	8	7
## 12	SYM01284	8	7
## 13	SYM01286	8	7
## 14	SYM02496	1	19
## 15	SYM02513	5	15
## 16	SYM01276	8	15
## 17	SYM01283	8	15
## 18	SYM02509	8	15
## 19	SYM02521	8	19
## 20	SYM01277	21	7
## 21	SYM01263	8	23
## 22	SYM01264	21	19
## 23	SYM01281	21	19

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