

NSFPGRP_HostMutant_C86Meliloti

Code ▾

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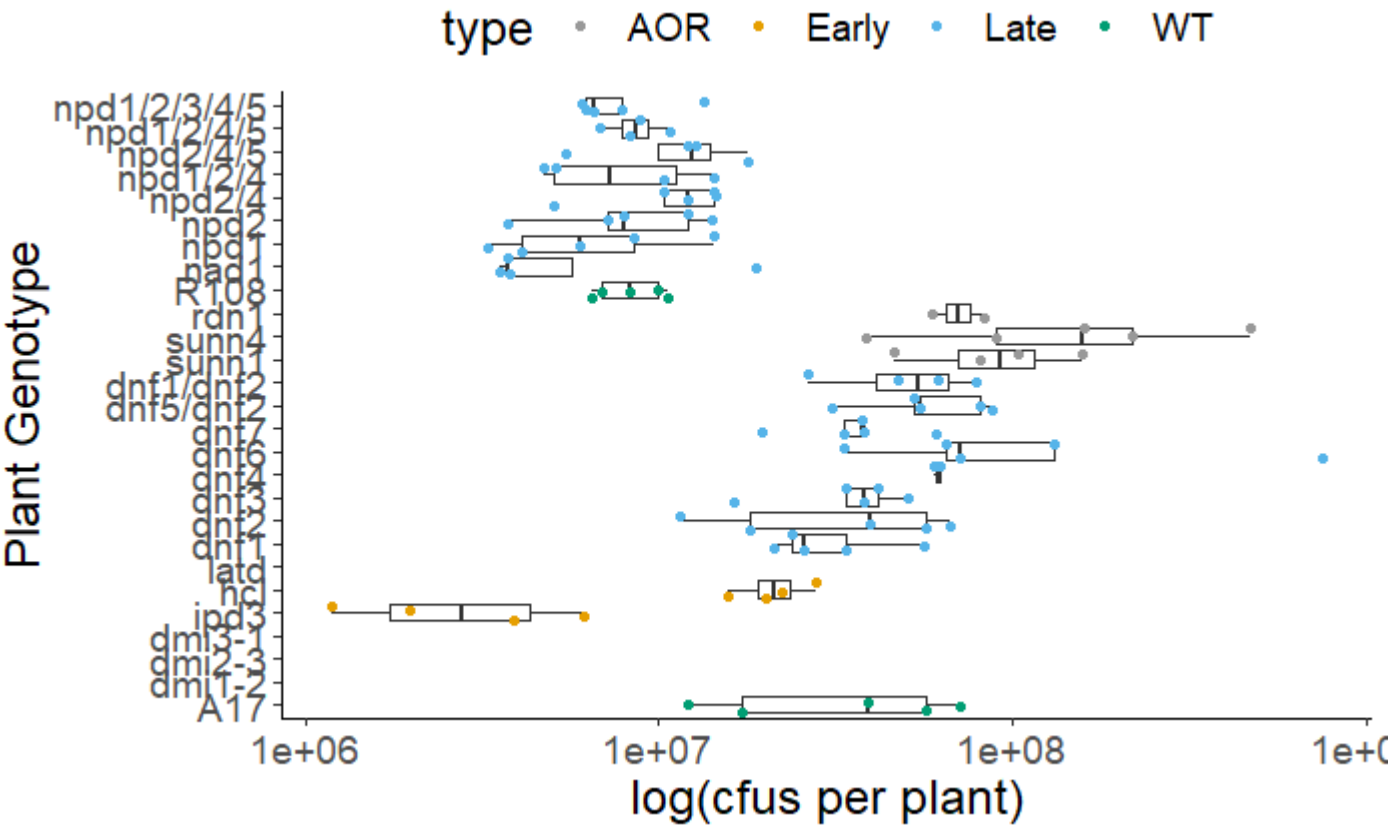
Analysis file for NSF Host Mutant C86 Ensifer meliloti select and resequence project.

Summary

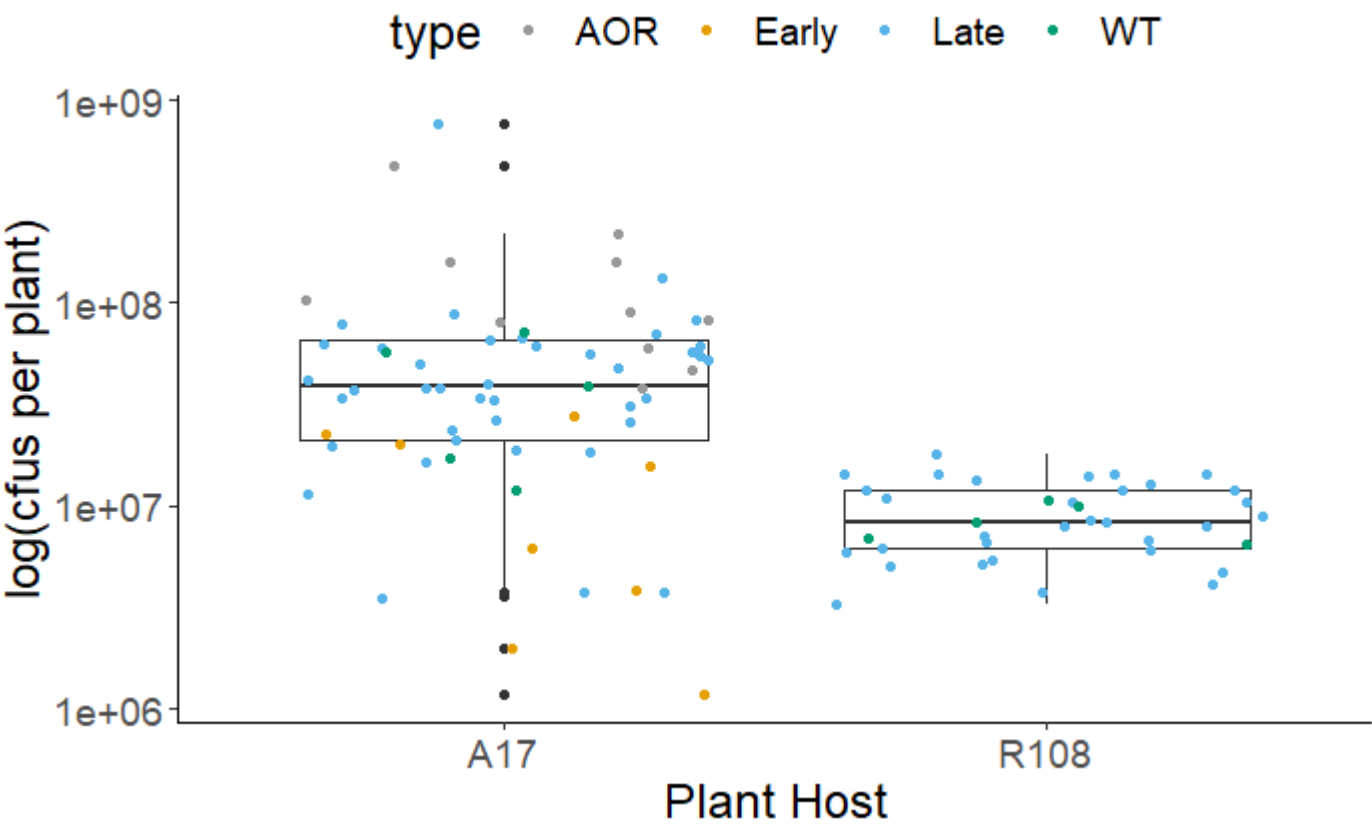
Results for dilution plating of nodule homogenate.

(1)Variation among genotypes. (2) Sunn1, Sunn4 are highly numerated with nodules. (3) A17 and R108 wild types show trend that A17 has higher rhizobial load than R108.

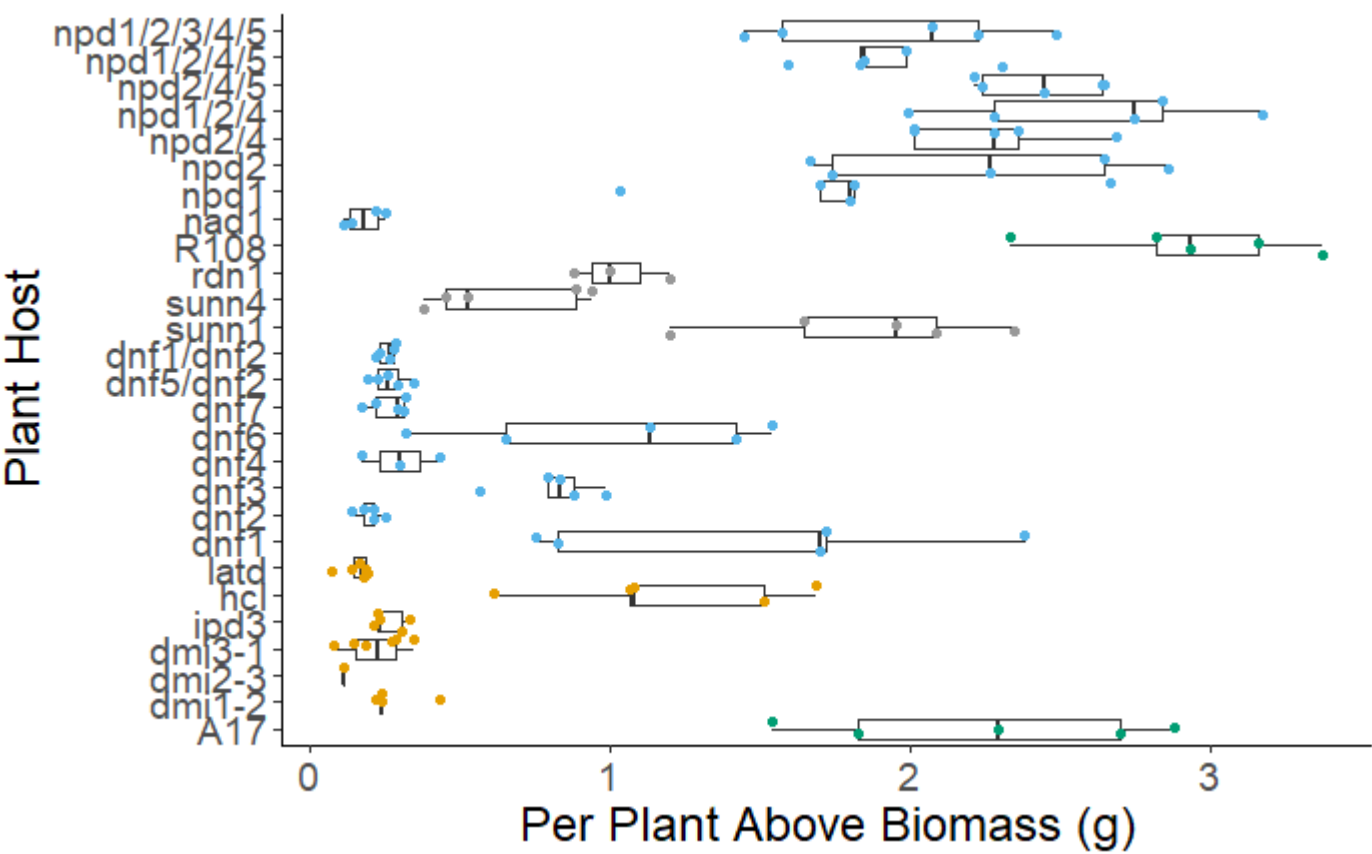
This plot depicts cfu per plant for each genotype.

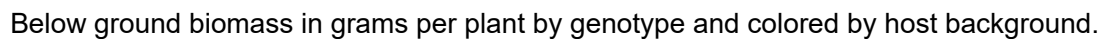


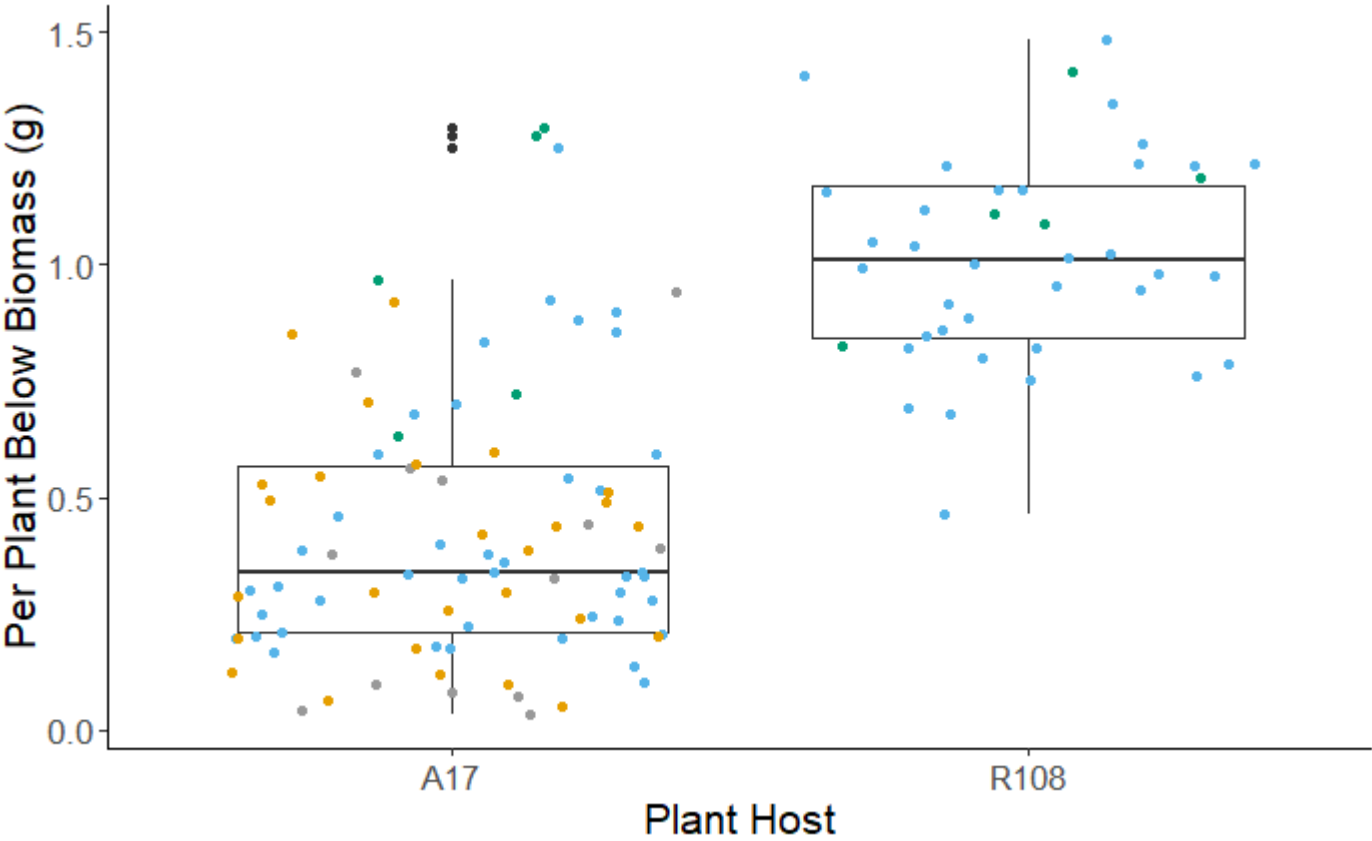
This plot depicts cfu per plant for each host background which could be Medicago truncatula A17 or R108.



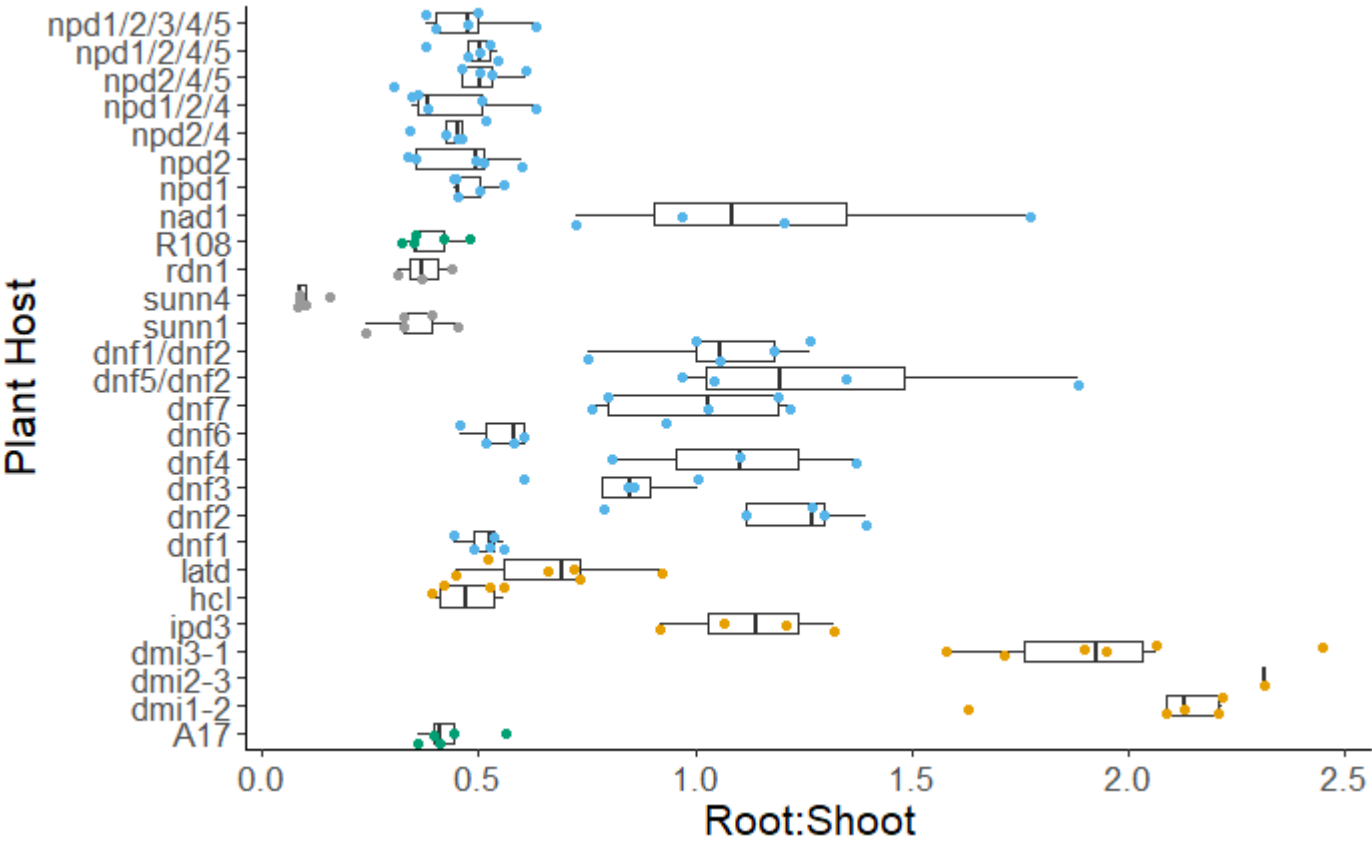
Above ground biomass in grams per plant by genotype and colored by host background.

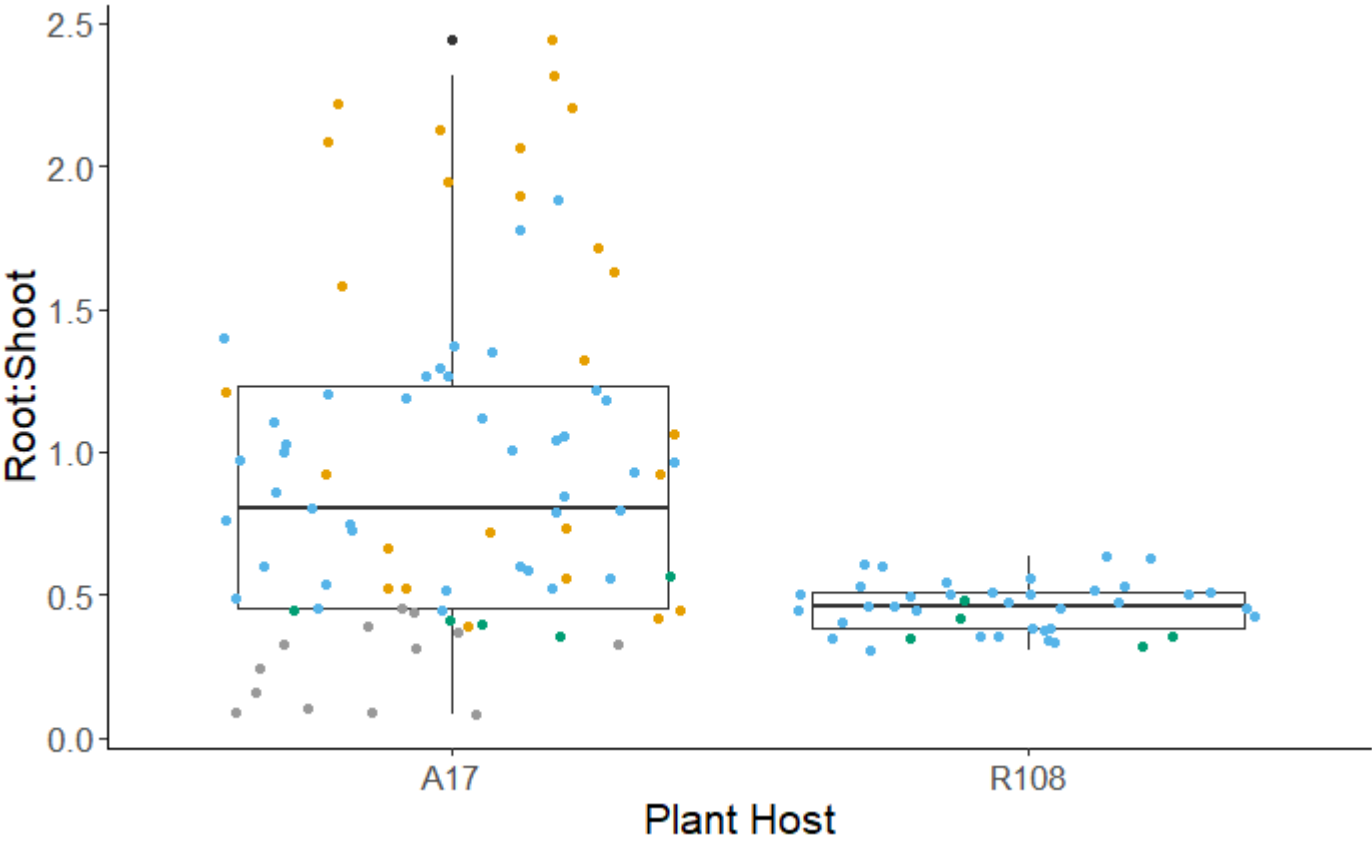






Root to Shoot ratio in grams per plant by genotype and colored by host background.





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```
#This chunk is for setting global options for all chunks
knitr::opts_knit$set(root.dir = '/GitHub')
knitr::opts_chunk$set(message = FALSE)

#Add a new chunk by clicking the *Insert Chunk* button on the toolbar or by pressing *Ctrl+Alt+I*.
```

#When you save the notebook, an HTML file containing the code and output will be saved alongside it (click the *Preview* button or press *Ctrl+Shift+K* to preview the HTML file).

#The preview shows you a rendered HTML copy of the contents of the editor. Consequently, unlike *Knit*, *Preview* does not run any R code chunks. Instead, the output of the chunk when it was last run in the editor is displayed.

#To display output in the plots pane Preferences>> OR Tools>>Global_Options>> RMarkdown>>uncheck "Show output inline...")

#Searchable R Markdown reference: <https://bookdown.org/yihui/rmarkdown-cookbook/>

#Code that may once again be useful

```
#Combining plots
#require(ggpubr)
#cfu_combo <- ggarrange(p_cfu_A17, p_cfu_R108, common.legend = TRUE)

#facet zoom
#facet_grid(. ~ background)
#facet_zoom(ylim = c(1000000, 10000000)) #require(ggforce))
```

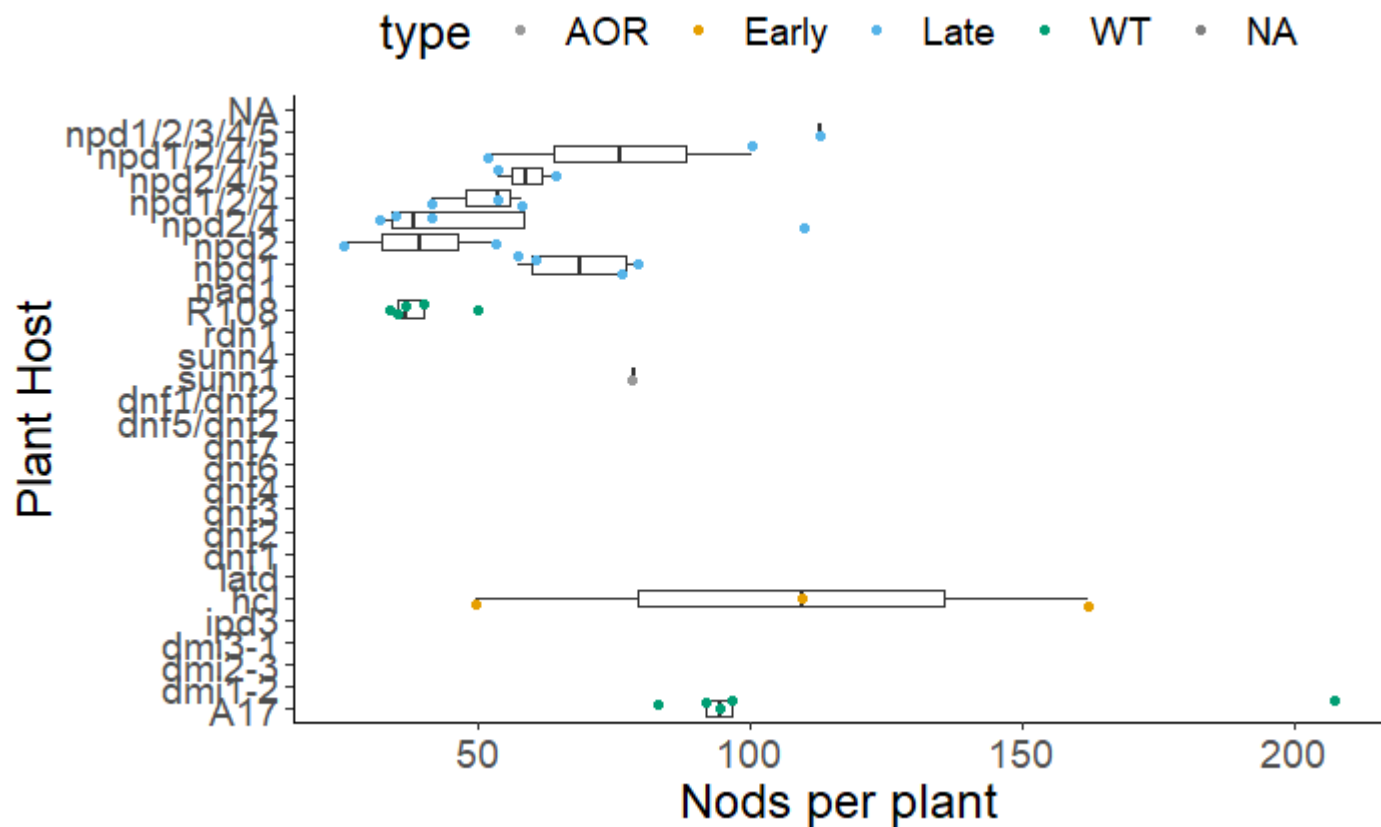
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```
nod_data <- read.table("../data/data_nod_img_measurements.txt", sep = "\t", header=TRUE)
#nod_data$genotype_id = as.factor(nod_data$genotype_id)
all_data <- all_data %>% full_join(nod_data, by="sample_id") %>% mutate(nod_cnt_plant = nod_count/num_plants, tot_area_plant = nod_total_area_cm2/num_plants )
```

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```
###mutation for count per plant and total area per plant

p_nod_cnt <-ggplot(all_data, aes(x=reorder(name,order), y=nod_cnt_plant)) +
  geom_boxplot(outlier.shape=NA) +
  geom_jitter(aes(x=name, y=nod_cnt_plant, color=type)) +
  coord_flip() +
  scale_color_manual(values=cbPalette) +
  labs(x="Plant Host",y="Nods per plant") +
  theme_classic() + theme(legend.position="top", text = element_text(size=18))
p_nod_cnt
```



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```
p_bg_nod_cnt <-ggplot(all_data, aes(x=background, y=nod_cnt_plant)) +
  geom_boxplot(aes(x=background, y=nod_cnt_plant)) +
  geom_jitter(aes(x=background, y=nod_cnt_plant, color=type)) +
  scale_color_manual(values=cbPalette) +
  scale_fill_manual(values=c("#D55E00", "#CC79A7")) +
  labs(x="Plant Host",y="Nods per plant")+
  theme_classic() + theme(legend.position="top", text = element_text(size=18))
p_bg_nod_cnt
```



p_tot_area



```
p_bg_tot_area <-ggplot(all_data, aes(x=background, y=tot_area_plant)) +
  geom_boxplot(aes(x=background, y=tot_area_plant)) +
  geom_jitter(aes(x=background, y=tot_area_plant, color=type)) +
  scale_color_manual(values=cbPalette) +
  scale_fill_manual(values=c("#D55E00", "#CC79A7")) +
  labs(x="Plant Host",y="Total Nod area per plant")+
  theme_classic() + theme(legend.position="top", text = element_text(size=18))
p_bg_tot_area
```

