NSFPGRP_HostMutant_C86Meliloti

Code **▼**

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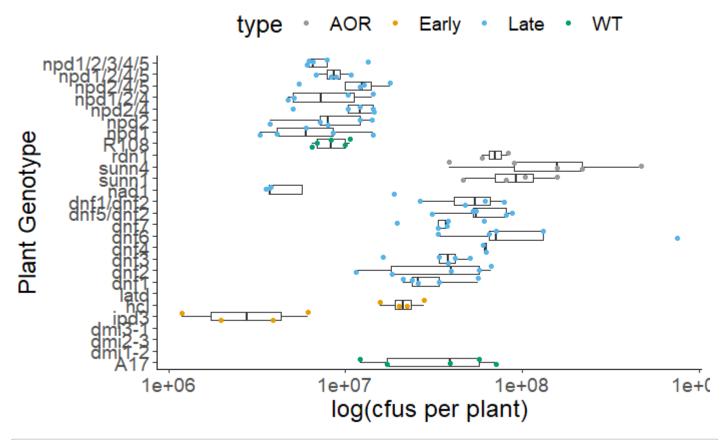
Analysis file for NSF Host Mutant C86 Ensifer meliloti select and resequence project.

Summary

Results for dilution plating of nodule homogenate.

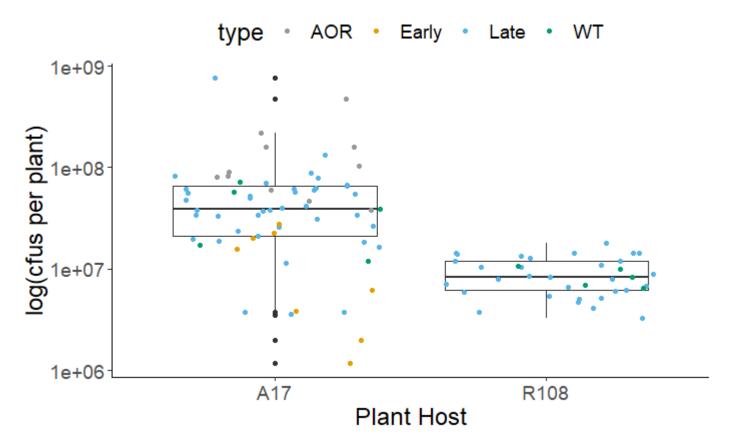
(1) Variation among backgrounds and genotypes. (2) Sunn1, Sunn4 are highly numerated with nodules. (3) A17 and R108 wild types show trend that A17 has higher rhizobial load than R108.

This plot depicts cfu per plant for each genotype.

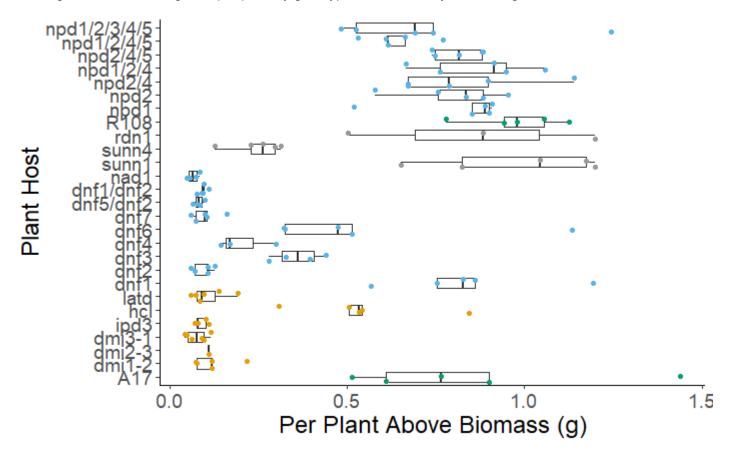


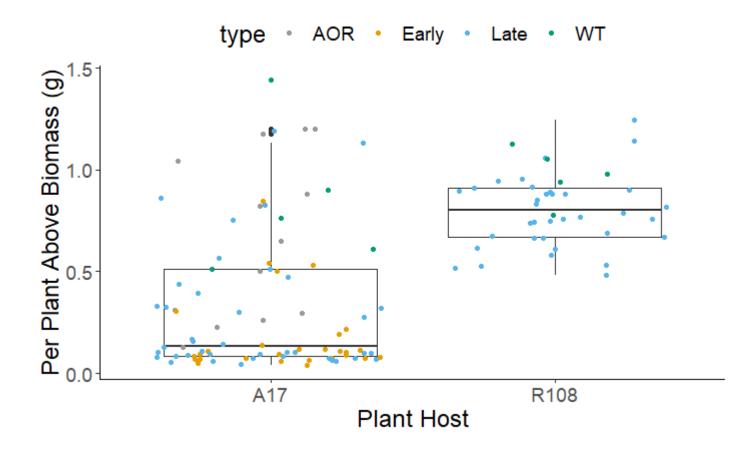
```
Df Sum Sq Mean Sq F value Pr(>F)
background 1 7.743e+16 7.743e+16 10.06 0.00201 **
Residuals 99 7.615e+17 7.692e+15
---
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
28 observations deleted due to missingness
function (x, which, ordered = FALSE, conf.level = 0.95, ...)
UseMethod("TukeyHSD")
<br/>
<
```

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

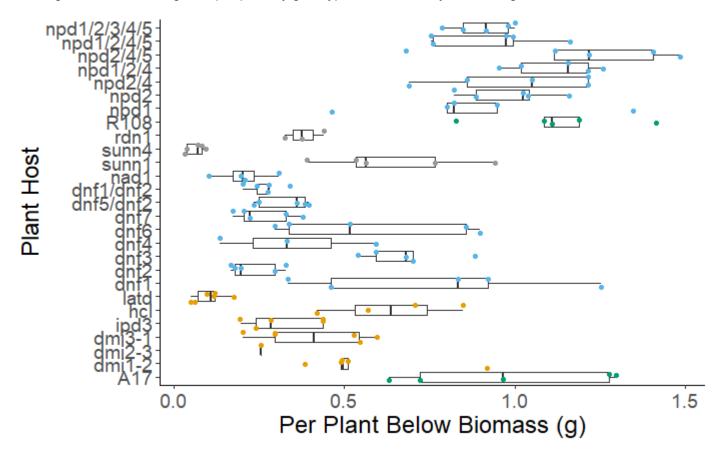


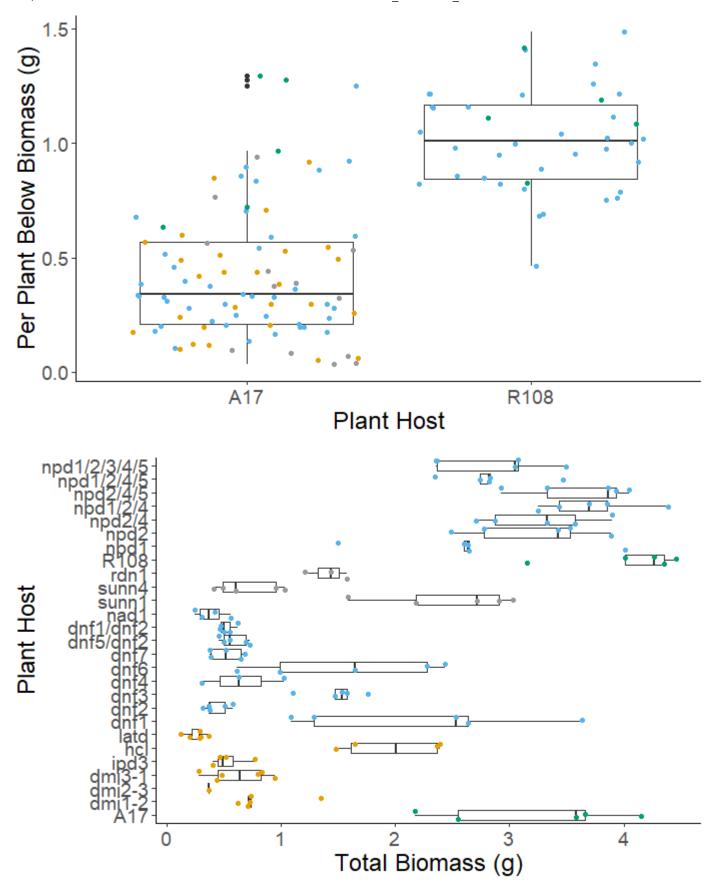
Above ground biomass in grams per plant by genotype and colored by host background.

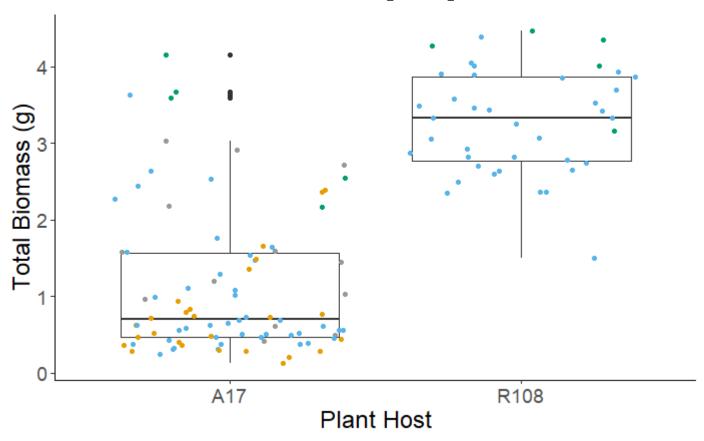




Below ground biomass in grams per plant by genotype and colored by host background.







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

