

# NSFPGRP\_HostMutant\_C86Meliloti

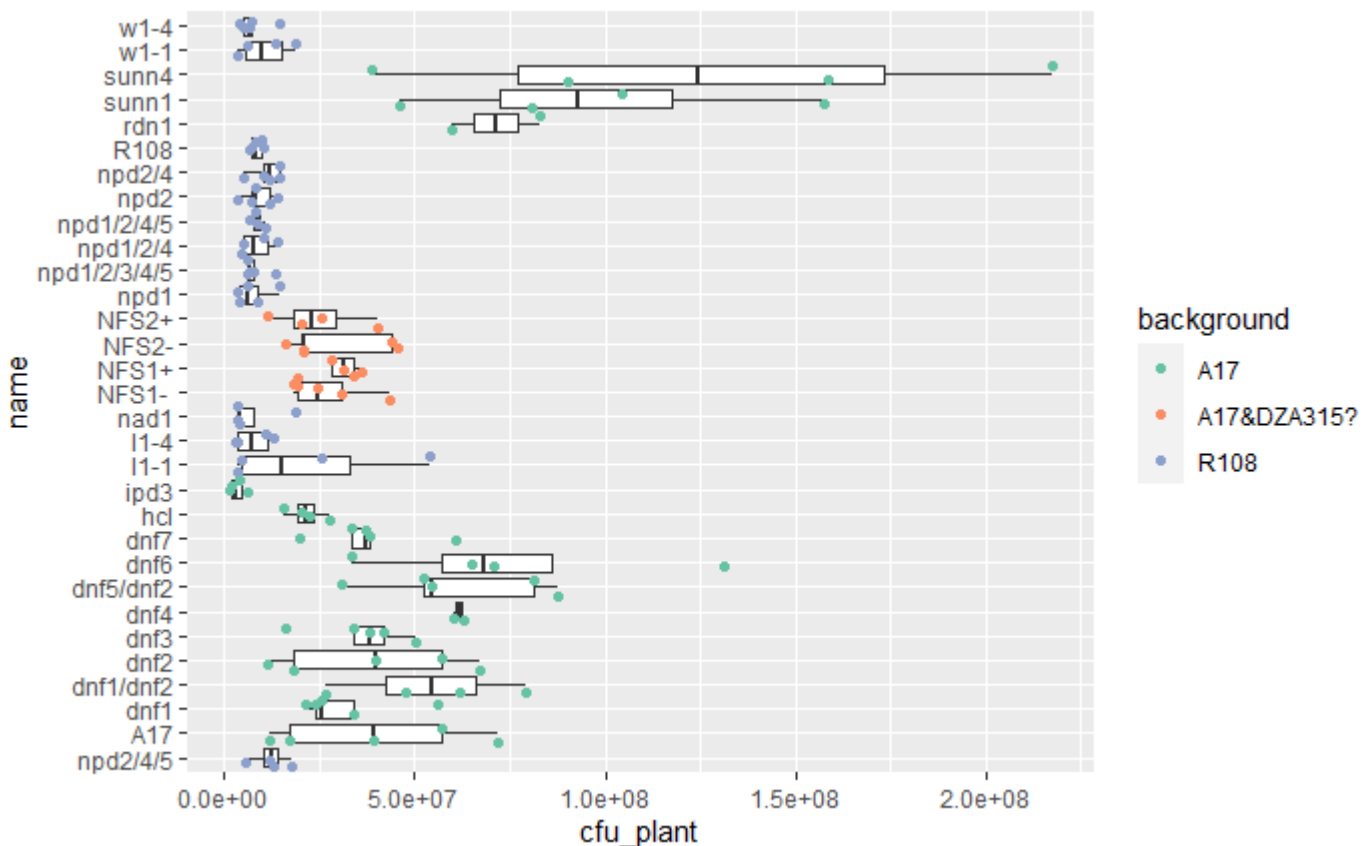
Code ▼

This file is the analysis of data gathered for the NSF Host Mutant C86 Ensifer meliloti select and resequence project.

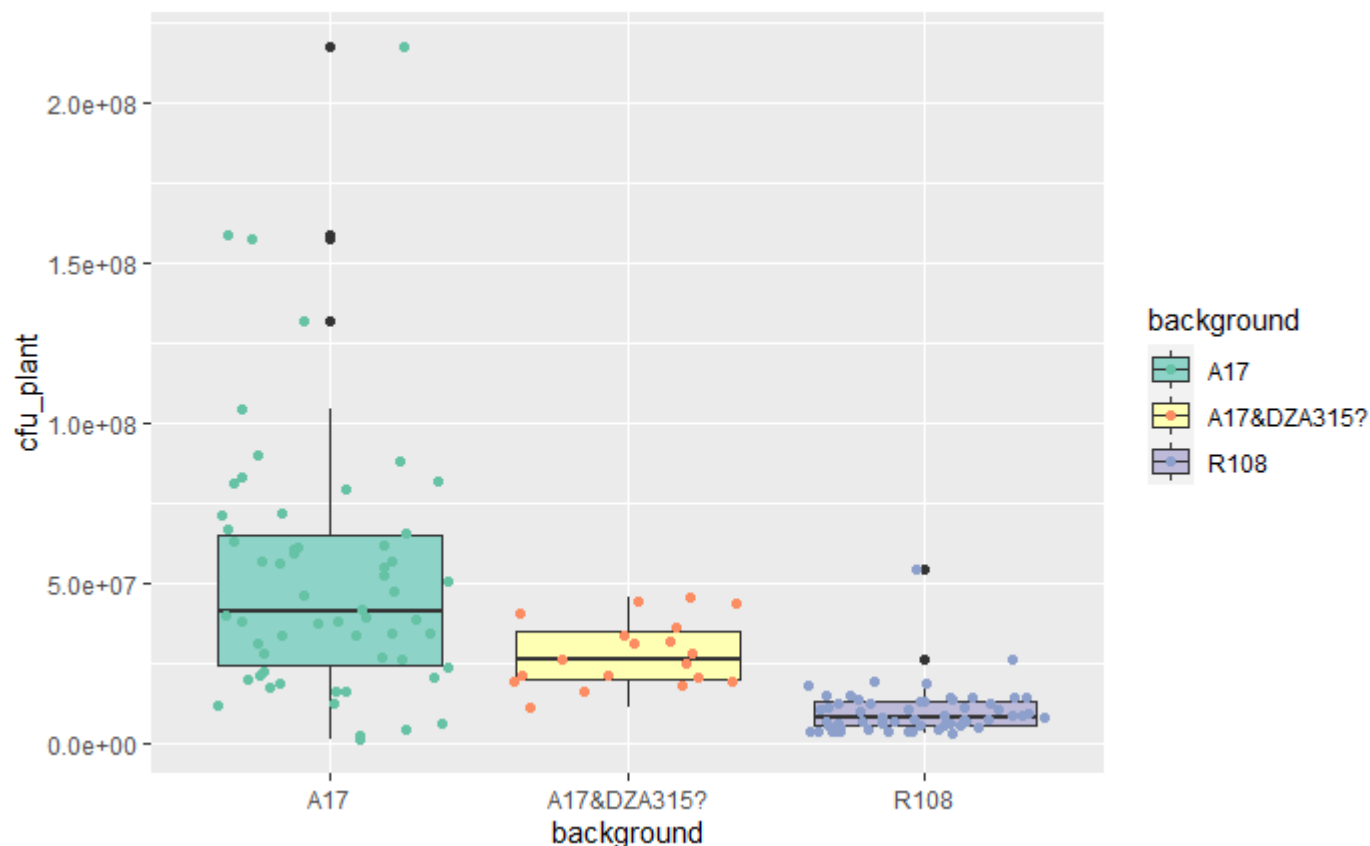
## Results for dilution plating of nodule homogenate.

(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.

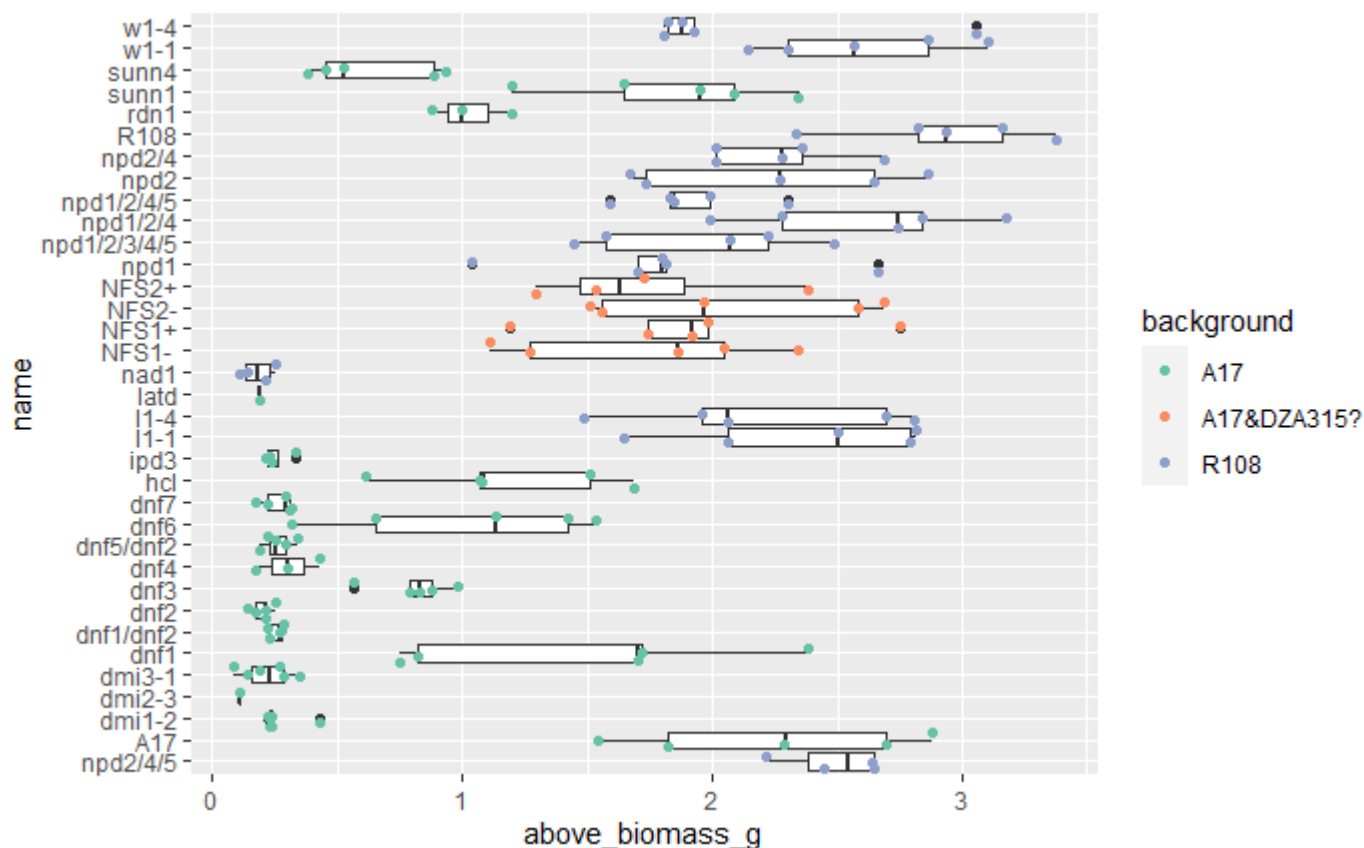
This plot depicts cfu per ml/plant for each genotype. Boxplot per genotype and point color host background.



This plot depicts cfu per ml/plant for each host background which could be *Medicago truncatula* A17 or R108 or A17 & DZA hybrid. This confirms what we seen in the last plot and also that... size does matter. That is generally even though A17 typically has smaller nodules than R108, A17 tends to have higher (and more variable) rhizobial presence. Liana called it! :)



Above ground biomass in grams per genotype colored by host background. At first glance it appears that there are host background differences in above ground biomass and within mutated versions of A17 (more so than R108). This is interesting bc it indicates the host mutation maybe indirectly responsible for reduced host performance by reducing symbiotic benefit.



Below ground biomass by genotype, colored by host background. A similar trend to above ground in that there seems to be host background differences in belowground biomass but definitely more variation... this could be attributed to loss of fine root hairs in the harvest and nodule picking processes, partly due to large quantities of substrate in some samples due to differences in cleaning effort.

