NSFPGRP_HostMutant_C86Meliloti

Code

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

Summary

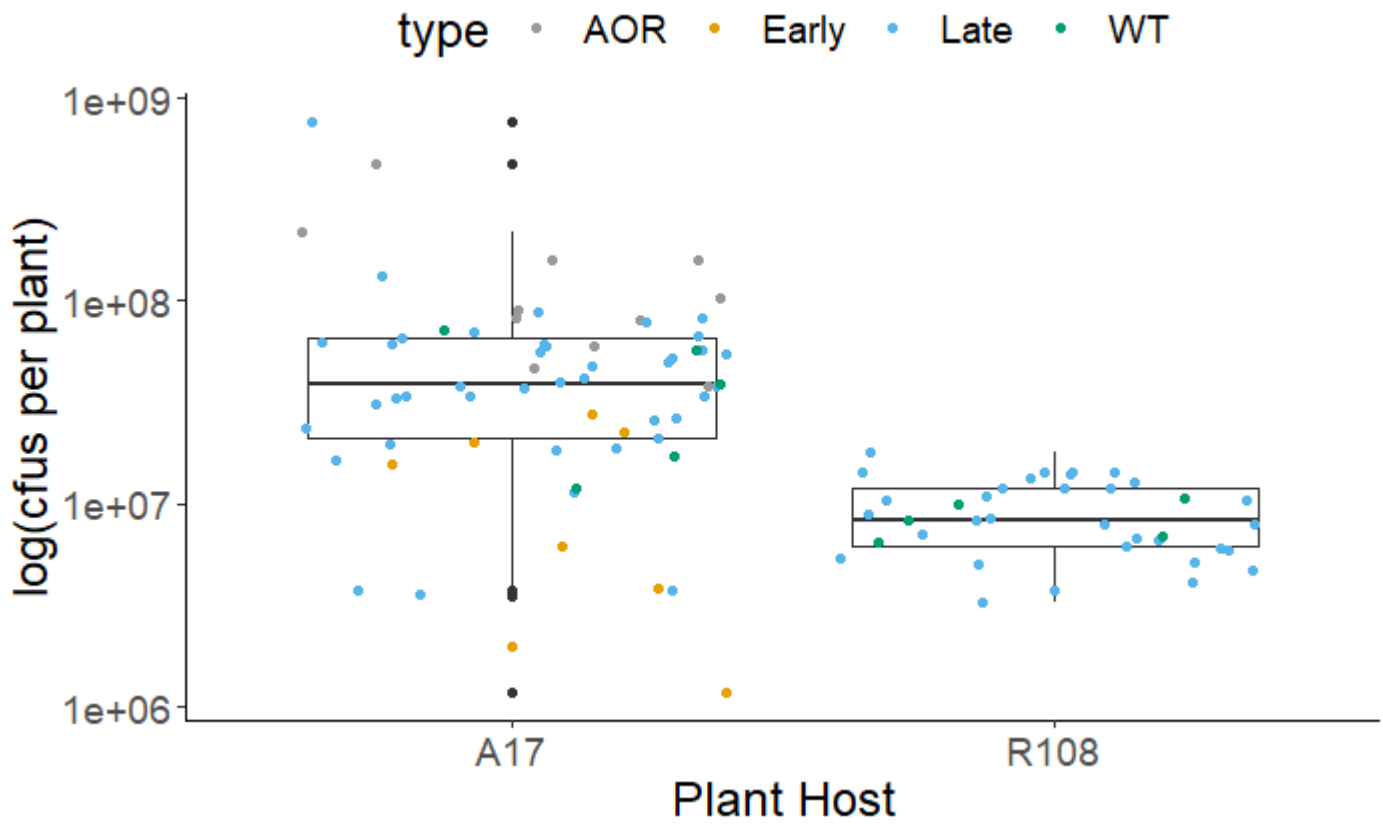
Results for dilution plating of nodule homogenate.
(1)Variation among backgrounds and genotypes. (2) Sunn1, Sunn4 are highly numerated with nodules. (3) A17 and R108 wild types show trend that A17 has higher rhizobial load than R108.

This plot depicts cfu per plant for each genotype.

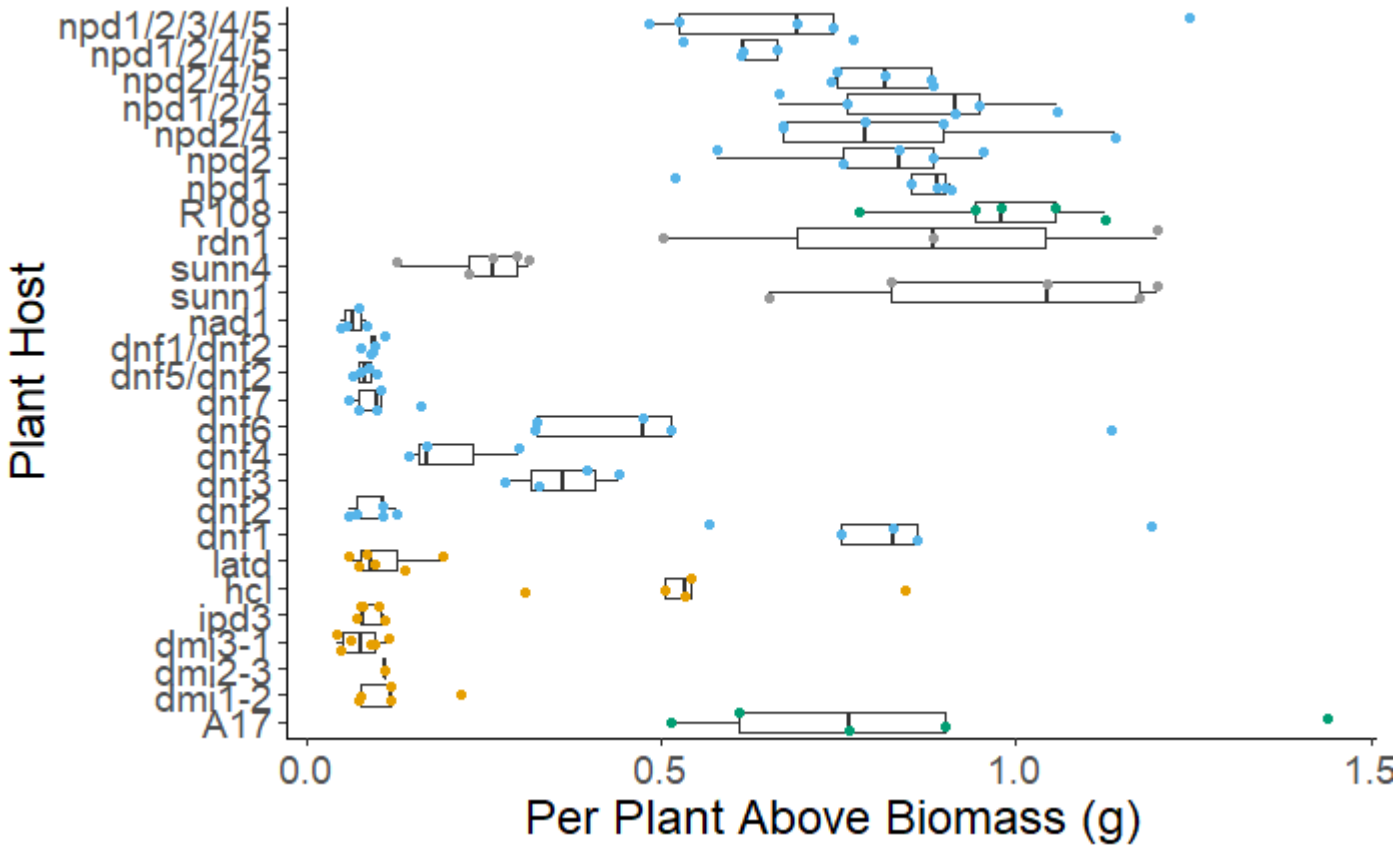
STATS ARE ORDERED BY: BACKGROUND; A17 TYPE THEN TUKEY; R108 TYPE (ONLY TWO wt & early so no tukey) ***

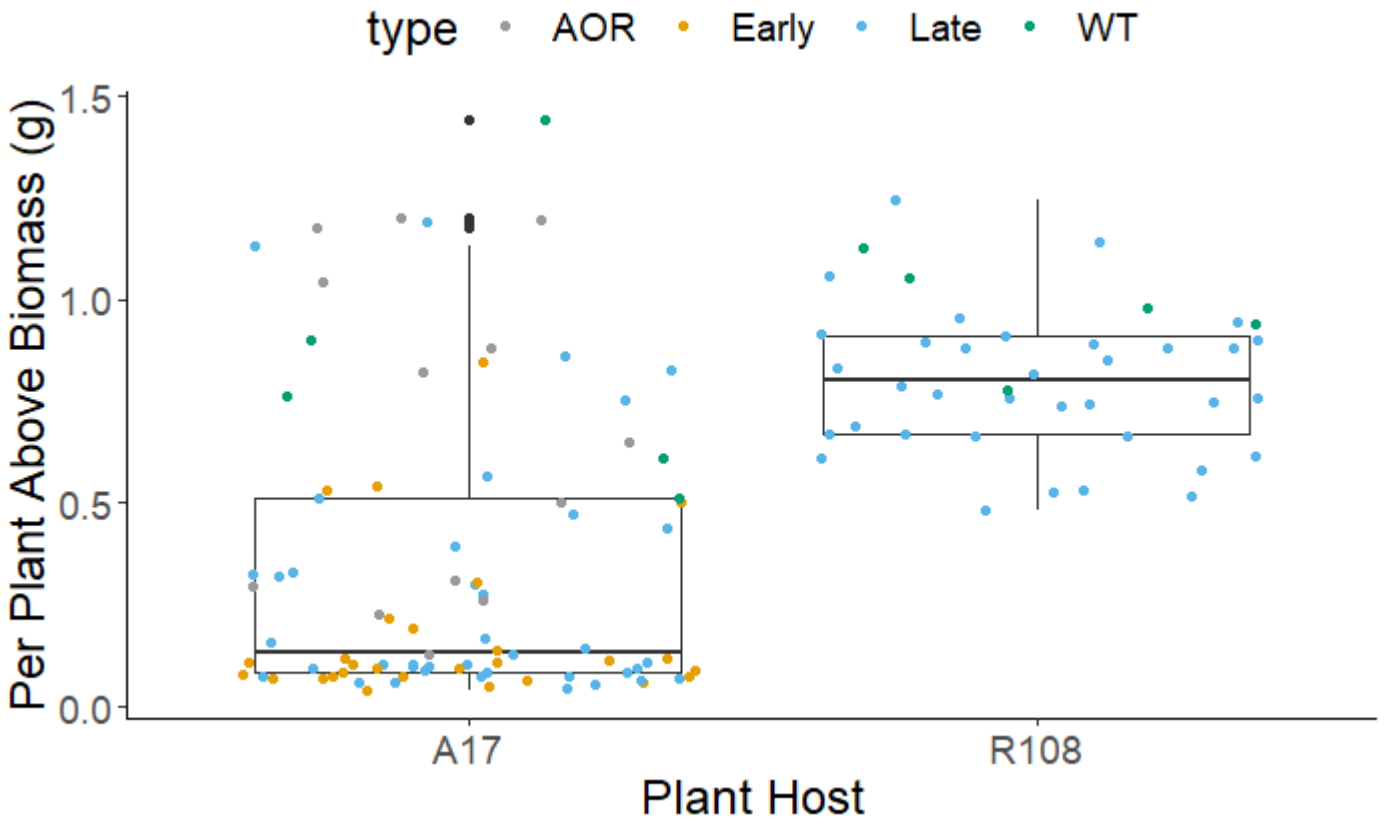
```
            Df    Sum Sq   Mean Sq F value Pr(>F)
type         1 2.604e+12 2.604e+12   0.187  0.668
Residuals   35 4.867e+14 1.391e+13
3 observations deleted due to missingness
```

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



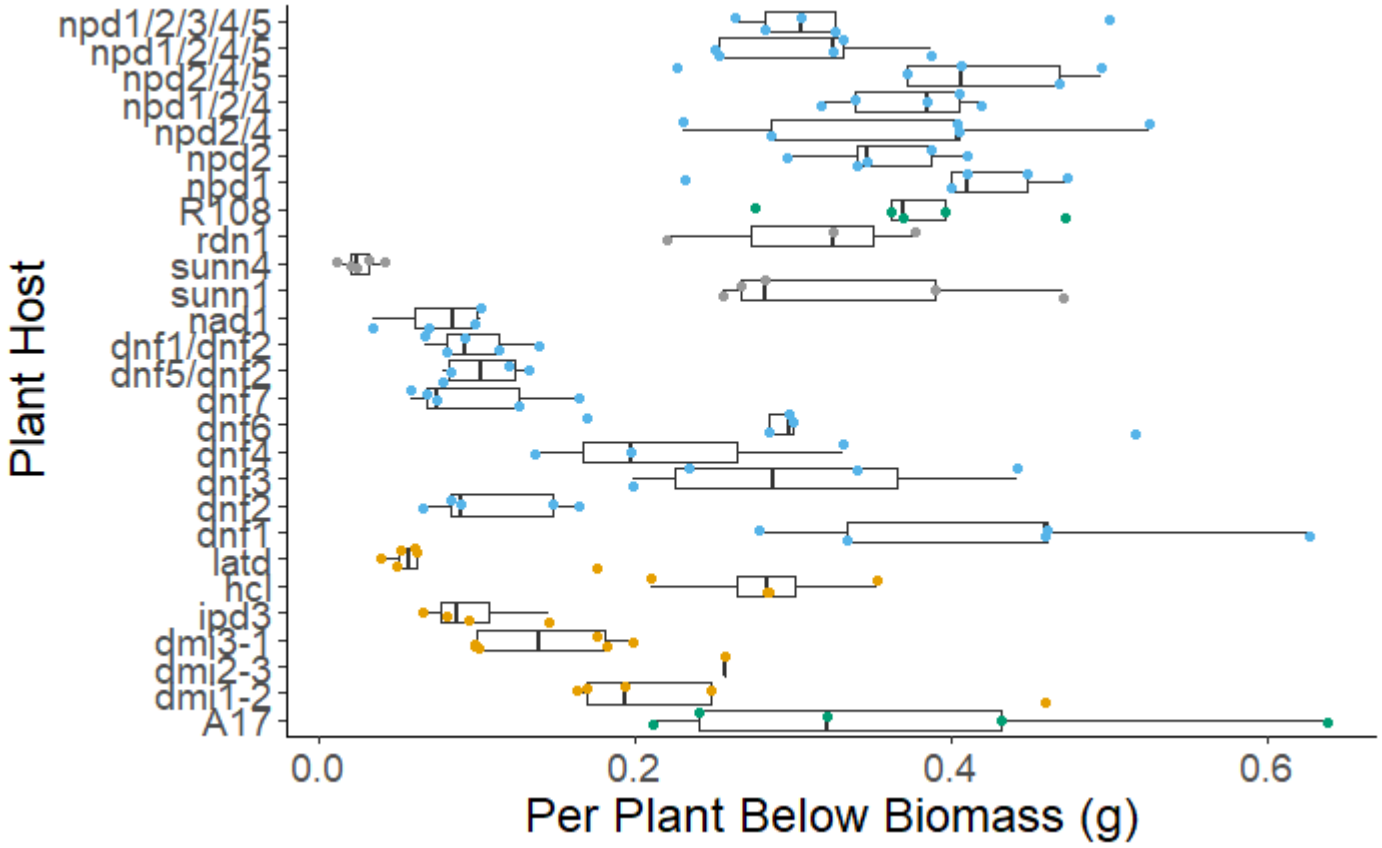
Above ground biomass in grams per plant by genotype and colored by host background.

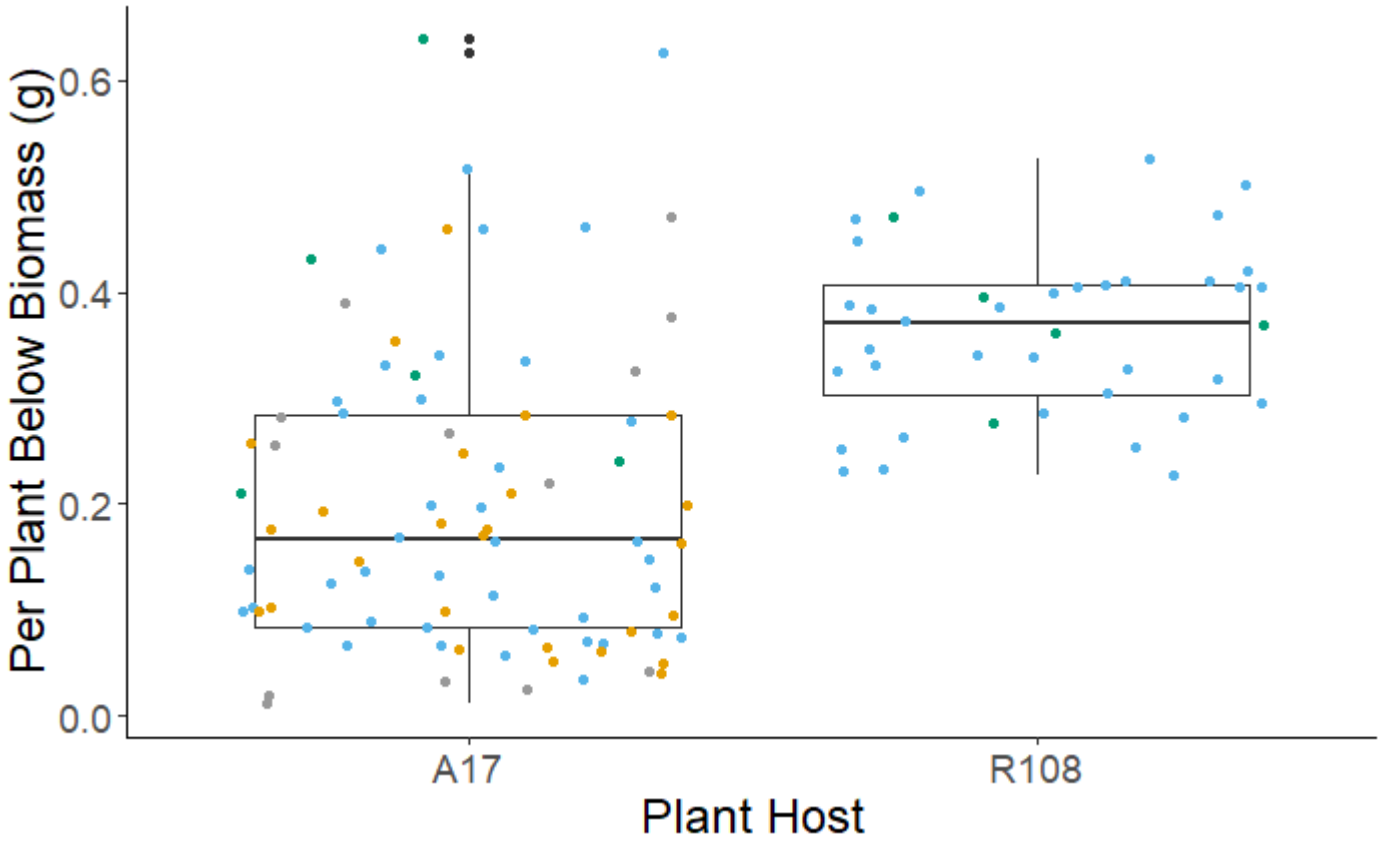

Plant Host
npd1/2/3/4/5
npd1/2/4/5
npd2/4/5
npd1/2/4
npd2/4
npd2
npd1
R108
rdn1
sunn4
sunn1
nad1
dnf1/dnf2
dnf5/dnf2
dnf7
dnf6
dnf4
dnf3
dnf2
dnf1
latd
hcl
ipd3
dmi3-1
dmi2-3
dmi1-2
A17
0.0
0.5
1.0
1.5
Per Plant Above Biomass (g)


type
AOR
Early
Late
WT
Per Plant Above Biomass (g)
1.5
1.0
0.5
0.0
A17
R108
Plant Host

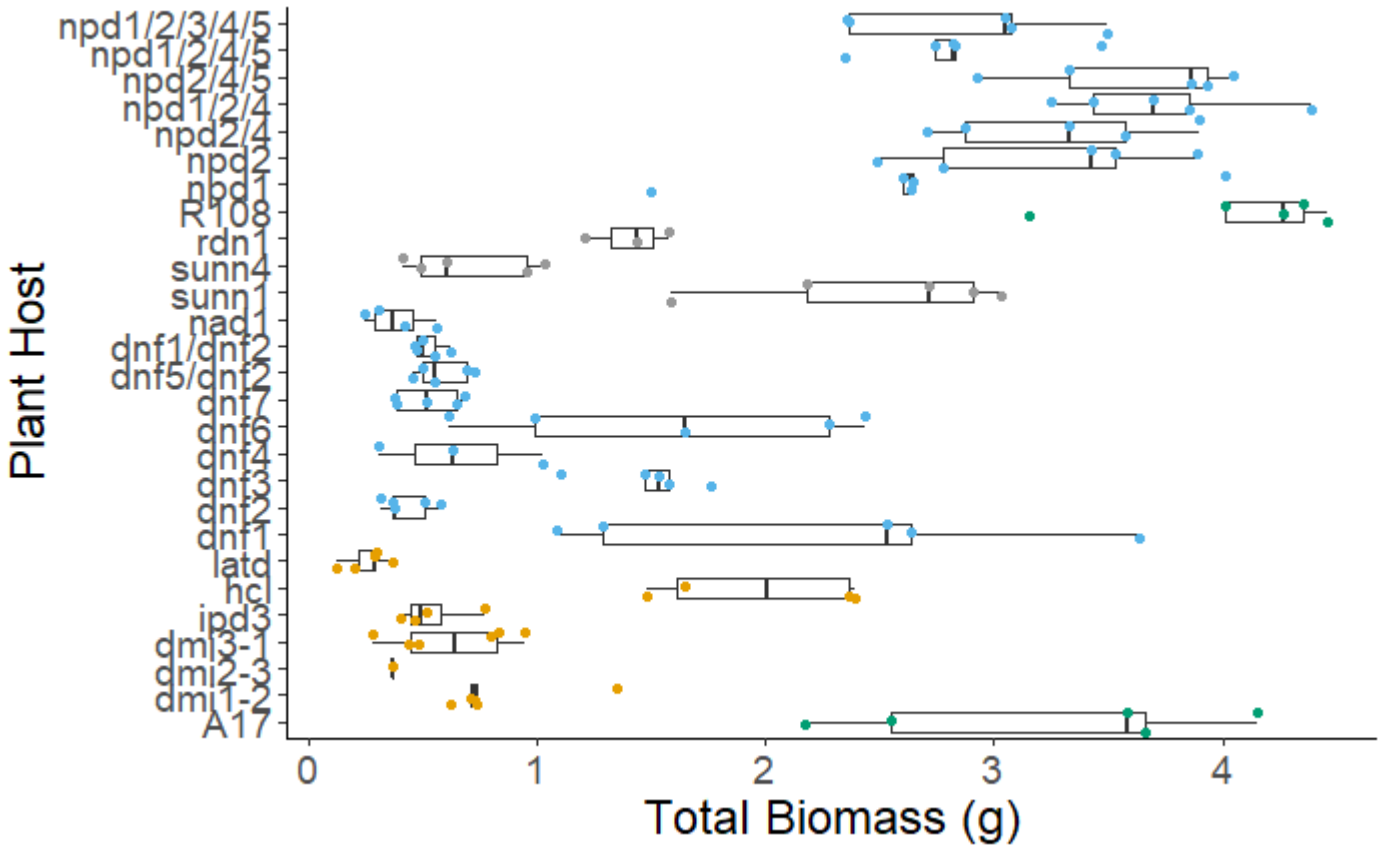
```
             Df Sum Sq Mean Sq F value   Pr(>F)
background    1  6.123   6.123   63.78 8.08e-13 ***
Residuals   124 11.903   0.096
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
3 observations deleted due to missingness
            Df Sum Sq Mean Sq F value   Pr(>F)
type         3  3.586   1.195    13.9 2.07e-07 ***
Residuals   82  7.052   0.086
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
3 observations deleted due to missingness
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = above_plant ~ type, data = filter(all_data, background == "A17"))

$type
                  diff         lwr        upr     p adj
Early-AOR  -0.49122894 -0.74934011 -0.2331178 0.0000195
Late-AOR   -0.39336346 -0.63889191 -0.1478350 0.0003845
WT-AOR      0.17636154 -0.22834958  0.5810727 0.6642557
Late-Early  0.09786548 -0.09163531  0.2873663 0.5314077
WT-Early    0.66759048  0.29420406  1.0409769 0.0000631
WT-Late     0.56972500  0.20492333  0.9345267 0.0005603

            Df Sum Sq Mean Sq F value Pr(>F)
type         1 0.1562 0.15615    5.35 0.0262 *
Residuals   38 1.1091 0.02919
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

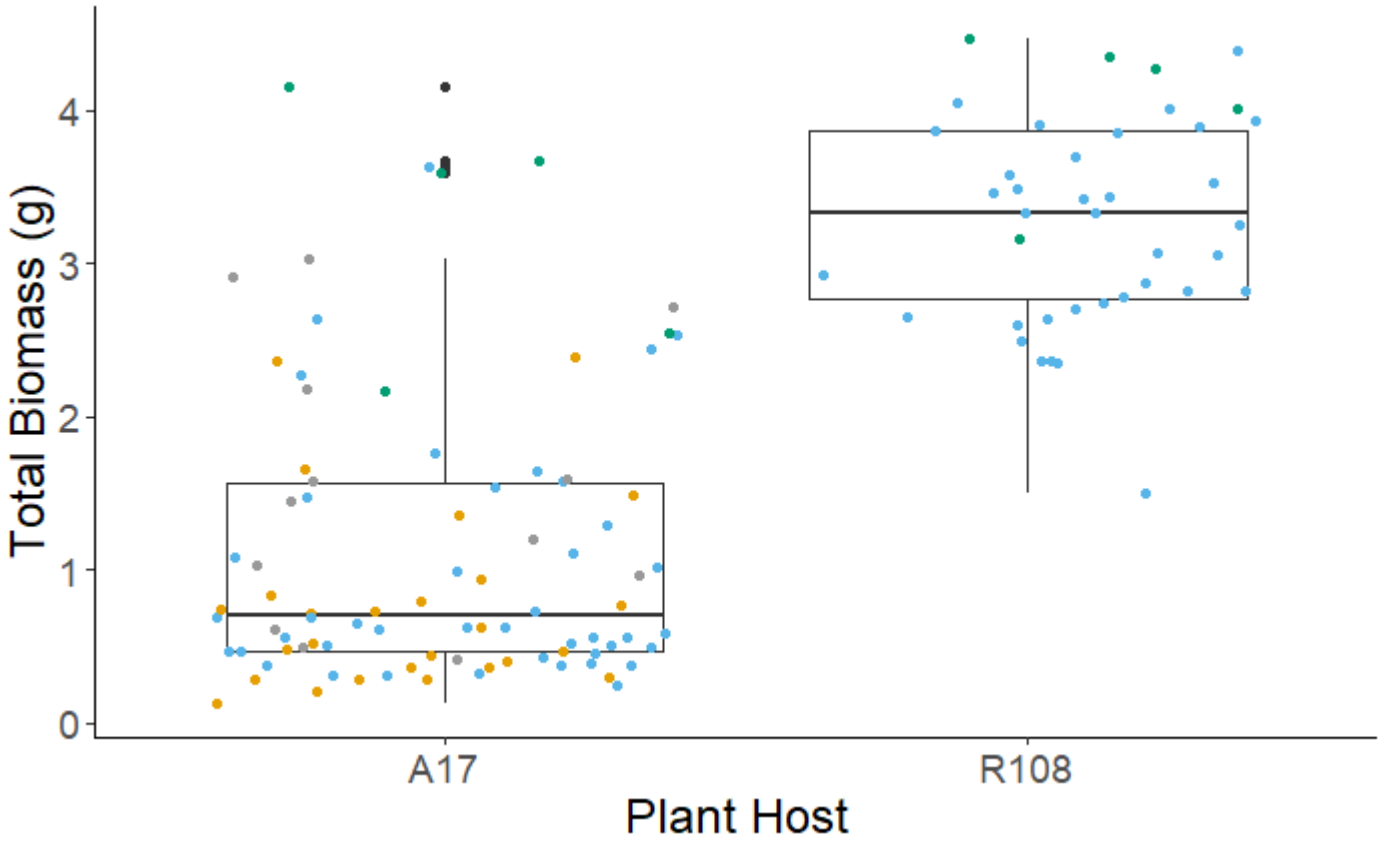
Below ground biomass in grams per plant by genotype and colored by host background.


Plant Host
npd1/2/3/4/5
npd1/2/4/5
npd2/4/5
npd1/2/4
npd2/4
npd2
npd1
R108
rdn1
sunn4
sunn1
nad1
dnf1/dnf2
dnf5/dnf2
dnf7
dnf6
dnf4
dnf3
dnf2
dnf1
latd
hcl
ipd3
dmi3-1
dmi2-3
dmi1-2
A17
0.0
0.2
0.4
0.6
Per Plant Below Biomass (g)


Per Plant Below Biomass (g)
0.0
0.2
0.4
0.6
A17
R108
Plant Host

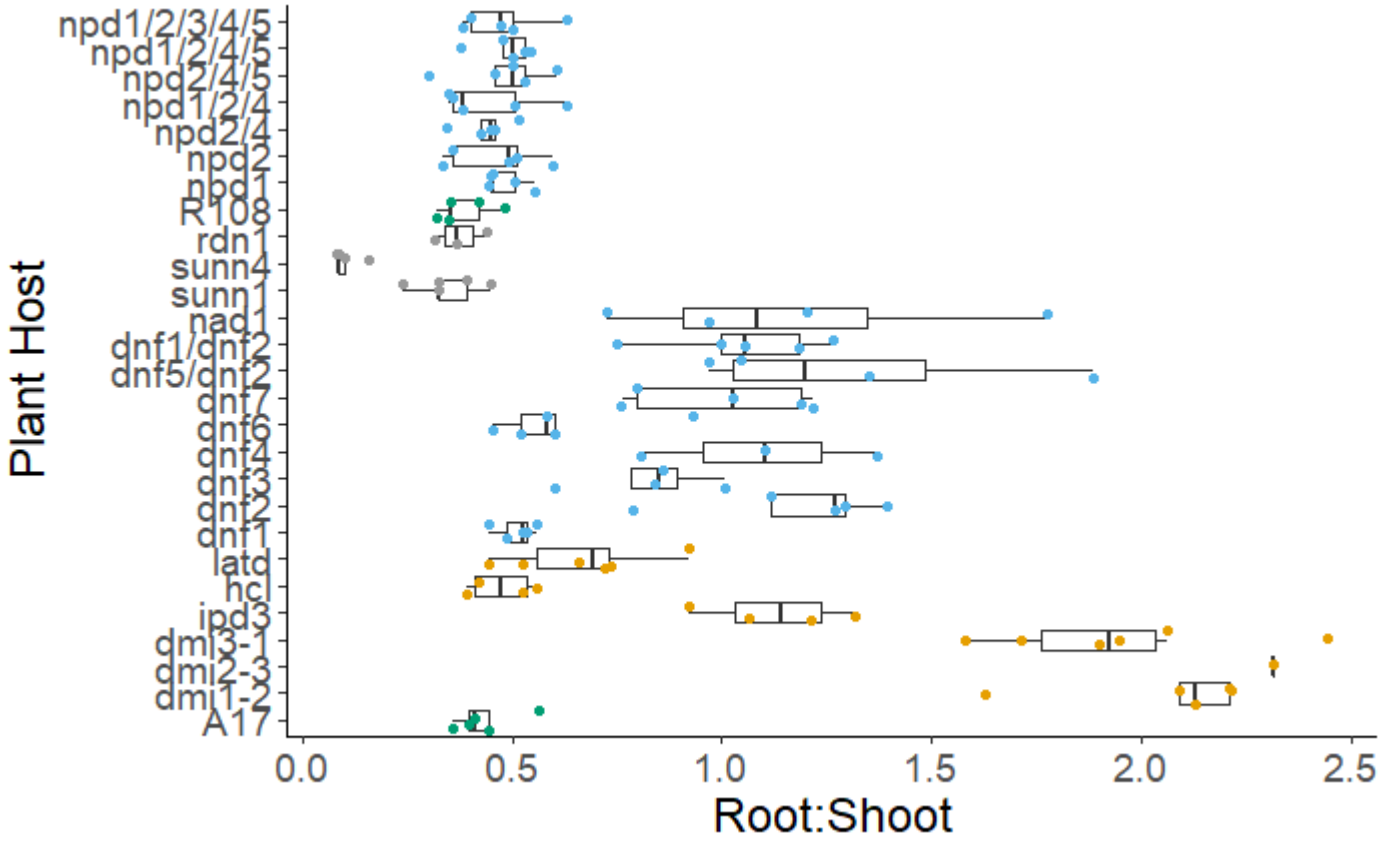
```
             Df Sum Sq Mean Sq F value   Pr(>F)
background    1 0.7302  0.7302   45.29 5.88e-10 ***
Residuals   122 1.9671  0.0161
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
5 observations deleted due to missingness
            Df Sum Sq Mean Sq F value Pr(>F)
type         3 0.1747 0.05823   3.014 0.0348 *
Residuals   80 1.5453 0.01932
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
5 observations deleted due to missingness
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = below_plant ~ type, data = filter(all_data, background == "A17"))

$type
                  diff          lwr        upr     p adj
Early-AOR  -0.04336538 -0.167236787 0.08050602 0.7950055
Late-AOR   -0.01237340 -0.128794944 0.10404815 0.9923714
WT-AOR      0.15983077 -0.032069982 0.35173152 0.1361340
Late-Early  0.03099199 -0.060873503 0.12285748 0.8125349
WT-Early    0.20319615  0.025119793 0.38127251 0.0188211
WT-Late     0.17220417 -0.000772833 0.34518117 0.0514742

            Df  Sum Sq  Mean Sq F value Pr(>F)
type         1 0.00079 0.000792   0.122  0.729
Residuals   38 0.24638 0.006484
```

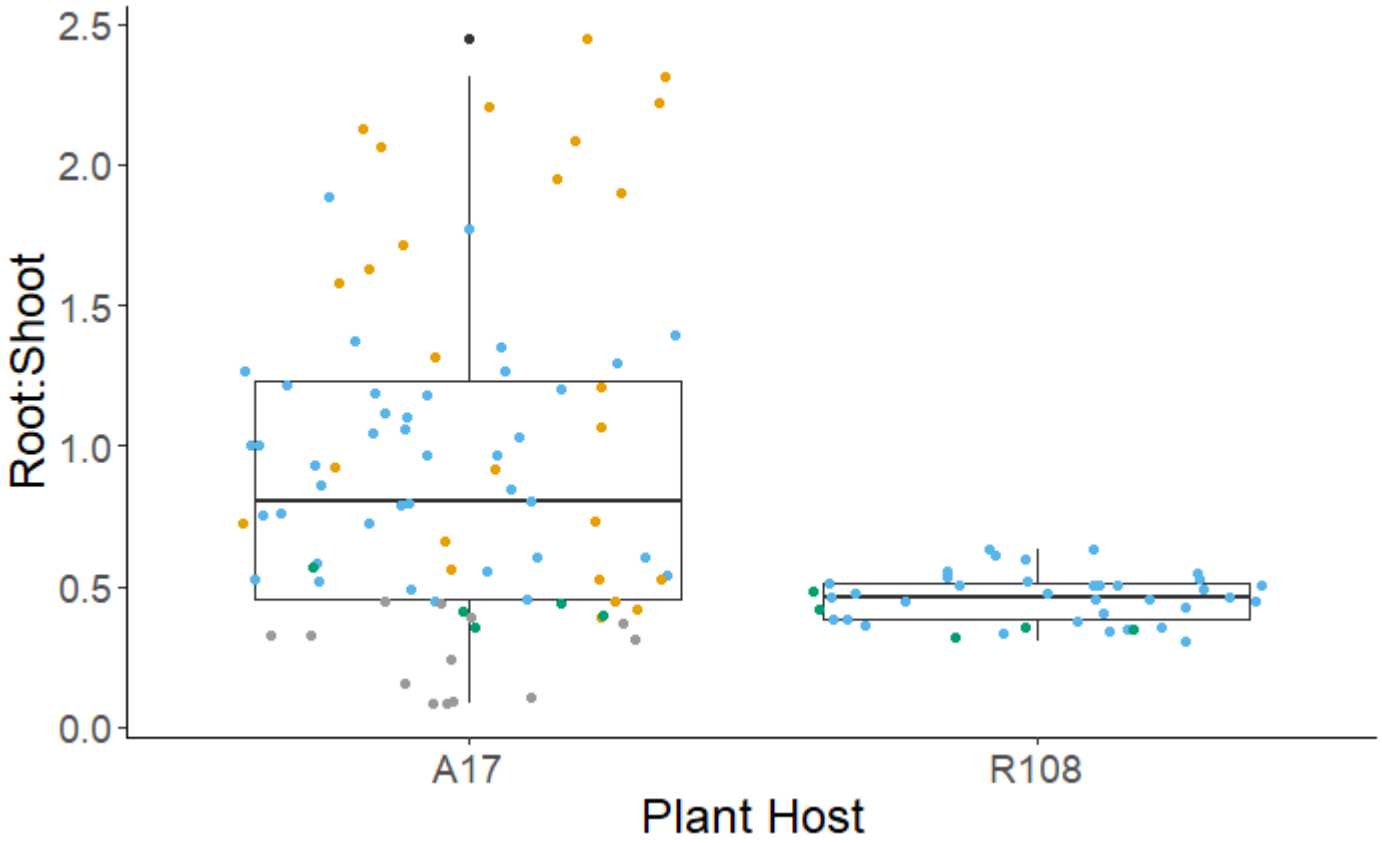

Plant Host
npd1/2/3/4/5
npd1/2/4/5
npd2/4/5
npd1/2/4
npd2/4
npd2
npd1
R108
rdn1
sunn4
sunn1
nad1
dnf1/dnf2
dnf5/dnf2
dnf7
dnf6
dnf4
dnf3
dnf2
dnf1
latd
hcl
ipd3
dmi3-1
dmi2-3
dmi1-2
A17
0
1
2
3
4
Total Biomass (g)


Total Biomass (g)
0
1
2
3
4
A17
R108
Plant Host

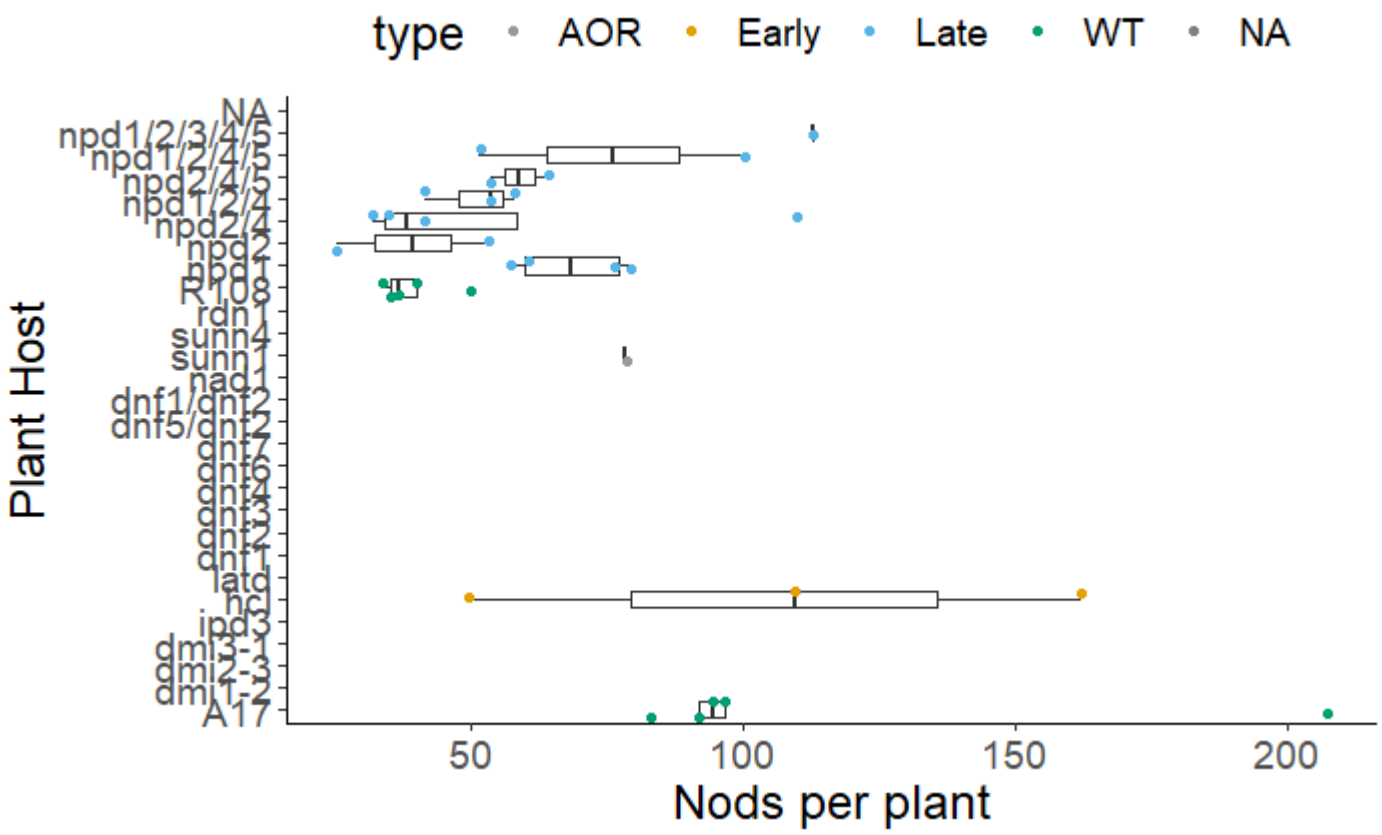
```
            Df Sum Sq Mean Sq F value Pr(>F)
background    1 127.53  127.53   168.8 <2e-16 ***
Residuals   124  93.67    0.76
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
3 observations deleted due to missingness
            Df Sum Sq Mean Sq F value   Pr(>F)
type         3  28.87   9.622   16.87 1.26e-08 ***
Residuals   82  46.76   0.570
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
3 observations deleted due to missingness
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = tot_biomass ~ type, data = filter(all_data, background == "A17"))

$type
                 diff        lwr        upr     p adj
Early-AOR  -0.7838462 -1.4565765 -0.1111158 0.0157253
Late-AOR   -0.5873681 -1.2159359  0.0411996 0.0756772
WT-AOR      1.6756462  0.6334568  2.7178355 0.0003644
Late-Early  0.1964780 -0.2977305  0.6906865 0.7249832
WT-Early    2.4594923  1.4923815  3.4266031 0.0000000
WT-Late     2.2630143  1.3260860  3.1999425 0.0000001

            Df Sum Sq Mean Sq F value  Pr(>F)
type         1  3.344   3.344   8.649 0.00555 **
Residuals   38 14.692   0.387
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

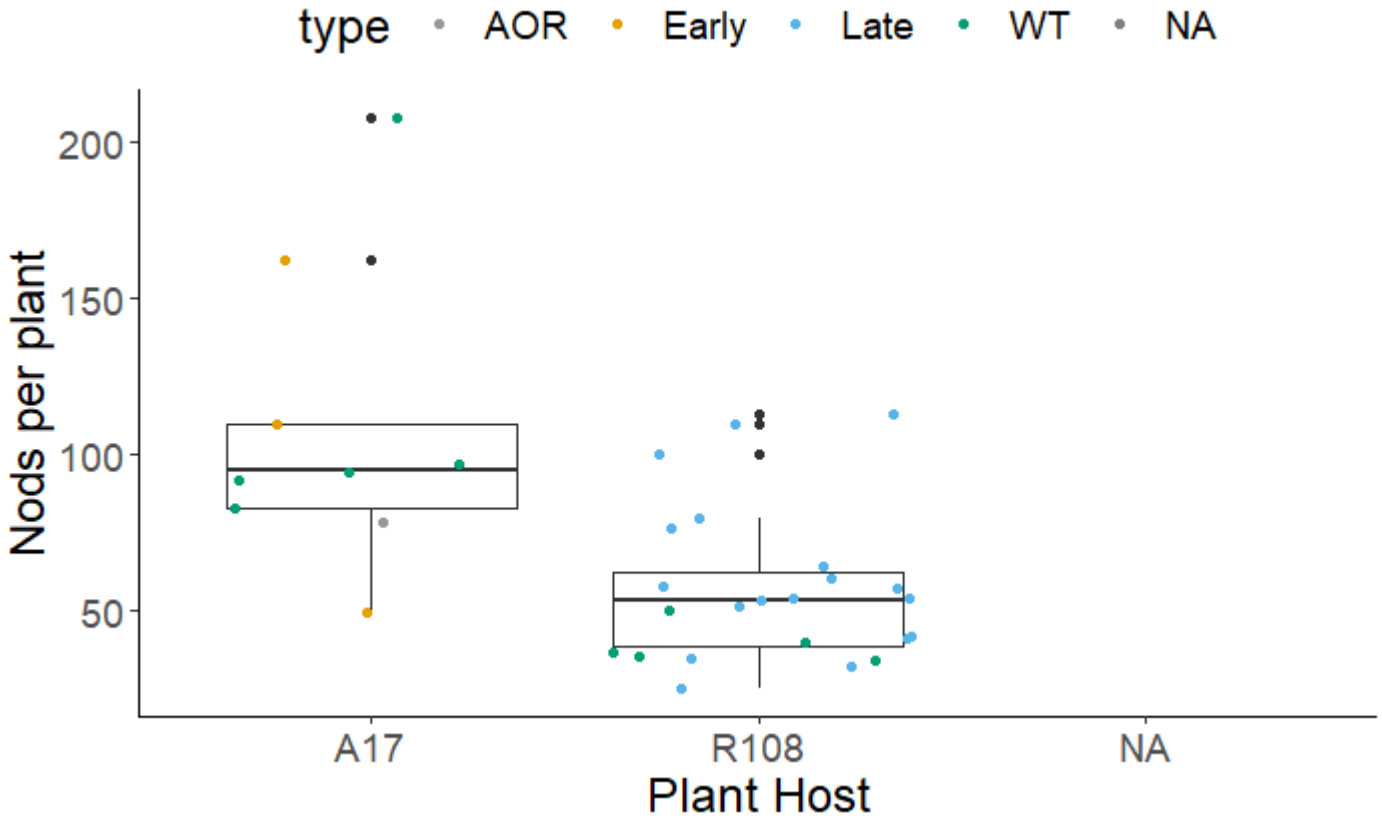
Root to shoot ratio in grams per plant by genotype and colored by host background.


Plant Host
npd1/2/3/4/5
npd1/2/4/5
npd2/4/5
npd1/2/4
npd2/4
npd2
npd1
R108
rdn1
sunn4
sunn1
nad1
dnf1/dnf2
dnf5/dnf2
dnf7
dnf6
dnf4
dnf3
dnf2
dnf1
latd
hcl
ipd3
dmi3-1
dmi2-3
dmi1-2
A17
0.0
0.5
1.0
1.5
2.0
2.5
Root:Shoot

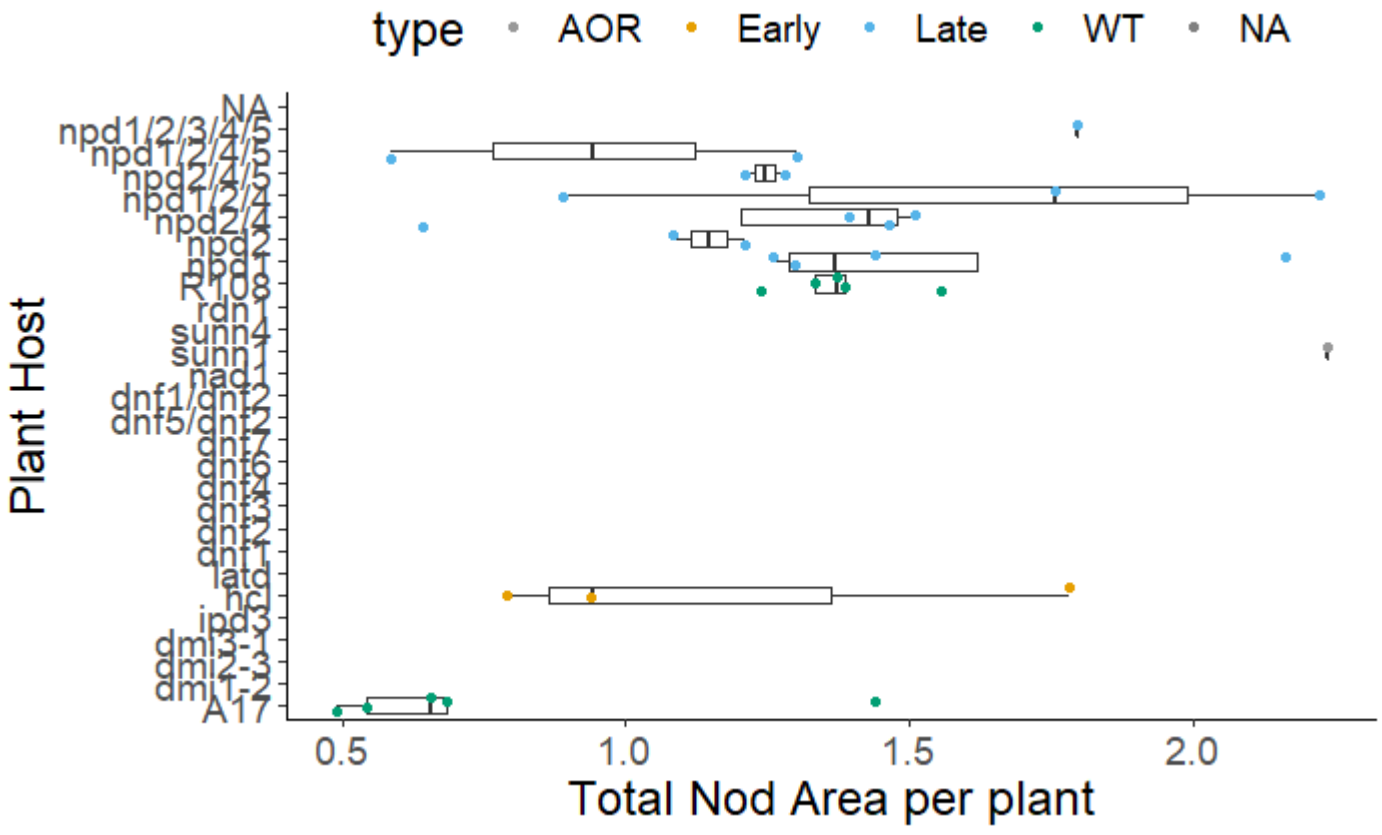

Root:Shoot
2.5
2.0
1.5
1.0
0.5
0.0
A17
R108
Plant Host

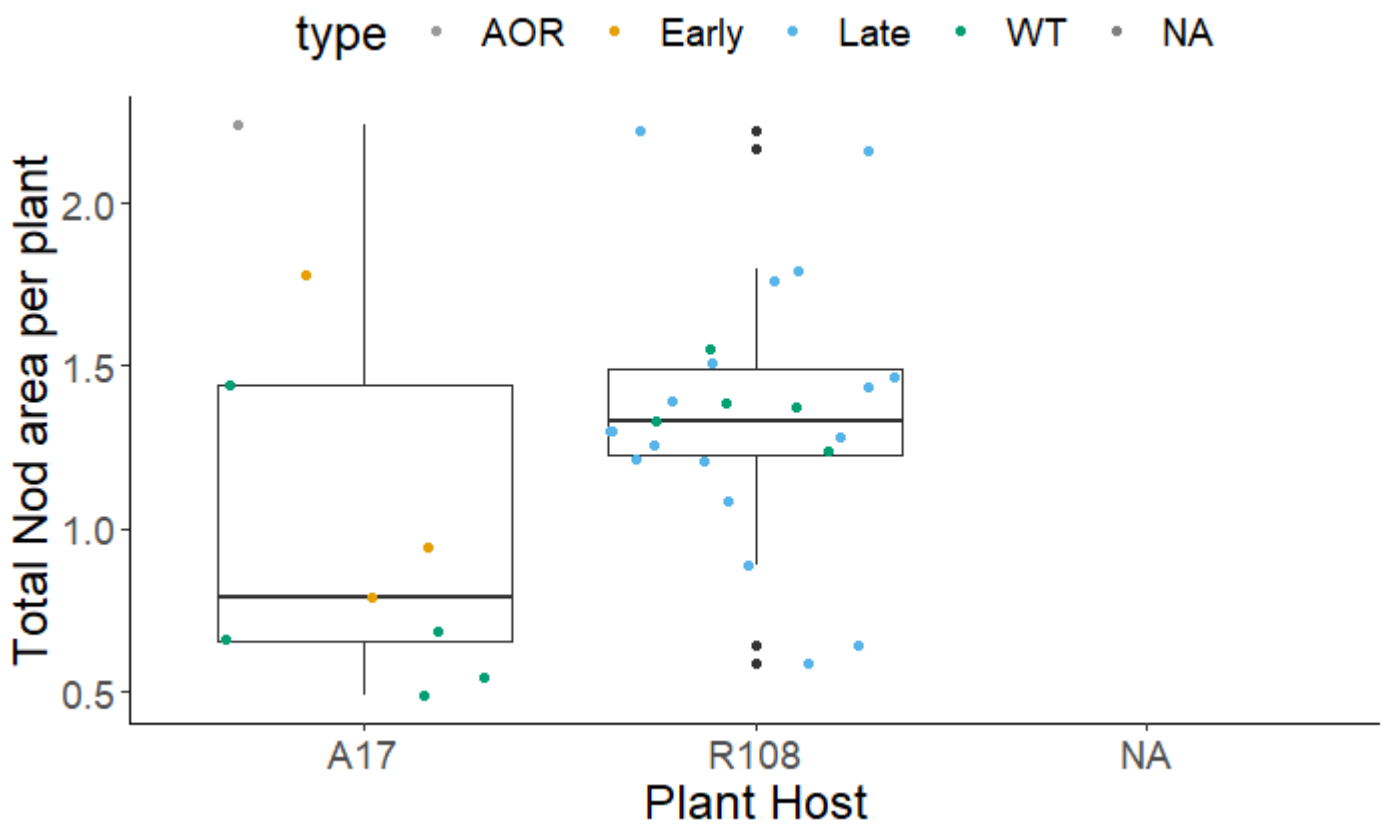
```
             Df Sum Sq Mean Sq F value   Pr(>F)
background    1  6.174   6.174   25.86 1.34e-06 ***
Residuals   122 29.124   0.239
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
5 observations deleted due to missingness
            Df Sum Sq Mean Sq F value  Pr(>F)
type         3  11.33   3.776   17.26 9.8e-09 ***
Residuals   80  17.50   0.219
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
5 observations deleted due to missingness
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = root_shoot ~ type, data = filter(all_data, background == "A17"))

$type
                 diff        lwr         upr     p adj
Early-AOR   1.0737502  0.6569099  1.49059059 0.0000000
Late-AOR    0.6975030  0.3057322  1.08927380 0.0000694
WT-AOR      0.1750090 -0.4707573  0.82077533 0.8924236
Late-Early -0.3762472 -0.6853843 -0.06711015 0.0106250
WT-Early   -0.8987412 -1.4979870 -0.29949543 0.0009953
WT-Late    -0.5224940 -1.1045799  0.05959192 0.0943413

            Df  Sum Sq  Mean Sq F value Pr(>F)
type         1 0.02872 0.028717   4.053 0.0512 .
Residuals   38 0.26925 0.007086
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```


type
AOR
Early
Late
WT
NA
Plant Host
NA
npd1/2/3/4/5
npd1/2/4/5
npd2/4/5
npd1/2/4
npd2/4
npd2
npd1
R108
rdn1
sunn4
sunn1
nad1
dnf1/dnf2
dnf5/dnf7
dnf7
dnf6
dnf4
dnf3
dnf2
dnf1
latd
nc
ipd3
dmi3-1
dmi2-3
dmi1-2
A17
50
100
150
200
Nods per plant

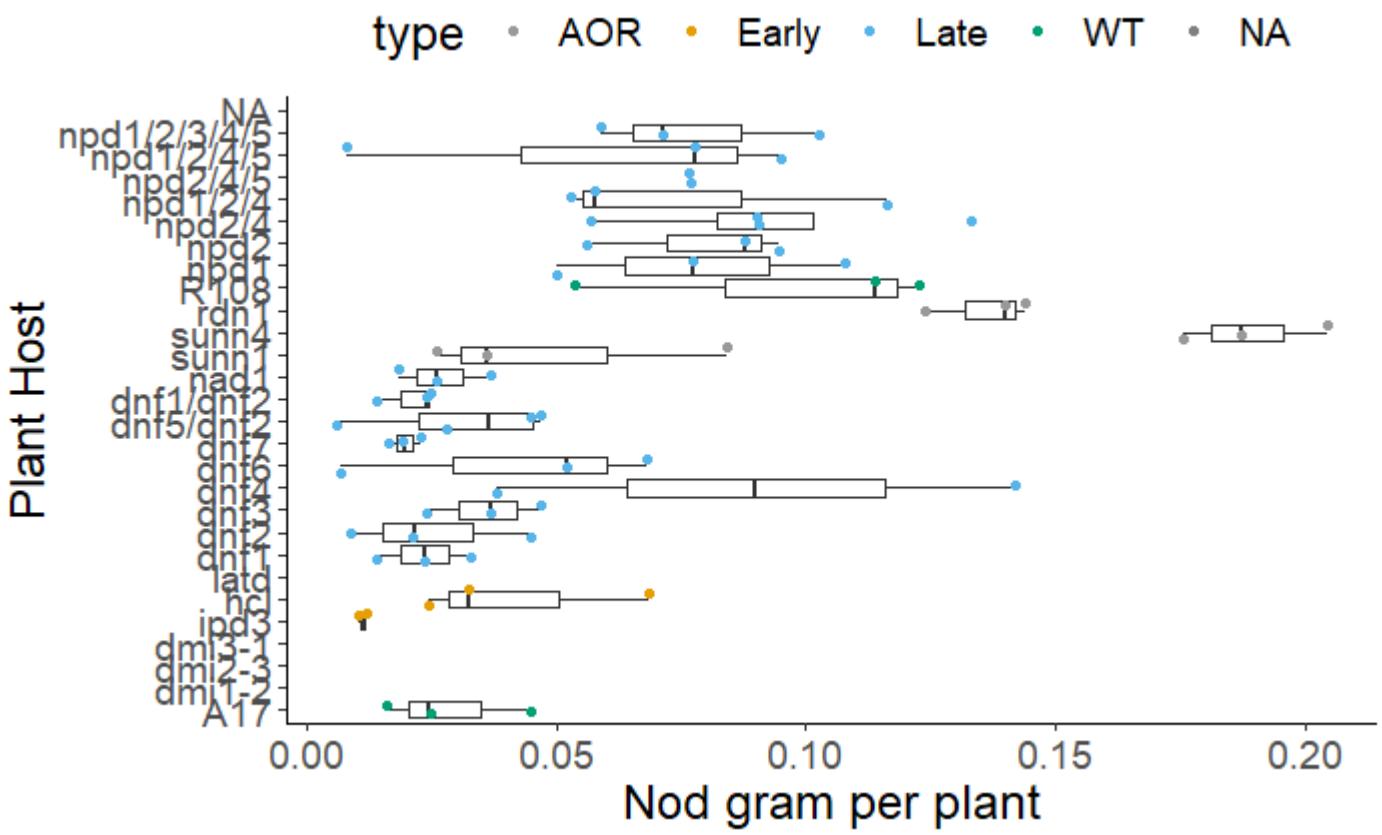

type
AOR
Early
Late
WT
NA
Nods per plant
200
150
100
50
A17
R108
NA
Plant Host

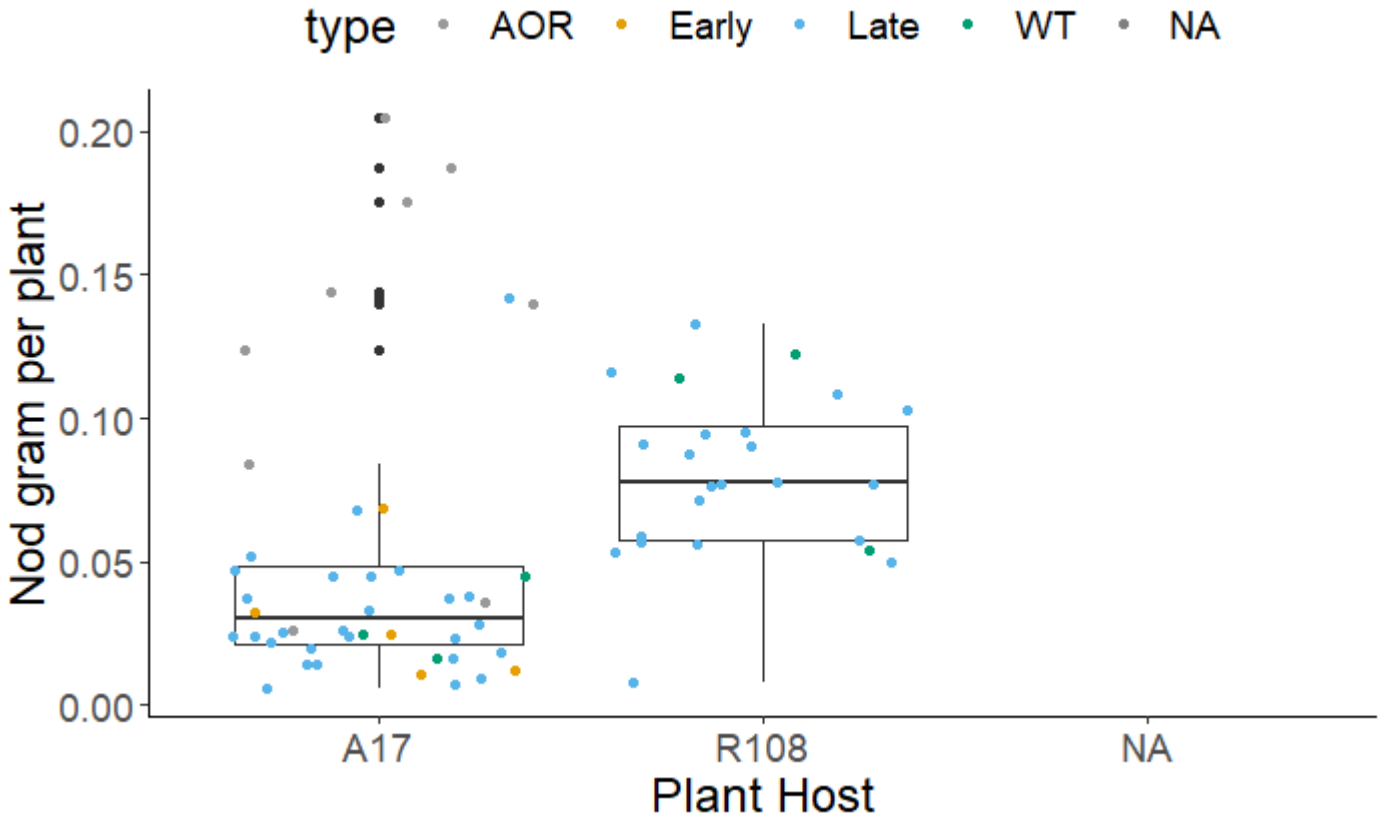
```
            Df Sum Sq Mean Sq F value   Pr(>F)
background   1  17130   17130   16.33 0.000341 ***
Residuals   30  31473    1049
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
127 observations deleted due to missingness
            Df Sum Sq Mean Sq F value Pr(>F)
type         2   1102     551   0.192   0.83
Residuals    6  17196    2866
80 observations deleted due to missingness
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = nod_cnt_plant ~ type, data = filter(all_data, background == "A17"))

$type
               diff       lwr      upr     p adj
Early-AOR 28.500000 -161.1715 218.1715 0.8914618
WT-AOR    36.266667 -143.6715 216.2049 0.8158125
WT-Early   7.766667 -112.1921 127.7255 0.9785569

            Df Sum Sq Mean Sq F value Pr(>F)
type         1   1954  1954.0   3.657 0.0696 .
Residuals   21  11221   534.4
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
17 observations deleted due to missingness
```






```
           Df Sum Sq Mean Sq F value Pr(>F)
background   1  0.591  0.5911    2.79  0.105
Residuals   30  6.357  0.2119
127 observations deleted due to missingness
           Df Sum Sq Mean Sq F value Pr(>F)
type         2  1.868  0.9339   4.785 0.0572 .
Residuals    6  1.171  0.1952
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
80 observations deleted due to missingness
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = tot_area_plant ~ type, data = filter(all_data, background == "A17"))

$type
               diff       lwr         upr     p adj
Early-AOR -1.068333 -2.633620 0.496952978 0.1712713
WT-AOR    -1.476033 -2.960994 0.008927647 0.0511495
WT-Early  -0.407700 -1.397674 0.582273987 0.4632009

           Df Sum Sq Mean Sq F value Pr(>F)
type         1  0.001 0.00095   0.006  0.939
Residuals   21  3.317 0.15795
17 observations deleted due to missingness
```


type
AOR
Early
Late
WT
NA
Plant Host
NA
npd1/2/3/4/5
npd1/2/4/5
npd2/4/5
npd1/2/4
npd2/4
npd2
npd1
R108
rdn1
sunn4
sunn1
nad1
dnf1/dnf2
dnf5/dnf7
dnf7
dnf6
dnf4
dnf3
dnf2
dnf1
latd
nc
ipd3
dmi3-1
dmi2-3
dmi1-2
A17
0.00
0.05
0.10
0.15
0.20
Nod gram per plant


type
AOR
Early
Late
WT
NA
Nod gram per plant
0.20
0.15
0.10
0.05
0.00
A17
R108
NA
Plant Host

```
            Df Sum Sq  Mean Sq F value Pr(>F)
background   1 0.0134 0.013398    6.62 0.0123 *
Residuals   66 0.1336 0.002024
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
91 observations deleted due to missingness
            Df  Sum Sq  Mean Sq F value   Pr(>F)
type         3 0.06125 0.020418   15.25 9.12e-07 ***
Residuals   40 0.05356 0.001339
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
45 observations deleted due to missingness
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = nod_wt_plant ~ type, data = filter(all_data, background == "A17"))

$type
                   diff         lwr         upr     p adj
Early-AOR  -0.094988889 -0.14969458 -0.04028320 0.0002009
Late-AOR   -0.091574074 -0.12932459 -0.05382356 0.0000005
WT-AOR     -0.095888889 -0.16127470 -0.03050308 0.0017916
Late-Early  0.003414815 -0.04433623  0.05116586 0.9974610
WT-Early   -0.000900000 -0.07252657  0.07072657 0.9999860
WT-Late    -0.004314815 -0.06400362  0.05537399 0.9973784

            Df   Sum Sq   Mean Sq F value Pr(>F)
type         1 0.000919 0.0009193   1.134  0.299
Residuals   22 0.017843 0.0008110
16 observations deleted due to missingness
```