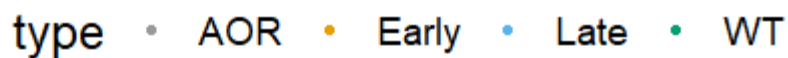


Code ▼

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

Results for dilution plating of nodule homogenate.

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 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
28 observations deleted due to missingness

      Df    Sum Sq   Mean Sq F value   Pr(>F)
type      3 8.273e+16 2.758e+16   2.439 0.0731 .
Residuals 60 6.783e+17 1.131e+16
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
25 observations deleted due to missingness
  Tukey multiple comparisons of means
    95% family-wise confidence level

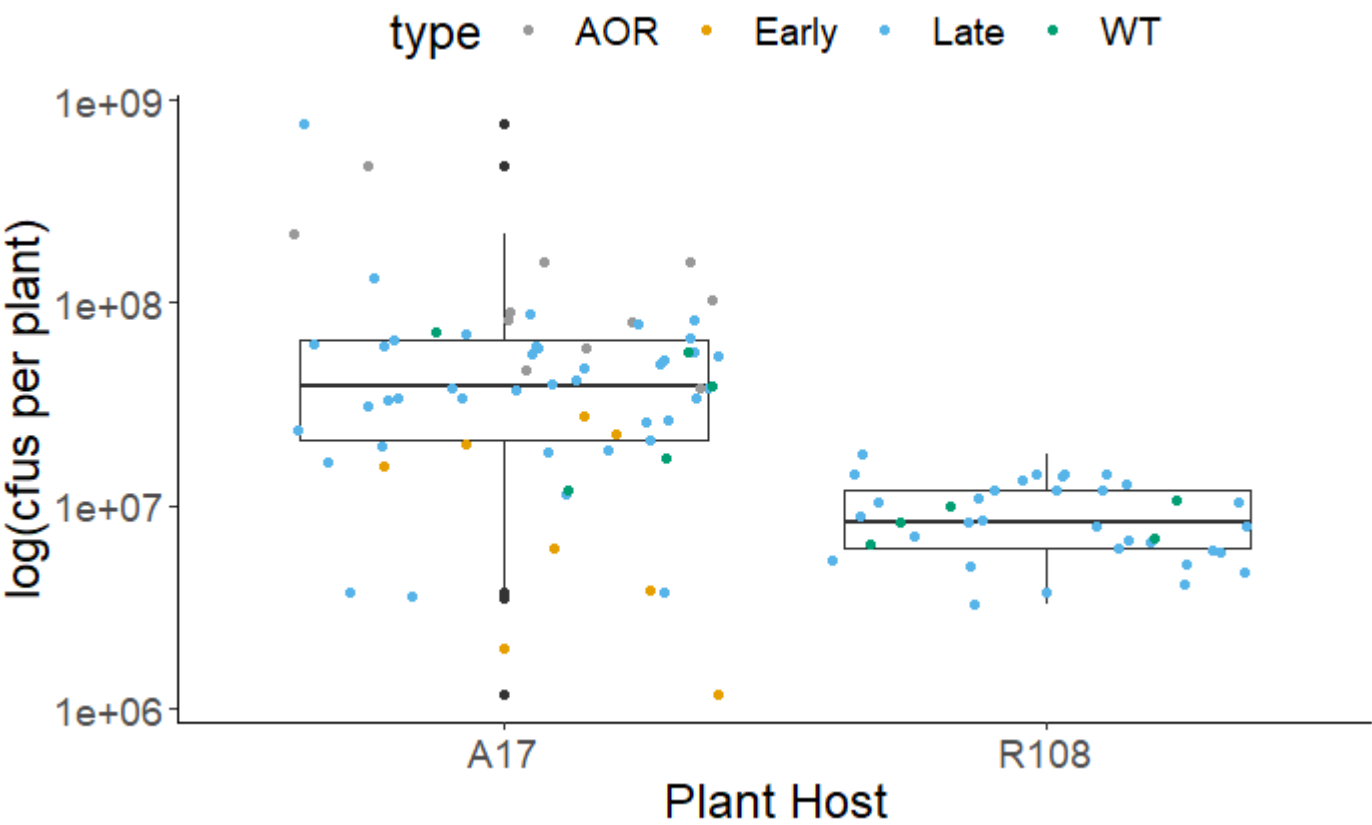
Fit: aov(formula = cfu_plant ~ type, data = filter(all_data, background == "A17"))

$type
      diff      lwr      upr    p adj
Early-AOR -124566335 -255122187  5989516 0.0667292
Late-AOR   -75501544 -171159176 20156089 0.1695090
WT-AOR     -97602273 -249146544 53941998 0.3317244
Late-Early  49064792  -59754653 157884237 0.6345667
WT-Early    26964063 -133213823 187141948 0.9703672
WT-Late     -22100729 -155376786 111175328 0.9716097

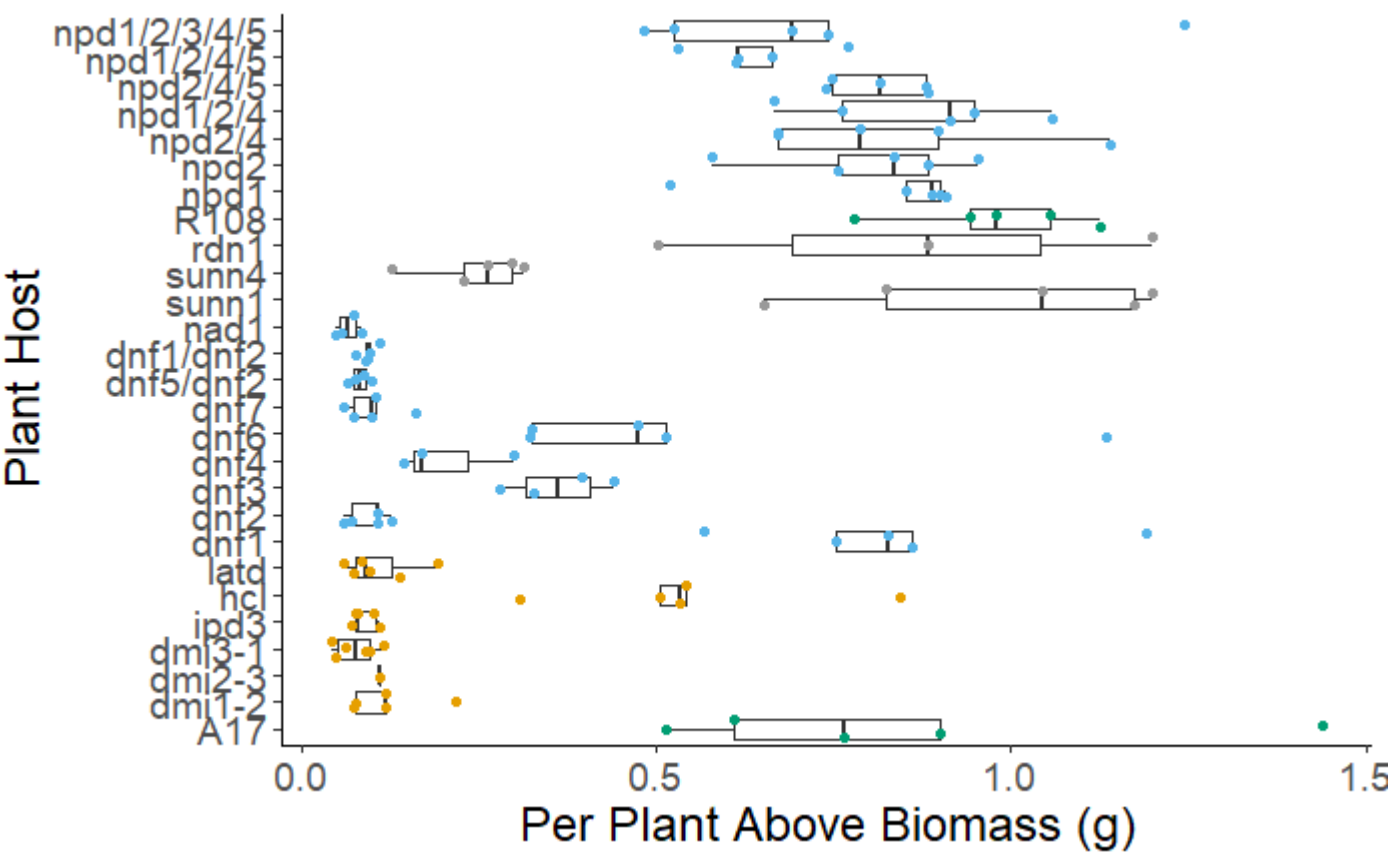
      Df    Sum Sq   Mean Sq F value   Pr(>F)
type      1 2.604e+12 2.604e+12   0.187  0.668
Residuals 35 4.867e+14 1.391e+13
3 observations deleted due to missingness

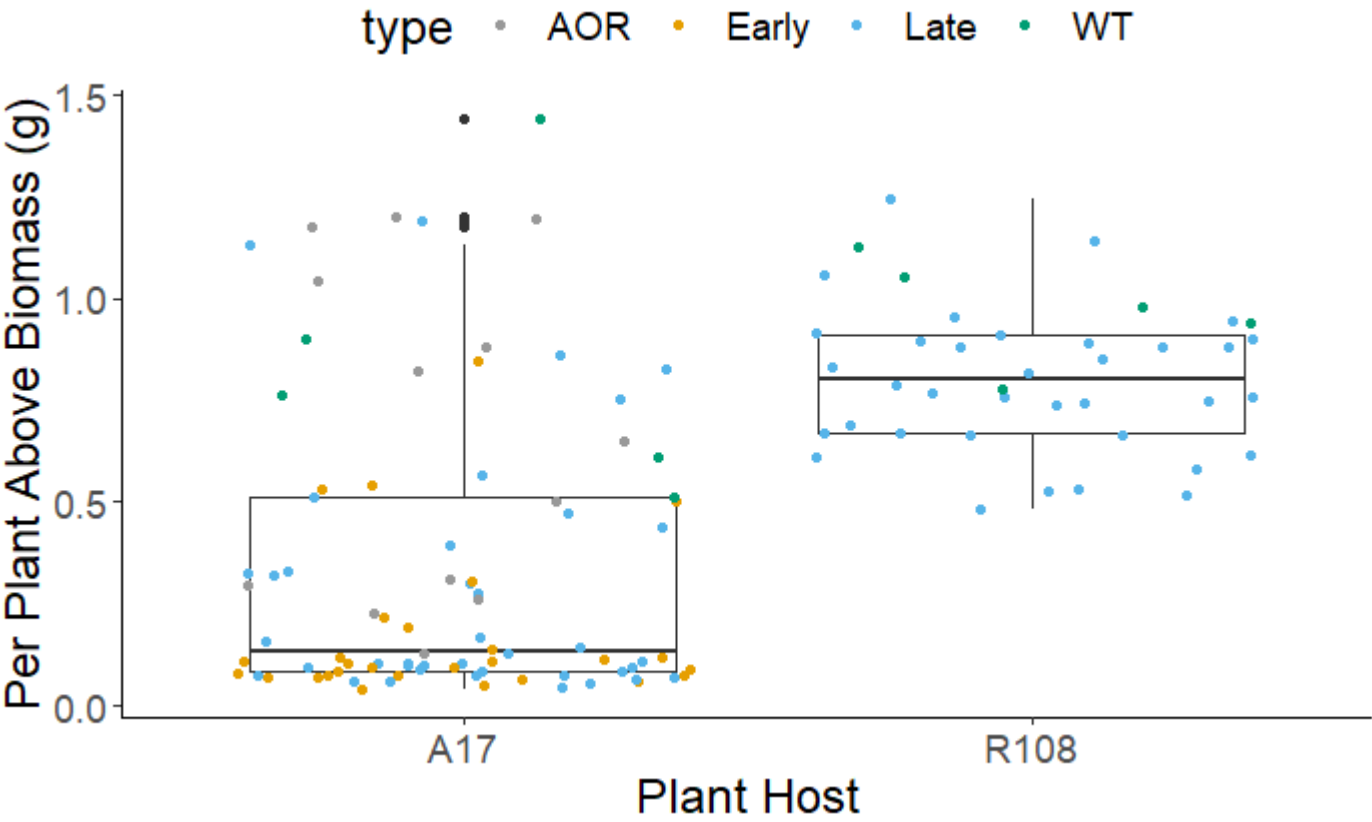
```

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.





```

      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

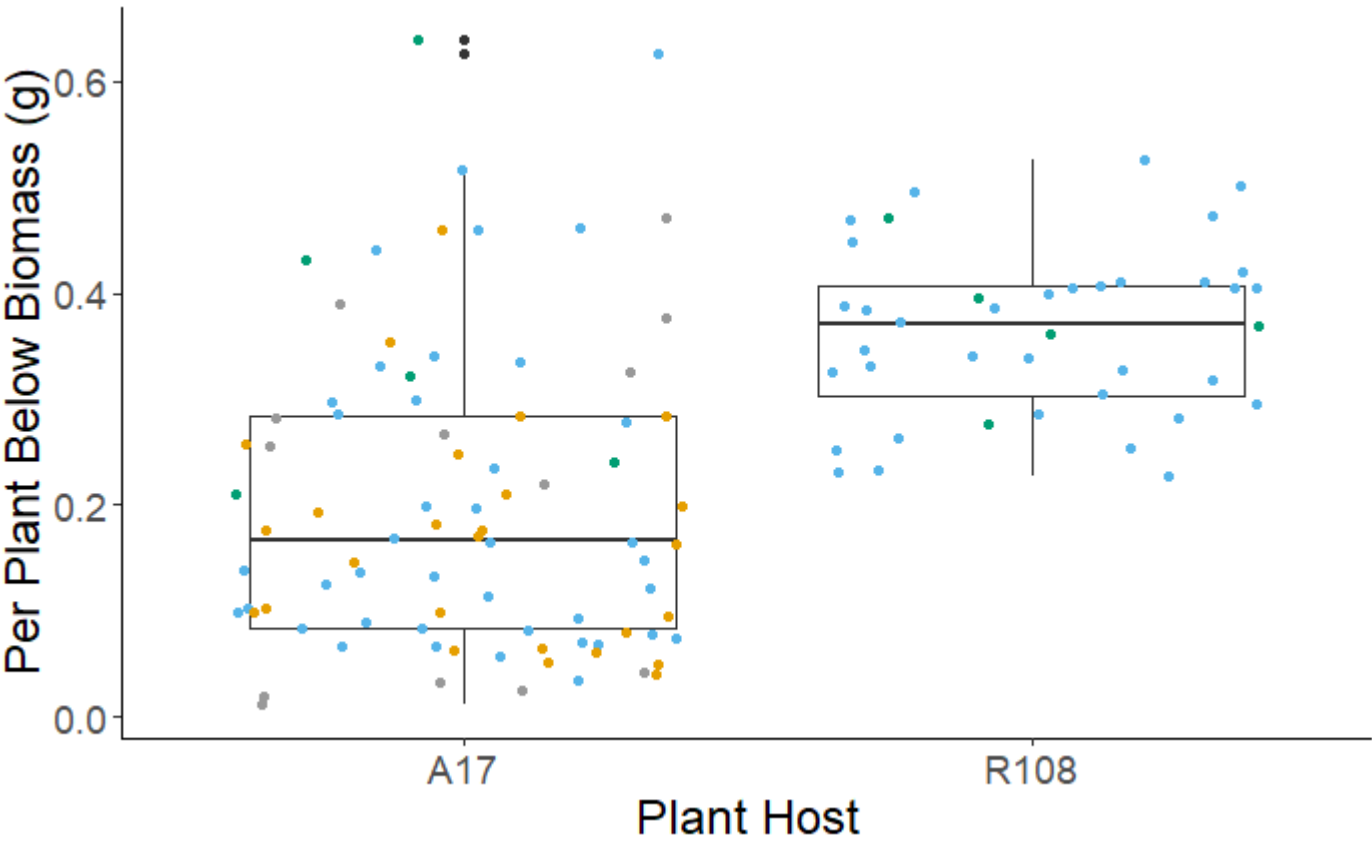
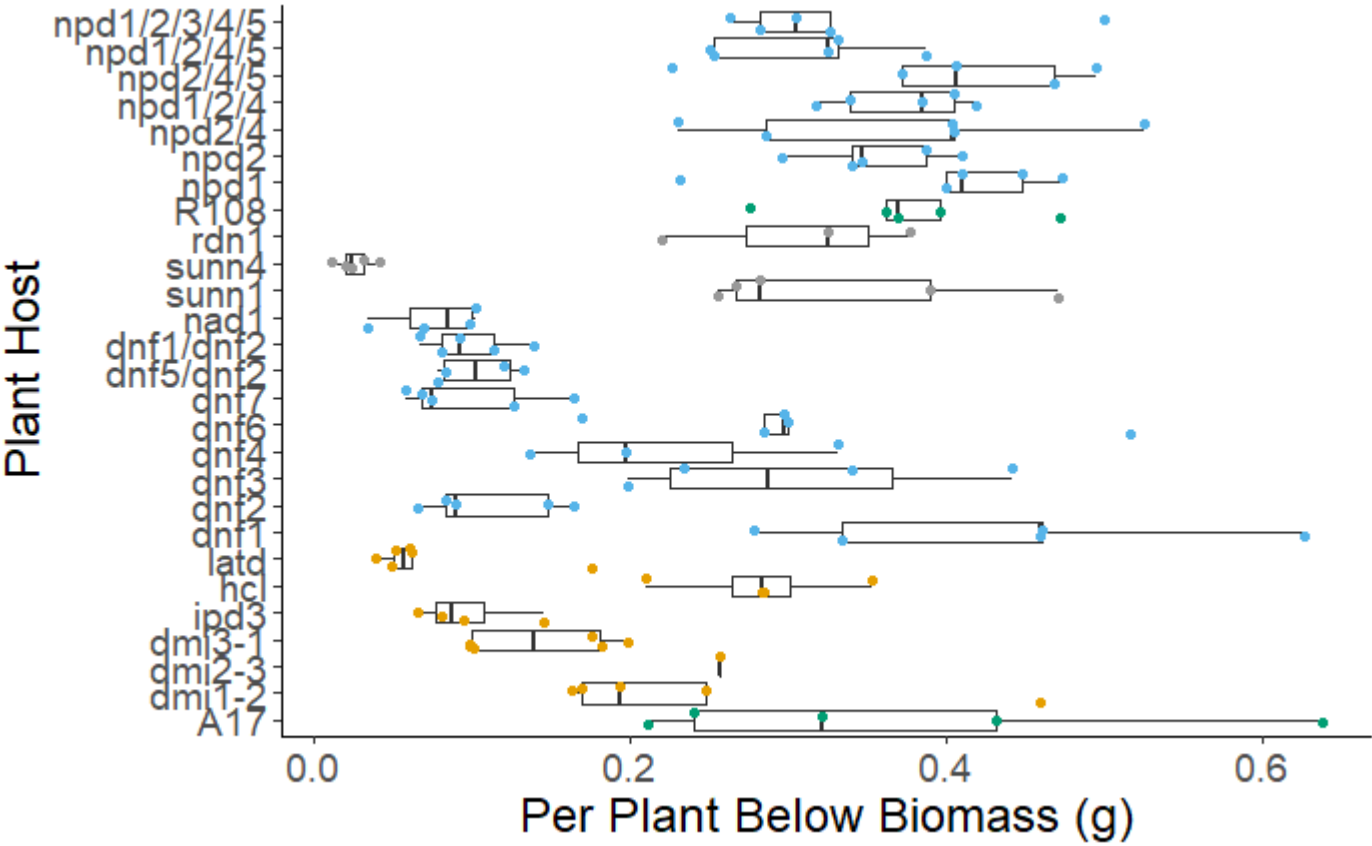
Fit: aov(formula = above_plant ~ type, data = filter(all_data, background == "A17"))

$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.



```

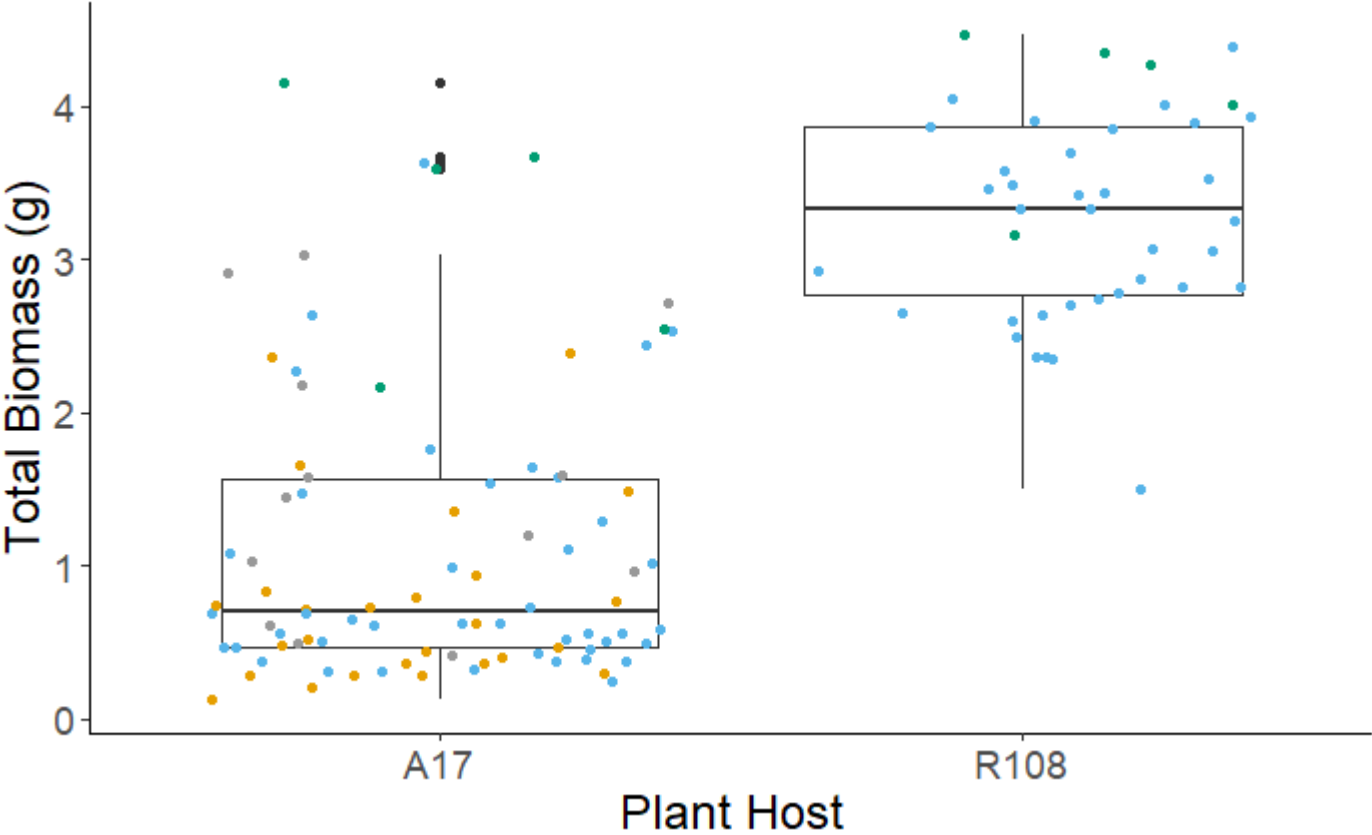
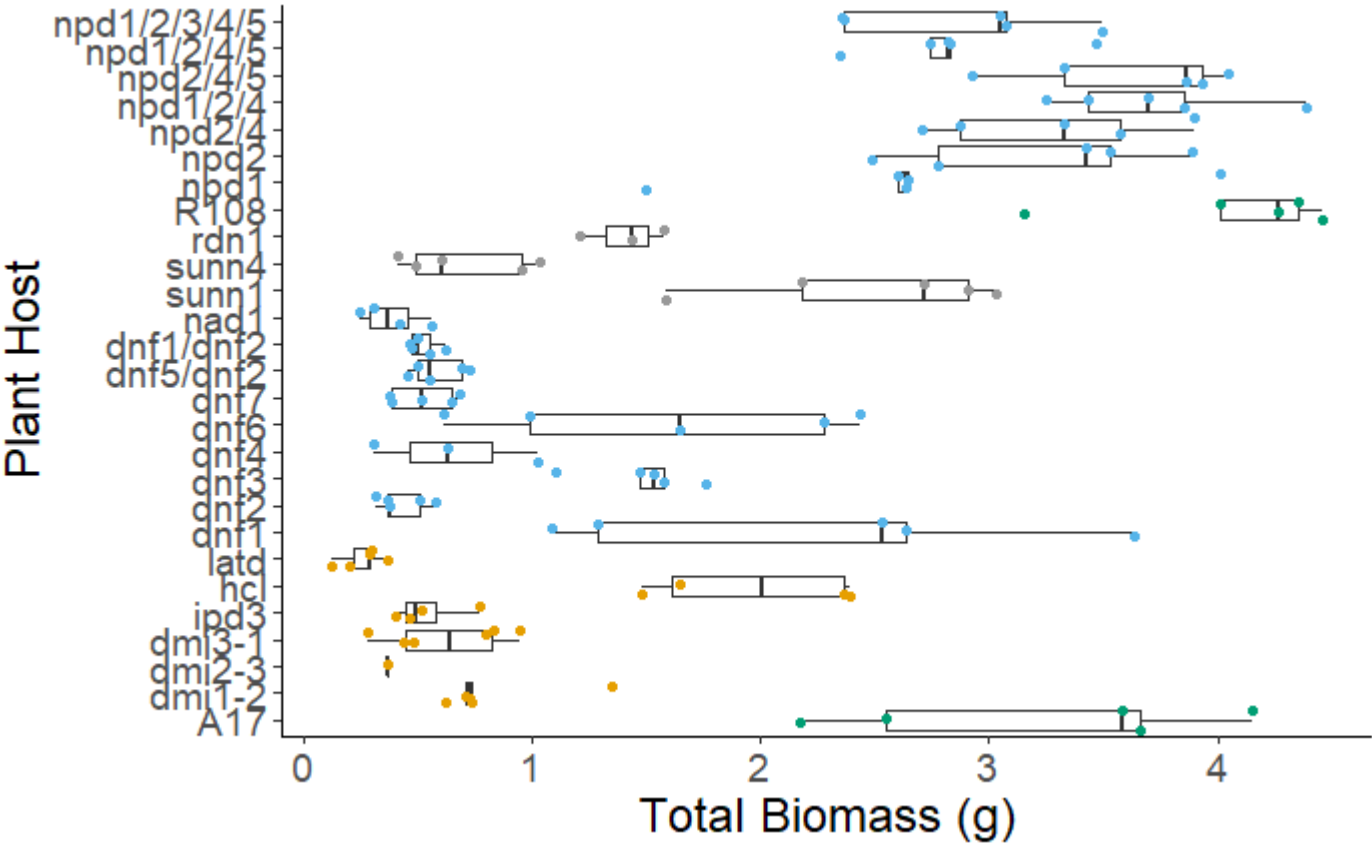
      Df Sum Sq Mean Sq F value    Pr(>F)
background    1 0.7302   0.7302   45.29 5.88e-10 ***
Residuals   122 1.9671   0.0161
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
5 observations deleted due to missingness
      Df Sum Sq Mean Sq F value    Pr(>F)
type        3 0.1747   0.05823    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

```




```

      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

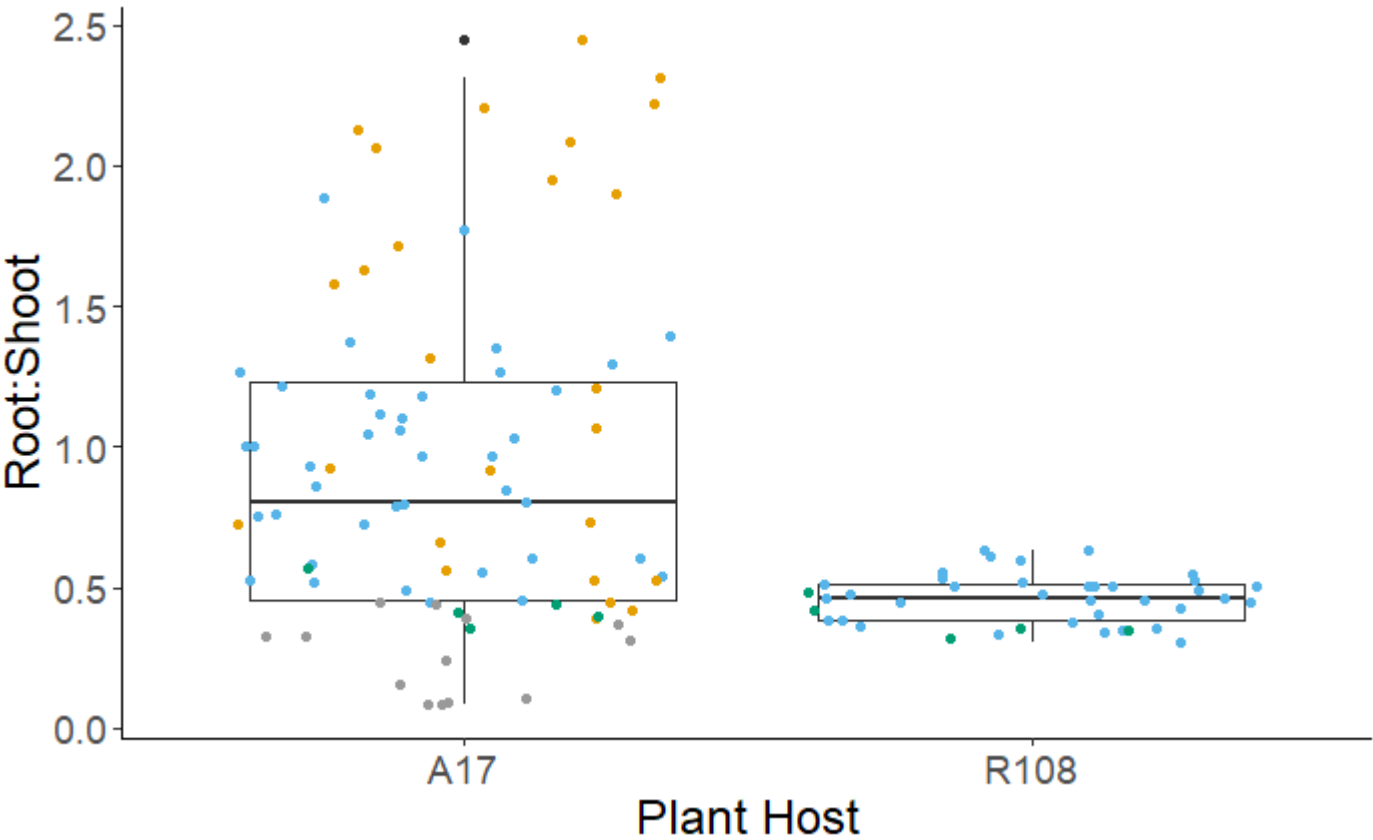
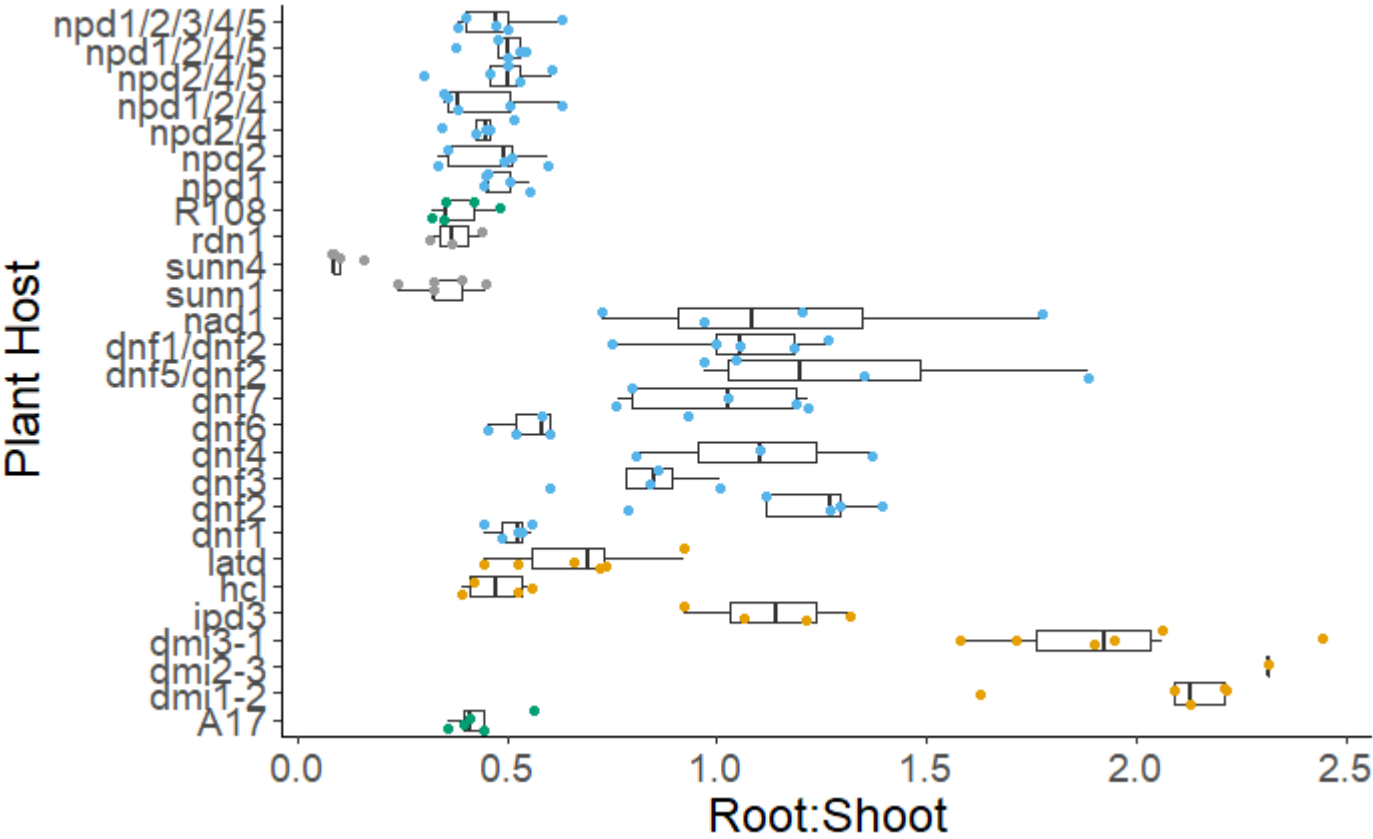
Fit: aov(formula = tot_biomass ~ type, data = filter(all_data, background == "A17"))

$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.



```

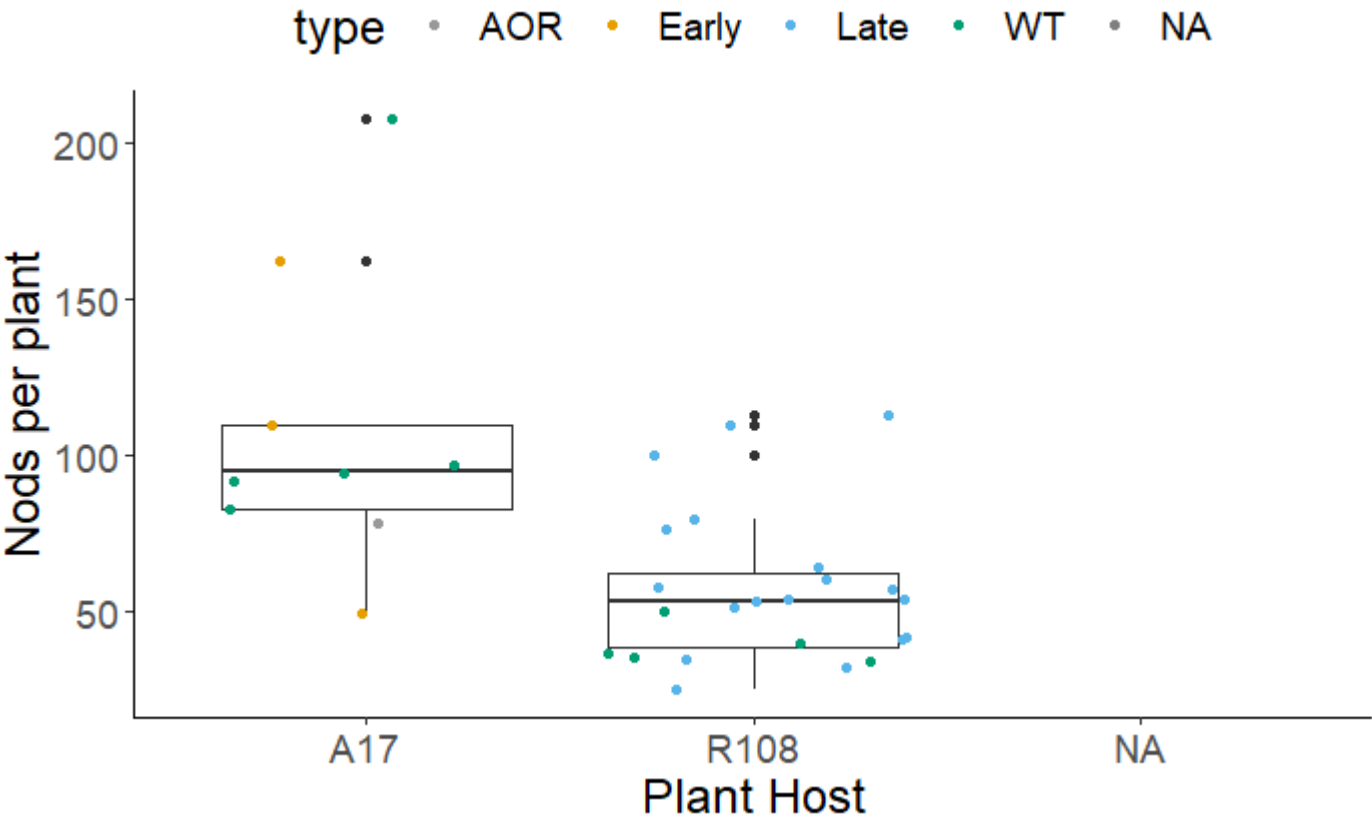
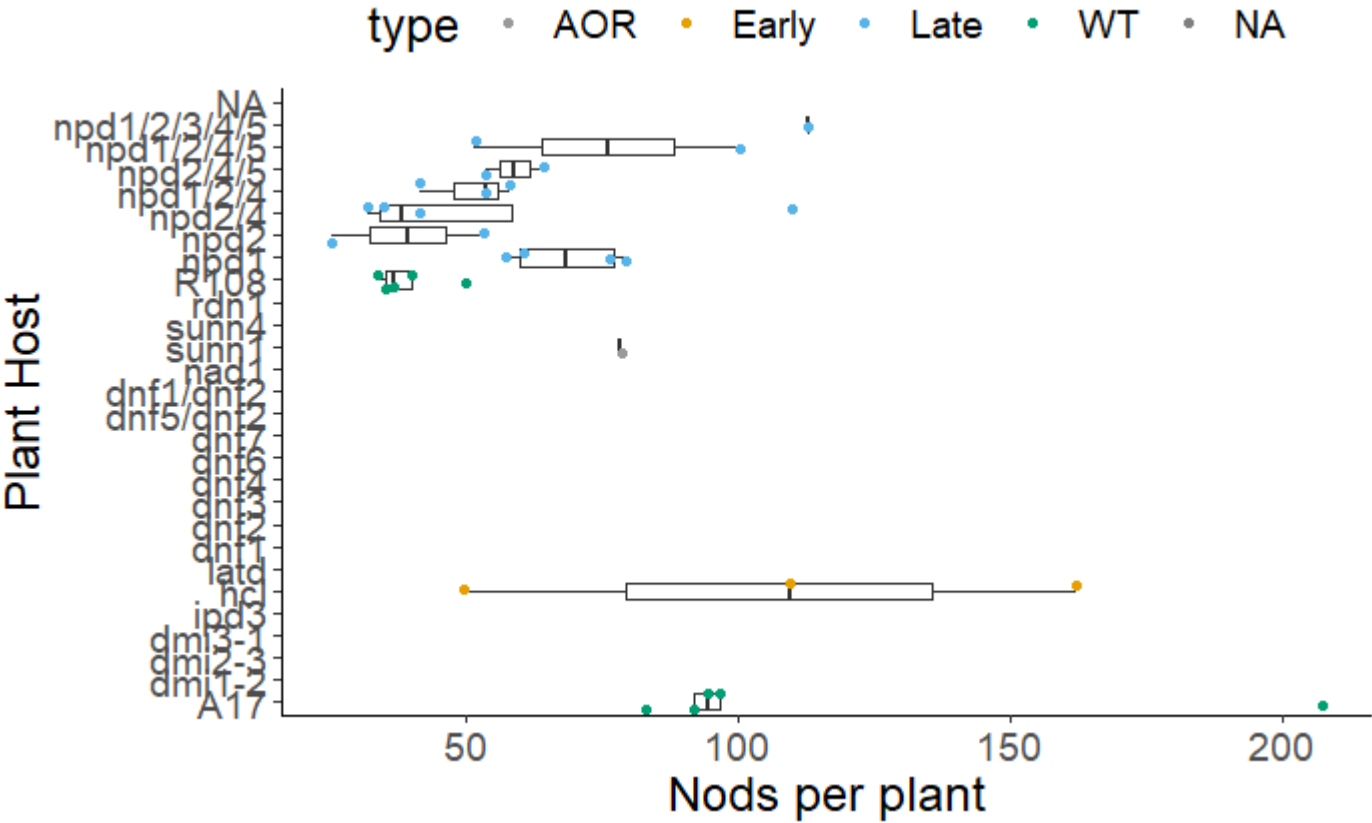
      Df Sum Sq Mean Sq F value    Pr(>F)
background    1  6.174    6.174   25.86 1.34e-06 ***
Residuals   122 29.124    0.239
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
5 observations deleted due to missingness
      Df Sum Sq Mean Sq F value    Pr(>F)
type      3 11.33    3.776   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

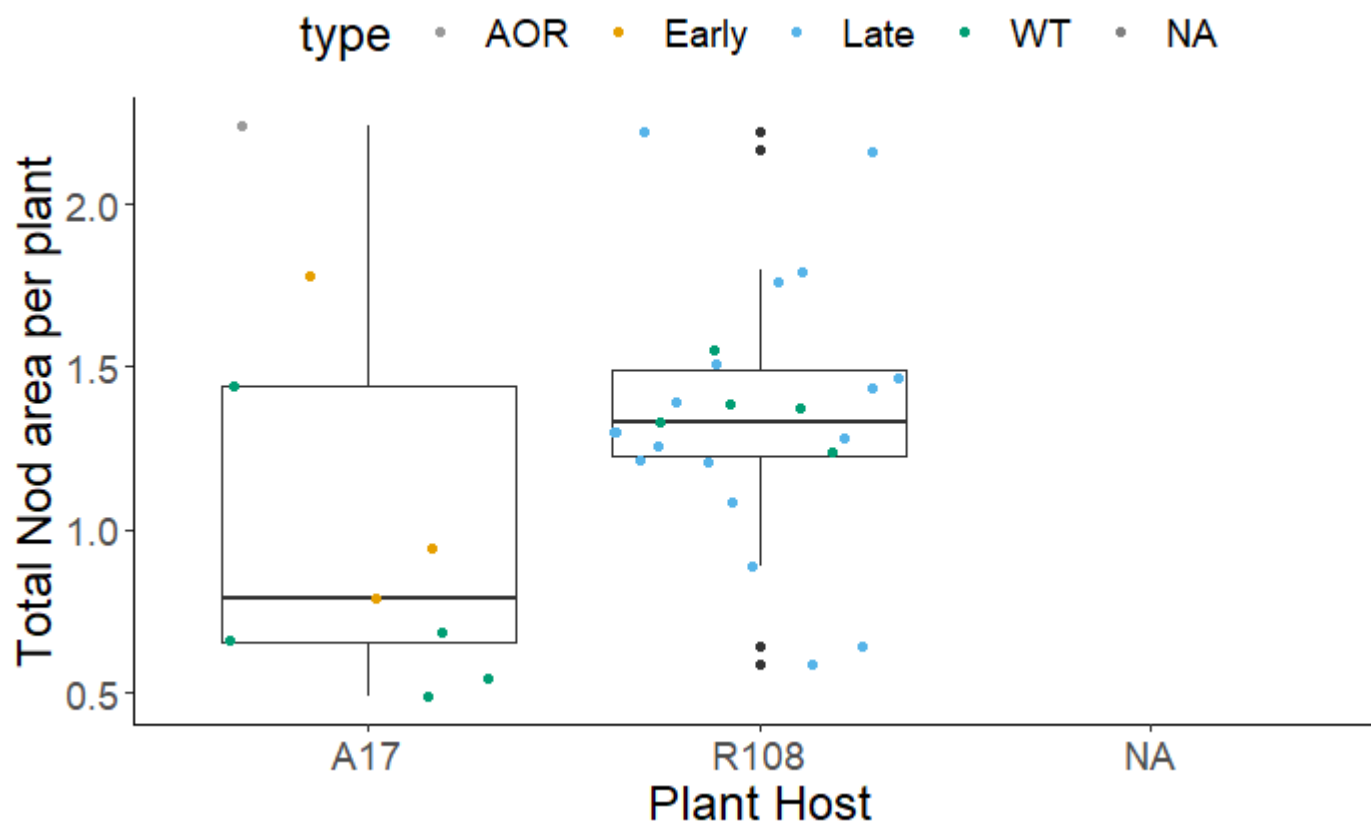
Fit: aov(formula = root_shoot ~ type, data = filter(all_data, background == "A17"))

$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

```





```

      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

```

```

      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

```