

Statistical analyses of experiments

The list of statistical analyses includes the models employed and their detailed results, organized according to the figures presented in this study.

This list offers comprehensive information on the statistical analyses featured in the Ph.D. thesis titled “Ecological Genetics of *Arabidopsis thaliana* Growth under Plant-Plant Competition” by Jessica Thome, arranged by the figures presented.

The statistical analyses were performed as outlined in the “Materials and Methods” section, including details on the factors utilized in the models listed below.

FIGURE 3.1.1.1 D

```
welch Two Sample t-test

data: flowering$flowering_dpg by flowering$condition
t = -2.3793, df = 9.349, p-value = 0.04029
alternative hypothesis: true difference in means between group single and group competition is not
equal to 0
95 percent confidence interval:
-4.4743727 -0.1256273
sample estimates:
mean in group single mean in group competition
27.2                      29.5
```

FIGURE 3.1.1.1 E

```
welch Two Sample t-test

data: flowering$leaves_flowering by flowering$condition
t = 2.8947, df = 17.941, p-value = 0.009679
alternative hypothesis: true difference in means between group single and group competition is not
equal to 0
95 percent confidence interval:
0.4932842 3.1067158
sample estimates:
mean in group single mean in group competition
15.4                      13.6
```

Figure 3.1.1.1 F

```
welch Two Sample t-test

data: data$Height by data$condition
t = 14.289, df = 16.84, p-value = 7.647e-11
alternative hypothesis: true difference in means between group single and group competition is not
equal to 0
95 percent confidence interval:
13.37309 18.01046
sample estimates:
mean in group single mean in group competition
31.09400                  15.40222
```

Figure 3.1.1.2 B

```
welch Two Sample t-test

data: data_tidy[which(data_tidy$metric_ID == "RI"), ]$metric_output by data_tidy[which(data_tidy
$metric_ID == "RI"), ]$condition
t = 6.5, df = 9, p-value = 0.0001115
alternative hypothesis: true difference in means between group single and group competition is not
equal to 0
95 percent confidence interval:
1.695137 3.504863
sample estimates:
mean in group single mean in group competition
2.6                      0.0
```

```
welch Two Sample t-test

data: data_tidy[which(data_tidy$metric_ID == "RII"), ]$metric_output by data_tidy[which(data_tidy
$metric_ID == "RI"), ]$condition
t = 1.4746, df = 9, p-value = 0.1744
alternative hypothesis: true difference in means between group single and group competition is not
equal to 0
95 percent confidence interval:
-0.6408765 3.0408765
sample estimates:
mean in group single mean in group competition
1.2                      0.0
```

```
welch Two Sample t-test

data: data_tidy[which(data_tidy$metric_ID == "CI"), ]$metric_output by data_tidy[which(data_tidy
$metric_ID == "RI")], ]$condition
t = 3.2844, df = 17.609, p-value = 0.004216
alternative hypothesis: true difference in means between group single and group competition is not
equal to 0
95 percent confidence interval:
0.4671069 2.1328931
sample estimates:
mean in group single mean in group competition
4.3 3.0
```

```
welch Two Sample t-test

data: data_tidy[which(data_tidy$metric_ID == "CII"), ]$metric_output by data_tidy[which(data_tidy
$metric_ID == "RI")], ]$condition
t = 9.0331, df = 9, p-value = 8.286e-06
alternative hypothesis: true difference in means between group single and group competition is not
equal to 0
95 percent confidence interval:
5.54681 9.25319
sample estimates:
mean in group single mean in group competition
7.4 0.0
```

```
welch Two Sample t-test

data: data_tidy[which(data_tidy$metric_ID == "Total"), ]$metric_output by data_tidy[which(data_tidy
$metric_ID == "RI")], ]$condition
t = 13.739, df = 10.565, p-value = 4.477e-08
alternative hypothesis: true difference in means between group single and group competition is not
equal to 0
95 percent confidence interval:
10.48738 14.51262
sample estimates:
mean in group single mean in group competition
15.5 3.0
```

Figure 3.1.2 D

```
welch Two Sample t-test

data: data_tidy[which(data_tidy$metric_ID == "siliques"), ]$metric_output by data_tidy[which(data_tidy
$metric_ID == "siliques"), ]$condition
t = 15.644, df = 11.056, p-value = 6.869e-09
alternative hypothesis: true difference in means between group single and group competition is not
equal to 0
95 percent confidence interval:
169.9882 225.6118
sample estimates:
mean in group single mean in group competition
237.2 39.4
```

Figure 3.1.3 A

```
Call:  
glm(formula = output ~ condition * fertilization + tray * position,  
    family = negative.binomial(theta = 20), data = branches[which(branches$ID ==  
        "Total"), ])  
  
Coefficients:  
Estimate Std. Error t value Pr(>|t|)  
(Intercept) 3.7336 0.3197 11.677 1.10e-12 ***  
conditioncompetition -2.0206 0.2404 -8.404 2.23e-09 ***  
fertilizationfertilization 0.8954 0.1578 5.675 3.47e-06 ***  
tray -0.5907 0.1993 -2.964 0.0059 **  
positionB -1.0037 0.3780 -2.655 0.0126 *  
positionC -0.8195 0.4668 -1.756 0.0894 .  
conditioncompetition:fertilizationfertilization 0.3290 0.3103 1.060 0.2975  
tray:positionB 0.5876 0.2167 2.712 0.0110 *  
tray:positionC 0.5459 0.2576 2.119 0.0425 *  
---  
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1  
  
(Dispersion parameter for Negative Binomial(20) family taken to be 0.8897663)  
  
Null deviance: 306.476 on 38 degrees of freedom  
Residual deviance: 26.382 on 30 degrees of freedom  
(1 Beobachtung als fehlend gelöscht)  
AIC: 219.62  
  
Number of Fisher Scoring iterations: 5
```

Figure 3.1.3 B

```
Call:  
glm(formula = siliques ~ condition * fertilization + tray * position,  
    family = negative.binomial(theta = 18), data = data)  
  
Coefficients:  
Estimate Std. Error t value Pr(>|t|)  
(Intercept) 5.33466 0.24236 22.011 < 2e-16 ***  
conditioncompetition -2.08042 0.13590 -15.309 1.02e-15 ***  
fertilizationfertilization 1.01700 0.13851 7.342 3.53e-08 ***  
tray -0.07570 0.13220 -0.573 0.5712  
positionB 0.12135 0.29112 0.417 0.6798  
positionC 0.35337 0.37083 0.953 0.3482  
conditioncompetition:fertilizationfertilization -0.36673 0.20869 -1.757 0.0891 .  
tray:positionB 0.05469 0.14949 0.366 0.7171  
tray:positionC -0.06047 0.19563 -0.309 0.7594  
---  
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1  
  
(Dispersion parameter for Negative Binomial(18) family taken to be 1.148085)  
  
Null deviance: 859.540 on 38 degrees of freedom  
Residual deviance: 38.814 on 30 degrees of freedom  
(1 Beobachtung als fehlend gelöscht)  
AIC: 389.47  
  
Number of Fisher Scoring iterations: 4
```

Figure 3.1.3D

```
Call:  
glm(formula = leaf_length_04.09 ~ condition * fertilization +  
    tray * position, family = negative.binomial(theta = 18),  
    data = data)  
  
Coefficients:  
Estimate Std. Error t value Pr(>|t|)  
(Intercept) 4.030048 0.176501 22.833 < 2e-16 ***  
conditioncompetition -0.774800 0.098820 -7.841 7.55e-09 ***  
fertilizationfertilization 0.174719 0.101879 1.715 0.0963 .  
tray -0.019479 0.094876 -0.205 0.8387  
positionB -0.206550 0.212526 -0.972 0.3386  
positionC 0.058193 0.274049 0.212 0.8332  
conditioncompetition:fertilizationfertilization 0.180122 0.151392 1.190 0.2432  
tray:positionB 0.074111 0.107789 0.688 0.4968  
tray:positionC -0.005234 0.144098 -0.036 0.9713  
---  
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1  
  
(Dispersion parameter for Negative Binomial(18) family taken to be 0.5457082)  
  
Null deviance: 90.251 on 39 degrees of freedom  
Residual deviance: 26.855 on 31 degrees of freedom  
AIC: 313.67  
  
Number of Fisher Scoring iterations: 4
```

Figure 3.1.3F

```
Call:  
glm(formula = leaf_length ~ soil * condition, family = negative.binomial(theta = 8870.097669),  
    data = leaf_length)  
  
Coefficients: (3 not defined because of singularities)  
Estimate Std. Error t value Pr(>|t|)  
(Intercept) 1.5339 0.1620 9.468 2.80e-12 ***  
soil60% vm + 40% 0 0.5342 0.1644 3.248 0.002198 **  
soil80% vm + 20% 0 0.6429 0.1577 4.077 0.000183 ***  
soilvm 1.5616 0.1393 11.213 1.28e-14 ***  
conditionsingle 0.6325 0.1025 6.173 1.73e-07 ***  
soil60% vm + 40% 0:conditionsingle NA NA NA NA  
soil80% vm + 20% 0:conditionsingle NA NA NA NA  
soilvm:conditionsingle NA NA NA NA  
---  
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1  
  
(Dispersion parameter for Negative Binomial(8870.098) family taken to be 1.510499)  
  
Null deviance: 343.295 on 49 degrees of freedom  
Residual deviance: 57.809 on 45 degrees of freedom  
AIC: 302.86  
  
Number of Fisher Scoring iterations: 4
```

Figure 3.1.3G

```
Call:  
glm(formula = siliques ~ condition * soil, family = negative.binomial(theta = 12),  
     data = data)  
  
Coefficients: (3 not defined because of singularities)  
              Estimate Std. Error t value Pr(>|t|)  
(Intercept)      2.2047    0.2003 11.007 2.37e-14 ***  
conditionsingle   1.5795    0.1649  9.576 1.98e-12 ***  
soil60% vm + 40% 0  0.4894    0.1655  2.956  0.00494 **  
soil80% vm + 20% 0  0.4205    0.1615  2.603  0.01246 *  
soilvm            1.2978    0.1579  8.221 1.65e-10 ***  
conditionsingle:soil60% vm + 40% 0    NA       NA       NA  
conditionsingle:soil80% vm + 20% 0    NA       NA       NA  
conditionsingle:soilvm                NA       NA       NA  
---  
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1  
  
(Dispersion parameter for Negative Binomial(12) family taken to be 1.340074)  
  
Null deviance: 209.52 on 49 degrees of freedom  
Residual deviance: 49.10 on 45 degrees of freedom  
AIC: 448.76  
  
Number of Fisher scoring iterations: 4
```

Figure 3.1.4B

```
Call:  
glm(formula = metric_output + 1 ~ time, family = negative.binomial(theta = 31356.15585),  
    data = branches[which(branches$metric_ID == "RI"), ])  
  
Coefficients:  
            Estimate Std. Error t value Pr(>|t|)  
(Intercept) 1.46634   0.07187 20.404 < 2e-16 ***  
time0       -0.17357   0.10838 -1.601  0.113  
time7       -0.04230   0.10668 -0.397  0.693  
time14      -0.11641   0.10668 -1.091  0.279  
time21      -0.73545   0.13265 -5.544 3.88e-07 ***  
time28      -1.22995   0.15110 -8.140 5.04e-12 ***  
---  
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1  
  
(Dispersion parameter for Negative Binomial(31356.16) family taken to be 0.3356532)  
  
Null deviance: 67.827 on 83 degrees of freedom  
Residual deviance: 27.813 on 78 degrees of freedom  
AIC: 285.51  
  
Number of Fisher Scoring iterations: 4  
  
Call:  
glm(formula = metric_output + 1 ~ time, family = negative.binomial(theta = 3.2),  
    data = branches[which(branches$metric_ID == "RII"), ])  
  
Coefficients:  
            Estimate Std. Error t value Pr(>|t|)  
(Intercept) 0.6931    0.2399  2.890 0.00499 **  
time0       0.4964    0.3230  1.537 0.12834  
time7       0.4796    0.3292  1.457 0.14914  
time14      0.5798    0.3201  1.811 0.07395 .  
time21     -0.4855    0.3866 -1.256 0.21289  
time28     -0.6931    0.3879 -1.787 0.07783 .  
---  
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1  
  
(Dispersion parameter for Negative Binomial(3.2) family taken to be 1.062064)  
  
Null deviance: 88.160 on 83 degrees of freedom  
Residual deviance: 64.155 on 78 degrees of freedom  
AIC: 323.54  
  
Number of Fisher Scoring iterations: 4
```

```

call:
glm(formula = metric_output ~ time, family = negative.binomial(theta = 282523.167),
     data = branches[which(branches$metric_ID == "CI"), ])

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.54045   0.06030 25.548 < 2e-16 ***
time0       -0.26748   0.09341 -2.864  0.00538 **
time7       -0.19337   0.09341 -2.070  0.04175 *
time14      -0.28768   0.09396 -3.062  0.00302 **
time21      -0.32120   0.09705 -3.310  0.00142 **
time28      -0.20544   0.09000 -2.283  0.02517 *
---
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(282523.2) family taken to be 0.2544802)

Null deviance: 28.034 on 83 degrees of freedom
Residual deviance: 24.116 on 78 degrees of freedom
AIC: 301.59

Number of Fisher Scoring iterations: 4

call:
glm(formula = metric_output + 1 ~ time, family = negative.binomial(theta = 18),
     data = branches[which(branches$metric_ID == "CII"), ])

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.7346    0.1186 14.622 < 2e-16 ***
time0       -0.2793    0.1812 -1.541   0.127
time7       -0.2922    0.1857 -1.573   0.120
time14      -0.2628    0.1805 -1.456   0.150
time21      -1.4663    0.2673 -5.485 4.95e-07 ***
time28      -1.7346    0.2795 -6.207 2.43e-08 ***
---
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(18) family taken to be 0.9097733)

Null deviance: 144.483 on 83 degrees of freedom
Residual deviance: 71.653 on 78 degrees of freedom
AIC: 336.33

Number of Fisher Scoring iterations: 4

```

```

call:
glm(formula = metric_output ~ time, family = negative.binomial(theta = 13),
     data = branches[which(branches$metric_ID == "Total"), ])

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.61496   0.09755 26.806 < 2e-16 ***
time0       -0.14807  0.14320 -1.034   0.304
time7       -0.09231  0.14496 -0.637   0.526
time14      -0.10652  0.14237 -0.748   0.457
time21      -1.00552  0.17255 -5.827 1.20e-07 ***
time28      -1.21214  0.17316 -7.000 7.87e-10 ***
---
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(13) family taken to be 0.9510014)

Null deviance: 160.101 on 83 degrees of freedom
Residual deviance: 72.778 on 78 degrees of freedom
AIC: 463.71

```

Number of Fisher scoring iterations: 4

Figure 3.1.4C

```

call:
glm(formula = metric_output ~ time, family = negative.binomial(theta = 24),
     data = pjt03_tidy[which(pjt03_tidy$metric_ID == "silques"),
                      ])

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 5.61653   0.05310 105.767 < 2e-16 ***
time0       -0.13977  0.07667 -1.823 0.072125 .
time7       -0.15957  0.07822 -2.040 0.044747 *
time14      -0.27044  0.07692 -3.516 0.000734 ***
time21      -0.91186  0.08039 -11.343 < 2e-16 ***
time28      -1.19689  0.07850 -15.246 < 2e-16 ***
---
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(24) family taken to be 0.933657)

Null deviance: 396.721 on 83 degrees of freedom
Residual deviance: 83.875 on 78 degrees of freedom
AIC: 860.42

```

Number of Fisher scoring iterations: 4

Figure 3.1.4D

```
call:  
glm(formula = metric_output ~ time, family = negative.binomial(theta = 3291731.616),  
    data = pjt03_tidy[which(pjt03_tidy$metric_ID == "Inflorescence Height [cm]"),  
    ])  
  
Coefficients:  
             Estimate Std. Error t value Pr(>|t|)  
(Intercept) 3.60550   0.01950 184.883 < 2e-16 ***  
time0        0.03771   0.02780   1.357   0.179  
time7       -0.01506   0.02937  -0.513   0.610  
time14      -0.00924   0.02869  -0.322   0.748  
time21       0.01884   0.02910   0.648   0.519  
time28      -0.13531   0.02910 -4.650 1.42e-05 ***  
---  
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1  
  
(Dispersion parameter for Negative Binomial(3291732) family taken to be 0.2099292)  
  
Null deviance: 24.778 on 79 degrees of freedom  
Residual deviance: 15.892 on 74 degrees of freedom  
(4 Beobachtungen als fehlend gelöscht)  
AIC: 462.06  
  
Number of Fisher Scoring iterations: 4
```

Figure 3.1.4H

```
welch Two Sample t-test  
  
data: pjt019$siliques by pjt019$condition  
t = -17.725, df = 16.922, p-value = 2.312e-12  
alternative hypothesis: true difference in means between group competition and group single is not  
equal to 0  
95 percent confidence interval:  
-217.3233 -171.0767  
sample estimates:  
mean in group competition     mean in group single  
          41.46667                  235.66667
```

Figure 3.1.5B

```
call:  
glm(formula = output + 1 ~ condition * soil_volume, family = negative.binomial(theta = 230633.338  
4),  
    data = branches[which(branches$ID == "RI"), ])  
  
Coefficients:  
             Estimate Std. Error t value Pr(>|t|)  
(Intercept) 1.16315   0.08694 13.380 < 2e-16 ***  
conditioncompetition -1.16315   0.17816 -6.529 4.65e-08 ***  
soil_volume9 cm pots  0.11778   0.10971   1.074   0.289  
conditioncompetition:soil_volume9 cm pots -0.05324   0.22658  -0.235   0.815  
---  
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1  
  
(Dispersion parameter for Negative Binomial(230633.3) family taken to be 0.241845)  
  
Null deviance: 46.353 on 49 degrees of freedom  
Residual deviance: 12.156 on 46 degrees of freedom  
AIC: 147  
  
Number of Fisher Scoring iterations: 4
```

```

Call:
glm(formula = output + 1 ~ condition * soil_volume, family = negative.binomial(theta = 6),
     data = branches[which(branches$ID == "RII"), ])

Coefficients:
                                         Estimate Std. Error t value Pr(>|t|)
(Intercept)                         1.632e-15  3.219e-01  0.000  1.0000
conditioncompetition                 -3.025e-16  4.552e-01  0.000  1.0000
soil_volume9 cm pots                  9.808e-01  3.683e-01  2.663  0.0106 *
conditioncompetition:soil_volume9 cm pots -9.808e-01  5.553e-01 -1.766  0.0840 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(6) family taken to be 0.8879707)

Null deviance: 38.876 on 49 degrees of freedom
Residual deviance: 25.014 on 46 degrees of freedom
AIC: 150.98

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output ~ condition * soil_volume, family = negative.binomial(theta = 458306.7746),
     data = branches[which(branches$ID == "CI"), ])

Coefficients:
                                         Estimate Std. Error t value Pr(>|t|)
(Intercept)                         1.54756   0.06116 25.303 <2e-16 ***
conditioncompetition                -0.18659   0.09082 -2.054  0.0456 *
soil_volume9 cm pots                 -0.05092   0.07978 -0.638  0.5265
conditioncompetition:soil_volume9 cm pots  0.09277   0.11728  0.791  0.4330
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(458306.8) family taken to be 0.1758045)

Null deviance: 9.3259 on 49 degrees of freedom
Residual deviance: 8.2962 on 46 degrees of freedom
AIC: 181.76

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output ~ condition * soil_volume, family = negative.binomial(theta = 458306.7746),
     data = branches[which(branches$ID == "CII"), ])

Coefficients:
                                         Estimate Std. Error t value Pr(>|t|)
(Intercept)                         1.9021    0.1574 12.085 7.08e-16 ***
conditioncompetition                 -4.2047    1.2979 -3.240  0.00223 **
soil_volume9 cm pots                  -0.1103    0.2079 -0.531  0.59810
conditioncompetition:soil_volume9 cm pots  2.3439    1.3496  1.737  0.08913 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(458306.8) family taken to be 1.65978)

Null deviance: 219.106 on 49 degrees of freedom
Residual deviance: 73.247 on 46 degrees of freedom
AIC: 186.55

Number of Fisher Scoring iterations: 6

```

```

call:
glm(formula = output ~ condition * soil_volume, family = negative.binomial(theta = 42.21309549),
     data = branches[which(branches$ID == "Total"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.61007 0.09547 27.339 < 2e-16 ***
conditioncompetition -1.22378 0.18648 -6.563 4.14e-08 ***
soil_volume9 cm pots 0.08004 0.12181 0.657 0.514
conditioncompetition:soil_volume9 cm pots 0.15635 0.23305 0.671 0.506
---
signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(42.2131) family taken to be 0.9375352)

Null deviance: 149.203 on 49 degrees of freedom
Residual deviance: 41.209 on 46 degrees of freedom
AIC: 254.06

Number of Fisher Scoring iterations: 4

```

Figure 3.1.5C

```

call:
glm(formula = siliques ~ condition * soil_volume, family = negative.binomial(theta = 27),
     data = compare)

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 4.98498 0.07248 68.779 < 2e-16 ***
conditioncompetition -1.11169 0.11035 -10.075 3.21e-13 ***
soil_volume9 cm pots 0.61122 0.09223 6.627 3.30e-08 ***
conditioncompetition:soil_volume9 cm pots -0.39461 0.14043 -2.810 0.00725 **
---
signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(27) family taken to be 1.197245)

Null deviance: 592.309 on 49 degrees of freedom
Residual deviance: 52.613 on 46 degrees of freedom
AIC: 466.91

Number of Fisher Scoring iterations: 4

```

Figure 3.1.5D

```

call:
glm(formula = Leaf.Length ~ condition * soil_volume, family = negative.binomial(theta = 1356744.1
2),
     data = compare)

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 3.87120 0.03866 100.140 < 2e-16 ***
conditioncompetition -0.19807 0.05953 -3.327 0.00183 **
soil_volume9 cm pots 0.11407 0.04790 2.381 0.02185 *
conditioncompetition:soil_volume9 cm pots -0.03267 0.07364 -0.444 0.65960
---
signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(1356744) family taken to be 0.6455783)

Null deviance: 57.577 on 45 degrees of freedom
Residual deviance: 27.216 on 42 degrees of freedom
(4 Beobachtungen als fehlend gelöscht)
AIC: 296.2

Number of Fisher Scoring iterations: 4

```

Figure 3.1.6B

```
Call:  
glm(formula = leaves_flowering ~ group + tray * position, family = negative.binomial(theta = 84796  
8.3478),  
    data = data)  
  
Coefficients:  
Estimate Std. Error t value Pr(>|t|)  
(Intercept) 2.8630691 0.1401247 20.432 < 2e-16 ***  
groupintraspecific competition -0.2101148 0.0638763 -3.289 0.00229 **  
groupinterspecific competition -0.3108027 0.0667371 -4.657 4.5e-05 ***  
tray 0.0087045 0.0316796 0.275 0.78511  
positionB 0.0777772 0.1515272 0.513 0.61097  
positionC 0.0230310 0.1967917 0.117 0.90750  
tray:positionB -0.0056133 0.0365722 -0.153 0.87890  
tray:positionC -0.0007991 0.0463578 -0.017 0.98634  
---  
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1  
  
(Dispersion parameter for Negative Binomial(847968.3) family taken to be 0.4455068)  
  
Null deviance: 28.045 on 42 degrees of freedom  
Residual deviance: 14.671 on 35 degrees of freedom  
AIC: 228.5  
  
Number of Fisher Scoring iterations: 4
```

Figure 3.1.6C

```
Call:  
glm(formula = number_leaves_30.03 ~ group + tray * position,  
    family = negative.binomial(theta = 896204.3158), data = data)  
  
Coefficients:  
Estimate Std. Error t value Pr(>|t|)  
(Intercept) 3.151886 0.132983 23.701 < 2e-16 ***  
groupintraspecific competition -0.358153 0.062106 -5.767 1.57e-06 ***  
groupinterspecific competition -0.520371 0.065576 -7.935 2.47e-09 ***  
tray 0.004465 0.030168 0.148 0.883  
positionB 0.001729 0.145132 0.012 0.991  
positionC -0.061636 0.192795 -0.320 0.751  
tray:positionB -0.007146 0.035076 -0.204 0.840  
tray:positionC 0.015565 0.044877 0.347 0.731  
---  
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1  
  
(Dispersion parameter for Negative Binomial(896204.3) family taken to be 0.4741387)  
  
Null deviance: 57.393 on 42 degrees of freedom  
Residual deviance: 18.559 on 35 degrees of freedom  
AIC: 236.81  
  
Number of Fisher Scoring iterations: 4
```

Figure 3.1.6D

```

Call:
glm(formula = leaves_flowering ~ group + tray * position, family = negative.binomial(theta = 84796
8.3478),
  data = data)

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.8630691 0.1401247 20.432 < 2e-16 ***
groupintraspecific competition -0.2101148 0.0638763 -3.289 0.00229 **
groupinterspecific competition -0.3108027 0.0667371 -4.657 4.5e-05 ***
tray 0.0087045 0.0316796 0.275 0.78511
positionB 0.0777772 0.1515272 0.513 0.61097
positionC 0.0230310 0.1967917 0.117 0.90750
tray:positionB -0.0056133 0.0365722 -0.153 0.87890
tray:positionC -0.0007991 0.0463578 -0.017 0.98634
---
signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(847968.3) family taken to be 0.4455068)

Null deviance: 28.045 on 42 degrees of freedom
Residual deviance: 14.671 on 35 degrees of freedom
AIC: 228.5

Number of Fisher Scoring iterations: 4

```

Figure 3.1.6E

```

Call:
glm(formula = DPG_flowering ~ group + tray * position, family = negative.binomial(theta = 4429044.
155),
  data = data)

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 3.12934 0.05899 53.047 <2e-16 ***
groupintraspecific competition 0.02646 0.02743 0.965 0.3414
groupinterspecific competition 0.02411 0.02766 0.872 0.3894
tray 0.04106 0.01302 3.154 0.0033 **
positionB 0.05217 0.06382 0.817 0.4192
positionC 0.05912 0.08045 0.735 0.4673
tray:positionB -0.01025 0.01519 -0.675 0.5044
tray:positionC -0.01911 0.01889 -1.011 0.3187
---
signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(4429044) family taken to be 0.1335487)

Null deviance: 8.3179 on 42 degrees of freedom
Residual deviance: 4.6222 on 35 degrees of freedom
AIC: 241.71

Number of Fisher Scoring iterations: 3

```

Figure 3.1.6F

```

Call:
glm(formula = siliques ~ group + tray * position, family = negative.binomial(theta = 9),
     data = data)

Coefficients:
                                         Estimate Std. Error t value Pr(>|t|)    
(Intercept)                         6.1072165  0.3108022 19.650 < 2e-16 ***
groupintraspecific competition -1.5226029  0.1469803 -10.359 4.69e-12 ***
groupinterspecific competition -1.8451849  0.1550270 -11.902 1.13e-13 ***
tray                                -0.0009205  0.0702342 -0.013   0.990  
positionB                            0.0798265  0.3363512  0.237   0.814  
positionC                            -0.4677452  0.4326850 -1.081   0.287  
tray:positionB                      -0.0292495  0.0818602 -0.357   0.723  
tray:positionC                      0.0753763  0.1028388  0.733   0.469  
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(9) family taken to be 1.197911)

Null deviance: 303.219 on 41 degrees of freedom
Residual deviance: 43.123 on 34 degrees of freedom
(1 Beobachtung als fehlend gelöscht)
AIC: 461.09

Number of Fisher Scoring iterations: 6

```

Figure 3.1.6G

```

Call:
glm(formula = output + 1 ~ group + tray * position, family = negative.binomial(theta = 149759.746
6),
     data = branches[which(branches$metric_ID == "RI"), ])

Coefficients:
                                         Estimate Std. Error t value Pr(>|t|)    
(Intercept)                         1.58161   0.27573  5.736 1.72e-06 ***
groupintraspecific competition -1.39855   0.13911 -10.054 7.37e-12 ***
groupinterspecific competition -1.60282   0.15370 -10.428 2.80e-12 ***
tray                                 0.04468   0.06101  0.732   0.469  
positionB                            0.22672   0.30239  0.750   0.458  
positionC                            -0.22667   0.50080 -0.453   0.654  
tray:positionB                      -0.03684   0.06948 -0.530   0.599  
tray:positionC                      0.01736   0.10466  0.166   0.869  
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(149759.7) family taken to be 0.2856147)

Null deviance: 82.4396 on 42 degrees of freedom
Residual deviance: 8.6326 on 35 degrees of freedom
AIC: 139.76

Number of Fisher Scoring iterations: 4

```

```

Call:
glm(formula = output + 1 ~ group + tray * position, family = negative.binomial(theta = 25.7054942
6),
  data = branches[which(branches$metric_ID == "RII"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.73010 0.41470 4.172 0.000189 ***
groupintraspecific competition -2.26790 0.22629 -10.022 8.0e-12 ***
groupinterspecific competition -2.25826 0.23297 -9.693 1.9e-11 ***
tray 0.08351 0.09029 0.925 0.361313
positionB 0.47957 0.45199 1.061 0.295953
positionC 0.45947 0.72734 0.632 0.531679
tray:positionB -0.04643 0.10116 -0.459 0.649072
tray:positionC -0.05375 0.14701 -0.366 0.716829
---
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(25.7055) family taken to be 0.5514234)

Null deviance: 177.263 on 42 degrees of freedom
Residual deviance: 18.438 on 35 degrees of freedom
AIC: 157.01

Number of Fisher scoring iterations: 4

Call:
glm(formula = output ~ group + tray * position, family = negative.binomial(theta = 485035.5236),
  data = branches[which(branches$metric_ID == "CI"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.58223 0.16668 9.493 3.25e-11 ***
groupintraspecific competition -0.07603 0.07799 -0.975 0.336280
groupinterspecific competition -0.36564 0.08574 -4.264 0.000144 ***
tray -0.04064 0.03900 -1.042 0.304524
positionB -0.04983 0.17945 -0.278 0.782899
positionC 0.06706 0.23286 0.288 0.775062
tray:positionB 0.01297 0.04511 0.287 0.775436
tray:positionC -0.01349 0.05755 -0.234 0.816029
---
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(485035.5) family taken to be 0.1592075)

Null deviance: 9.6447 on 42 degrees of freedom
Residual deviance: 5.5283 on 35 degrees of freedom
AIC: 157.49

Number of Fisher scoring iterations: 4

Call:
glm(formula = output + 1 ~ group + tray * position, family = negative.binomial(theta = 88083.7210
7),
  data = branches[which(branches$metric_ID == "CII"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.53425 0.40010 3.835 0.000502 ***
groupintraspecific competition -1.55253 0.18259 -8.503 4.93e-10 ***
groupinterspecific competition -2.24684 0.23931 -9.389 4.30e-11 ***
tray 0.15735 0.08484 1.855 0.072084 .
positionB 1.04708 0.42780 2.448 0.019541 *
positionC 0.61999 0.68702 0.902 0.372998
tray:positionB -0.22891 0.09475 -2.416 0.021051 *
tray:positionC -0.12138 0.13912 -0.872 0.388907
---
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(88083.72) family taken to be 0.6985563)

Null deviance: 178.604 on 42 degrees of freedom
Residual deviance: 22.979 on 35 degrees of freedom
AIC: 163.6

Number of Fisher scoring iterations: 5

```

```

Call:
glm(formula = output ~ group + tray * position, family = negative.binomial(theta = 334.3385694),
     data = branches[which(branches$metric_ID == "Total"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.86250  0.26997 10.603 1.79e-12 ***
groupintraspecific competition -1.58641  0.12989 -12.214 3.54e-14 ***
groupinterspecific competition -2.14417  0.16401 -13.073 4.98e-15 ***
tray          0.07728  0.05918  1.306  0.2001
positionB    0.55232  0.29236  1.889  0.0672 .
positionC    0.37321  0.46791  0.798  0.4305
tray:positionB -0.09795  0.06645 -1.474  0.1494
tray:positionC -0.06566  0.09704 -0.677  0.5031
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(334.3386) family taken to be 0.9268447)

Null deviance: 424.045 on 42 degrees of freedom
Residual deviance: 32.798 on 35 degrees of freedom
AIC: 217.98

Number of Fisher scoring iterations: 4

```

Figure 3.1.7B

```

Call:
glm(formula = output + 1 ~ condition * root_separation + tray,
     family = negative.binomial(theta = 261814.8663), data = branches[which(branches$metric_ID ==
      "RI"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.69057  0.12901 13.104 3.23e-13 ***
conditioncompetition -1.25988  0.14269 -8.829 1.91e-09 ***
root_separationw/ -0.42455  0.10274 -4.132 0.000312 ***
tray          0.03357  0.04660  0.720 0.477478
conditioncompetition:root_separationw/ 0.97796  0.18443  5.303 1.35e-05 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(261814.9) family taken to be 0.1946293)

Null deviance: 27.180 on 31 degrees of freedom
Residual deviance: 5.115 on 27 degrees of freedom
AIC: 112.16

Number of Fisher scoring iterations: 4

Call:
glm(formula = output + 1 ~ condition * root_separation + tray,
     family = negative.binomial(theta = 6), data = branches[which(branches$metric_ID ==
      "RII"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.07266  0.35361  5.861 3.05e-06 ***
conditioncompetition -2.07283  0.38683 -5.359 1.16e-05 ***
root_separationw/ -1.34590  0.29986 -4.488 0.000120 ***
tray          0.07254  0.12947  0.560 0.579879
conditioncompetition:root_separationw/ 2.00063  0.51591  3.878 0.000611 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(6) family taken to be 0.8463419)

Null deviance: 72.433 on 31 degrees of freedom
Residual deviance: 25.720 on 27 degrees of freedom
AIC: 137.82

Number of Fisher scoring iterations: 5

```

```

Call:
glm(formula = output ~ condition * root_separation + tray, family = negative.binomial(theta = 1068
728.771),
  data = branches[which(branches$metric_ID == "CI"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.17265 0.08288 14.149 5.24e-14 ***
conditioncompetition -0.09387 0.07522 -1.248 0.223
root_separationw/ 0.08046 0.06978 1.153 0.259
tray -0.01402 0.02794 -0.502 0.620
conditioncompetition:root_separationw/ 0.12319 0.09910 1.243 0.225
---
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(1068729) family taken to be 0.06256945)

Null deviance: 2.2913 on 31 degrees of freedom
Residual deviance: 1.6979 on 27 degrees of freedom
AIC: 109.25

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output + 1 ~ condition * root_separation + tray,
  family = negative.binomial(theta = 250518.6733), data = branches[which(branches$metric_ID ==
  "CII"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.27203 0.15530 14.630 2.35e-14 ***
conditioncompetition -0.64341 0.15460 -4.162 0.000288 ***
root_separationw/ -0.19454 0.13286 -1.464 0.154686
tray -0.04365 0.05445 -0.802 0.429724
conditioncompetition:root_separationw/ 0.79769 0.20032 3.982 0.000464 ***
---
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(250518.7) family taken to be 0.5487793)

Null deviance: 27.811 on 31 degrees of freedom
Residual deviance: 15.621 on 27 degrees of freedom
AIC: 146.53

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output ~ condition * root_separation + tray, family = negative.binomial(theta = 2014
29.0372),
  data = branches[which(branches$metric_ID == "Total"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 3.16405 0.13919 22.731 < 2e-16 ***
conditioncompetition -1.18263 0.15067 -7.849 1.94e-08 ***
root_separationw/ -0.56089 0.11740 -4.777 5.54e-05 ***
tray 0.01024 0.05040 0.203 0.84
conditioncompetition:root_separationw/ 1.20558 0.19649 6.136 1.48e-06 ***
---
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(201429) family taken to be 0.9619007)

Null deviance: 104.183 on 31 degrees of freedom
Residual deviance: 26.451 on 27 degrees of freedom
AIC: 178.34

Number of Fisher Scoring iterations: 4

```

Figure 3.1.7C

```
Call:  
glm(formula = siliques ~ condition * root_separation + tray,  
     family = negative.binomial(theta = 14.64167276), data = data)  
  
Coefficients:  
Estimate Std. Error t value Pr(>|t|)  
(Intercept) 5.81228 0.17218 33.757 < 2e-16 ***  
conditioncompetition -1.49310 0.15349 -9.727 2.56e-10 ***  
root_separationw/ -0.76589 0.14451 -5.300 1.36e-05 ***  
tray 0.03119 0.05883 0.530 0.6  
conditioncompetition:root_separationw/ 1.43589 0.20739 6.923 1.93e-07 ***  
---  
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
  
(Dispersion parameter for Negative Binomial(14.6417) family taken to be 1.137716)
```

```
Null deviance: 156.278 on 31 degrees of freedom  
Residual deviance: 32.536 on 27 degrees of freedom  
AIC: 343.69
```

Number of Fisher Scoring iterations: 4

Figure 3.1.8B

S pots

```
welch Two Sample t-test  
  
data: small$RI by small$condition  
t = 2.6833, df = 14.272, p-value = 0.0176  
alternative hypothesis: true difference in means between group single and group competition is not  
equal to 0  
95 percent confidence interval:  
 0.2425327 2.1574673  
sample estimates:  
 mean in group single mean in group competition  
 1.8 0.6  
  
welch Two Sample t-test  
  
data: small$RII by small$condition  
t = 2.0604, df = 9, p-value = 0.06943  
alternative hypothesis: true difference in means between group single and group competition is not  
equal to 0  
95 percent confidence interval:  
 -0.2447921 5.2447921  
sample estimates:  
 mean in group single mean in group competition  
 2.5 0.0  
  
welch Two Sample t-test  
  
data: small$CI by small$condition  
t = -1.0392, df = 17.845, p-value = 0.3126  
alternative hypothesis: true difference in means between group single and group competition is not  
equal to 0  
95 percent confidence interval:  
 -1.8137257 0.6137257  
sample estimates:  
 mean in group single mean in group competition  
 3.6 4.2
```

```

welch Two Sample t-test

data: small$CII by small$condition
t = 1.7192, df = 14.105, p-value = 0.1074
alternative hypothesis: true difference in means between group single and group competition is not
equal to 0
95 percent confidence interval:
-0.4933422 4.4933422
sample estimates:
mean in group single mean in group competition
5.1 3.1

welch Two Sample t-test

data: small$Total by small$condition
t = 3.1173, df = 16.248, p-value = 0.006539
alternative hypothesis: true difference in means between group single and group competition is not
equal to 0
95 percent confidence interval:
1.636025 8.563975
sample estimates:
mean in group single mean in group competition
13.0 7.9

```

M pots

```

welch Two Sample t-test

data: large$RI by large$condition
t = 2.0896, df = 17.385, p-value = 0.05165
alternative hypothesis: true difference in means between group single and group competition is not
equal to 0
95 percent confidence interval:
-0.005589717 1.405589717
sample estimates:
mean in group single mean in group competition
4.7 4.0

welch Two Sample t-test

data: large$RII by large$condition
t = 2.0169, df = 17.377, p-value = 0.05942
alternative hypothesis: true difference in means between group single and group competition is not
equal to 0
95 percent confidence interval:
-0.1728463 7.9728463
sample estimates:
mean in group single mean in group competition
12.6 8.7

welch Two Sample t-test

data: large$CI by large$condition
t = -1.2127, df = 15.94, p-value = 0.2429
alternative hypothesis: true difference in means between group single and group competition is not
equal to 0
95 percent confidence interval:
-1.3743261 0.3743261
sample estimates:
mean in group single mean in group competition
3.6 4.1

welch Two Sample t-test

data: large$CII by large$condition
t = -0.80356, df = 17.908, p-value = 0.4322
alternative hypothesis: true difference in means between group single and group competition is not
equal to 0
95 percent confidence interval:
-3.253943 1.453943
sample estimates:
mean in group single mean in group competition
9.6 10.5

```

```

welch Two Sample t-test

data: large$Total by large$condition
t = 1.2938, df = 17.71, p-value = 0.2124
alternative hypothesis: true difference in means between group single and group competition is not
equal to 0
95 percent confidence interval:
-2.002546 8.402546
sample estimates:
mean in group single mean in group competition
30.5 27.3

```

Figure 3.1.8C

S pots

```

welch Two Sample t-test

data: small$siliques by small$condition
t = 2.8878, df = 16.906, p-value = 0.01027
alternative hypothesis: true difference in means between group single and group competition is not
equal to 0
95 percent confidence interval:
4.870444 31.329556
sample estimates:
mean in group single mean in group competition
121.3 103.2

```

M pots

```

welch Two Sample t-test

data: large$siliques by large$condition
t = -0.44779, df = 13.864, p-value = 0.6612
alternative hypothesis: true difference in means between group single and group competition is not
equal to 0
95 percent confidence interval:
-53.30605 34.90605
sample estimates:
mean in group single mean in group competition
295.2 304.4

```

Figure 3.1.9 B

```

Call:
glm(formula = siliques ~ condition * root_separation * sowing_l.p. *
soil_volume + tray * position, family = negative.binomial(theta = 8.4),
data = data)

```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	6.1210839	0.5249121	11.6611588	4.196374e-10
conditioncompetition	-3.2200285	0.3697245	-8.7092651	4.640785e-08
root_separationw/	3.5347628	0.4768876	7.4121510	5.107964e-07
sowing_l.p.1 week	0.4317884	0.4348285	0.9930084	3.331847e-01
soil_volumeM	-1.1112460	0.3111163	-3.5718027	2.034852e-03
tray	-0.3825922	0.3396318	-1.1264911	2.739850e-01
positionB	-0.4865464	0.7156007	-0.6799133	5.047600e-01
positionC	-1.6608045	0.9964328	-1.6667501	1.119641e-01
root_separationw/:sowing_l.p.1 week	-1.1493771	0.5572117	-2.0627298	5.307847e-02
tray:positionB	0.3399355	0.4401056	0.7723953	4.493822e-01
tray:positionC	0.9215262	0.5895018	1.5632287	1.345017e-01

```

signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(8.4) family taken to be 1.660165)

Null deviance: 272.254 on 29 degrees of freedom
Residual deviance: 30.572 on 19 degrees of freedom
AIC: 283.73

Number of Fisher scoring iterations: 7

```

Figure 3.1.9 D

```

call:
glm(formula = output + 1 ~ condition * root_separation * sowing_l.p. *
soil_volume + tray, family = negative.binomial(theta = 116337.2669),
data = branches[which(branches$metric_id == "RI"), ])

              Estimate Std. Error      t value     Pr(>|t|)
(Intercept)    1.23448256  0.2596331  4.7547202 8.579344e-05
conditioncompetition -1.33500107  0.3116926 -4.2830698 2.780691e-04
root_separationw/ 1.00846912  0.3986767  2.5295412 1.873011e-02
sowing_l.p.1 week 0.31954036  0.3649839  0.8754918 3.903580e-01
soil_volumem -0.26997025  0.2261873 -1.1935697 2.448127e-01
tray          0.08329518  0.1789493  0.4654680 6.459738e-01
root_separationw/:sowing_l.p.1 week -0.77152566  0.4723418 -1.6334055 1.159998e-01

```

```

signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(116337.3) family taken to be 0.3845561)

Null deviance: 21.7502 on 29 degrees of freedom
Residual deviance: 8.1952 on 23 degrees of freedom
AIC: 97.902

Number of Fisher scoring iterations: 4

```

```

call:
glm(formula = output + 1 ~ condition * root_separation * sowing_l.p. *
soil_volume + tray, family = negative.binomial(theta = 40.47139748),
data = branches[which(branches$metric_id == "RII"), ])

              Estimate Std. Error      t value     Pr(>|t|)
(Intercept)    1.829636412  0.3905590  4.684661053 0.0001021472
conditioncompetition -1.856537536  0.4632897 -4.007293006 0.0005524449
root_separationw/ 1.969905611  0.6609725  2.980314151 0.0066922943
sowing_l.p.1 week -0.004496136  0.6068269 -0.007409255 0.9941522153
soil_volumem -1.395632805  0.4016567 -3.474690852 0.0020506563
tray          0.022385678  0.2883212  0.077641451 0.9387847653
root_separationw/:sowing_l.p.1 week -0.246777304  0.7766067 -0.317763550 0.7535313092

```

```

signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(40.4714) family taken to be 0.8901449)

Null deviance: 52.246 on 29 degrees of freedom
Residual deviance: 17.183 on 23 degrees of freedom
AIC: 104.48

Number of Fisher scoring iterations: 5

```

```

call:
glm(formula = output + 1 ~ condition * root_separation * sowing_l.p. *
soil_volume + tray, family = negative.binomial(theta = 344047.3541),
data = branches[which(branches$metric_id == "CI"), ])

```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	1.65581226	0.1404990	11.7852257	3.166569e-11
conditioncompetition	-0.73759893	0.1489717	-4.9512689	5.263562e-05
root_separationw/	0.97115221	0.2003999	4.8460725	6.835270e-05
sowing_l.p.1 week	-0.07401355	0.1784758	-0.4146980	6.822055e-01
soil_volumeM	-0.25922424	0.1351369	-1.9182346	6.757874e-02
tray	-0.10890346	0.0947234	-1.1496997	2.620826e-01
root_separationw/:sowing_l.p.1 week	-0.02606994	0.2200203	-0.1184888	9.067091e-01

signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(344047.4) family taken to be 0.1651374)

Null deviance: 12.9334 on 29 degrees of freedom
 Residual deviance: 3.9085 on 23 degrees of freedom
 AIC: 108.93

Number of Fisher Scoring iterations: 4

Call:

```
glm(formula = output + 1 ~ condition * root_separation * sowing_l.p. *
    soil_volume + tray, family = negative.binomial(theta = 117917.381),
    data = branches[which(branches$metric_id == "CII"), ])
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	2.3215981	0.2285428	10.1582645	5.679686e-10
conditioncompetition	-2.1041338	0.3519472	-5.9785490	4.270957e-06
root_separationw/	2.1421002	0.4215801	5.0811232	3.815309e-05
sowing_l.p.1 week	0.3717595	0.4361457	0.8523745	4.027952e-01
soil_volumeM	-0.5971847	0.2095003	-2.8505189	9.052448e-03
tray	-0.1833802	0.1679604	-1.0918060	2.862237e-01
root_separationw/:sowing_l.p.1 week	-0.7772248	0.5059052	-1.5363051	1.381073e-01

signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(117917.4) family taken to be 0.552007)

Null deviance: 59.173 on 29 degrees of freedom
 Residual deviance: 13.142 on 23 degrees of freedom
 AIC: 113.95

Number of Fisher Scoring iterations: 5

Call:

```
glm(formula = output + 1 ~ condition * root_separation * sowing_l.p. *
    soil_volume + tray, family = negative.binomial(theta = 87613.00543),
    data = branches[which(branches$metric_id == "Total"), ])
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	3.1183440	0.2192350	14.2237503	6.927324e-13
conditioncompetition	-2.2072741	0.3421567	-6.4510612	1.392143e-06
root_separationw/	2.2497679	0.4100053	5.4871684	1.404690e-05
sowing_l.p.1 week	0.2613049	0.4350739	0.6005988	5.539801e-01
soil_volumeM	-0.7358295	0.2019969	-3.6427766	1.359674e-03
tray	-0.1028681	0.1612646	-0.6378836	5.298496e-01
root_separationw/:sowing_l.p.1 week	-0.6457166	0.5002313	-1.2908360	2.095856e-01

signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(87613.01) family taken to be 1.160113)

Null deviance: 143.309 on 29 degrees of freedom
 Residual deviance: 24.062 on 23 degrees of freedom
 AIC: 147.75

Number of Fisher Scoring iterations: 5

Figure 3.1.9 F

```

call:
glm(formula = siliques ~ condition * root_separation * sowing_l.p.,
family = negative.binomial(theta = 6.165047973), data = data)

                               Estimate Std. Error   t value   Pr(>|t|)
(Intercept)                  6.6398758  0.2140306 31.023017 7.014506e-21
conditioncompetition          -4.5857521  0.3566085 -12.859345 2.946770e-12
root_separationw/             -0.9013699  0.3035688 -2.969245 6.675410e-03
sowing_l.p.1 week              1.0277862  0.3737040  2.750268 1.114093e-02
conditioncompetition:root_separationw/ 3.4362870  0.4709613  7.296326 1.547175e-07
root_separationw/:sowing_l.p.1 week -0.7219768  0.4852675 -1.487791 1.498281e-01

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(6.165) family taken to be 1.400788)

Null deviance: 339.76  on 29  degrees of freedom
Residual deviance: 31.07  on 24  degrees of freedom
AIC: 314.16

Number of Fisher Scoring iterations: 5

```

Figure 3.1.9 G

```

call:
glm(formula = output + 1 ~ condition * root_separation * sowing_l.p.,
family = negative.binomial(theta = 183139.9636), data = branches[which(branches$metric_id ==
"RI"), ])

                               Estimate Std. Error   t value   Pr(>|t|)
(Intercept)                  1.8870696  0.1015393 18.5846231 9.407720e-16
conditioncompetition          -1.8870696  0.2799208 -6.7414408 5.670668e-07
root_separationw/             -0.2006707  0.1513656 -1.3257354 1.974085e-01
sowing_l.p.1 week              0.3364722  0.3415371  0.9851703 3.343688e-01
conditioncompetition:root_separationw/ 1.4244461  0.3331225  4.2760431 2.617577e-04
root_separationw/:sowing_l.p.1 week -0.3970969  0.3973984 -0.9992413 3.276467e-01

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(183140) family taken to be 0.3402253)

Null deviance: 44.4622  on 29  degrees of freedom
Residual deviance: 8.3912  on 24  degrees of freedom
AIC: 107.83

Number of Fisher Scoring iterations: 4

call:
glm(formula = output + 1 ~ condition * root_separation * sowing_l.p.,
family = negative.binomial(theta = 6.593592463), data = branches[which(branches$metric_id ==
"RII"), ])

                               Estimate Std. Error   t value   Pr(>|t|)
(Intercept)                  3.025291e+00  0.2107599  1.435420e+01 2.819253e-13
conditioncompetition          -3.025291e+00  0.5476671 -5.523960e+00 1.110230e-05
root_separationw/             -6.273958e-01  0.3134312 -2.001702e+00 5.674449e-02
sowing_l.p.1 week              5.238858e-17  0.7148699  7.328407e-17 1.000000e+00
conditioncompetition:root_separationw/ 1.908330e+00  0.6701019  2.847820e+00 8.882502e-03
root_separationw/:sowing_l.p.1 week 7.335124e-09  0.8376091  8.757216e-09 1.000000e+00

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(6.5936) family taken to be 1.109351)

Null deviance: 124.515  on 29  degrees of freedom
Residual deviance: 26.144  on 24  degrees of freedom
AIC: 147.79

Number of Fisher Scoring iterations: 4

```

```

Call:
glm(formula = output + 1 ~ condition * root_separation * sowing_l.p.,
     family = negative.binomial(theta = 5.514668369), data = branches[which(branches$metric_id ==
      "RIII"), ])

              Estimate Std. Error      t value    Pr(>|t|)
(Intercept) 2.694627e+00  0.1784825  1.509743e+01 9.428333e-14
conditioncompetition -2.694627e+00  0.4278440 -6.298154e+00 1.644457e-06
root_separationw/ -1.819158e+00  0.3292276 -5.525534e+00 1.105866e-05
sowing_l.p.1 week  3.050740e-15  0.5498990  5.547819e-15 1.000000e+00
conditioncompetition:root_separationw/ 1.819158e+00  0.6409210  2.838351e+00 9.081084e-03
root_separationw/:sowing_l.p.1 week -2.927598e-15  0.7776746 -3.764554e-15 1.000000e+00

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(5.5147) family taken to be 0.6399307)

Null deviance: 98.957  on 29  degrees of freedom
Residual deviance: 14.850  on 24  degrees of freedom
AIC: 111.98

Number of Fisher scoring iterations: 4

Call:
glm(formula = output + 1 ~ condition * root_separation * sowing_l.p.,
     family = negative.binomial(theta = 255834.8634), data = branches[which(branches$metric_id ==
      "CI"), ])

              Estimate Std. Error      t value    Pr(>|t|)
(Intercept) 1.7578579  0.1039379 16.9125783 7.744927e-15
conditioncompetition -0.9694006  0.1982007 -4.8910051 5.480574e-05
root_separationw/ -0.1892420  0.1544564 -1.2252133 2.323837e-01
sowing_l.p.1 week  0.2411621  0.2255172  1.0693734 2.955393e-01
conditioncompetition:root_separationw/ 0.4993969  0.2705974  1.8455350 7.733305e-02
root_separationw/:sowing_l.p.1 week -0.0588405  0.2985776 -0.1970694 8.454327e-01

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(255834.9) family taken to be 0.3132825)

Null deviance: 19.5754  on 29  degrees of freedom
Residual deviance: 7.5287  on 24  degrees of freedom
AIC: 112.78

Number of Fisher scoring iterations: 4

Call:
glm(formula = output + 1 ~ condition * root_separation * sowing_l.p.,
     family = negative.binomial(theta = 117189.6822), data = branches[which(branches$metric_id ==
      "CII"), ])

              Estimate Std. Error      t value    Pr(>|t|)
(Intercept) 2.4510051  0.1134341 21.6073107 3.077633e-17
conditioncompetition -2.4510051  0.4026342 -6.0874236 2.749279e-06
root_separationw/ -0.1286174  0.1658327 -0.7755850 4.455698e-01
sowing_l.p.1 week  0.7884574  0.4659263  1.6922363 1.035456e-01
conditioncompetition:root_separationw/ 1.2272297  0.4759174  2.5786610 1.647927e-02
root_separationw/:sowing_l.p.1 week -0.2384110  0.5436355 -0.4385494 6.649105e-01

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(117189.7) family taken to be 0.7462288)

Null deviance: 107.047  on 29  degrees of freedom
Residual deviance: 17.798  on 24  degrees of freedom
AIC: 126.4

Number of Fisher scoring iterations: 5

Call:
glm(formula = output + 1 ~ condition * root_separation * sowing_l.p.,
     family = negative.binomial(theta = 333704.1645), data = branches[which(branches$metric_id ==
      "CIII"), ])

```

```

              Estimate Std. Error   t value   Pr(>|t|) 
(Intercept)      2.4510051 0.06129545 39.9867407 1.775022e-23
conditioncompetition -2.4510051 0.21757408 -11.2651518 4.570406e-11
root_separationw/ -2.2686835 0.20018721 -11.3328094 4.046162e-11
sowing_1.p.1 week  0.1823216 0.28266436  0.6450108 5.250387e-01
conditioncompetition:root_separationw/  2.2686835 0.35670383  6.3601323 1.415077e-06
root_separationw/:sowing_1.p.1 week -0.1823216 0.40873199 -0.4460663 6.595478e-01

signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(333704.2) family taken to be 0.2179061)

Null deviance: 116.8402 on 29 degrees of freedom
Residual deviance:  5.1965 on 24 degrees of freedom
AIC: 89.762

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output + 1 ~ condition * root_separation * sowing_1.p.,
     family = negative.binomial(theta = 18.22211237), data = branches[which(branches$metric_id ==
"Total"), ])

              Estimate Std. Error   t value   Pr(>|t|) 
(Intercept)      4.1896547 0.1274475 32.873560 1.800740e-21
conditioncompetition -3.4011974 0.3666055 -9.277540 2.082320e-09
root_separationw/ -0.7884574 0.1915800 -4.115552 3.933230e-04
sowing_1.p.1 week  0.7375989 0.4258018  1.732259 9.606221e-02
conditioncompetition:root_separationw/  2.3025851 0.4367865  5.271649 2.092112e-05
root_separationw/:sowing_1.p.1 week -0.5064872 0.4983640 -1.016300 3.196232e-01

signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(18.2221) family taken to be 1.15971)

Null deviance: 312.728 on 29 degrees of freedom
Residual deviance: 27.205 on 24 degrees of freedom
AIC: 185.46

Number of Fisher Scoring iterations: 4

```

Figure 3.1.10 B

```

Call:
glm(formula = output + 1 ~ condition * competitor + tray * position,
     family = negative.binomial(theta = 516419.3261), data = branches[which(branches$metric_ID ==
"RI"), ])

Coefficients: (3 not defined because of singularities)
              Estimate Std. Error   t value   Pr(>|t|) 
(Intercept)      1.134e+00 3.005e-01  3.772  0.00105 ** 
conditioncompetition -1.205e+00 1.257e-01 -9.580 2.62e-09 *** 
competitororg11  1.010e-01 1.459e-01  0.692  0.49624    
competitorwerewolf NA          NA        NA        NA      
tray             -1.410e-16 1.873e-01  0.000  1.00000    
positionB        2.381e-01 3.428e-01  0.694  0.49465    
positionC        2.649e-03 5.173e-01  0.005  0.99596    
conditioncompetition:competitororg11 NA          NA        NA        NA      
conditioncompetition:competitorwerewolf NA          NA        NA        NA      
tray:positionB   -5.638e-02 2.161e-01 -0.261  0.79663    
tray:positionC   8.327e-17 3.244e-01  0.000  1.00000    
--- 
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(516419.3) family taken to be 0.1052597)

Null deviance: 22.4623 on 29 degrees of freedom
Residual deviance:  2.3053 on 22 degrees of freedom
AIC: 90.044

Number of Fisher Scoring iterations: 4

```

```

Call:
glm(formula = output + 1 ~ condition * competitor + tray * position,
     family = negative.binomial(theta = 204627.3439), data = branches[which(branches$metric_ID ==
      "RII"), ])

Coefficients: (3 not defined because of singularities)
                                         Estimate Std. Error t value Pr(>|t|)
(Intercept)                         0.004567  0.506187  0.009   0.993
conditioncompetition                 -0.587260  0.197468 -2.974   0.007 **
competitororg11                     -0.023710  0.211712 -0.112   0.912
competitorwerewolf                  NA         NA       NA      NA
tray                                  0.405464  0.295542  1.372   0.184
positionB                            0.144653  0.594111  0.243   0.810
positionC                            0.598437  0.775625  0.772   0.449
conditioncompetition:competitororg11 NA         NA       NA      NA
conditioncompetition:competitorwerewolf NA         NA       NA      NA
tray:positionB                      -0.107214  0.357044 -0.300   0.767
tray:positionC                      -0.405464  0.476547 -0.851   0.404
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(204627.3) family taken to be 0.2096269)

Null deviance: 9.3544  on 29  degrees of freedom
Residual deviance: 4.5466  on 22  degrees of freedom
AIC: 85.024

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output ~ condition * competitor + tray * position,
     family = negative.binomial(theta = 335288.7426), data = branches[which(branches$metric_ID ==
      "CI"), ])

Coefficients: (3 not defined because of singularities)
                                         Estimate Std. Error t value Pr(>|t|)
(Intercept)                         1.287084  0.299796  4.293 0.000295 ***
conditioncompetition                 -0.380098  0.122088 -3.113 0.005065 **
competitororg11                     0.009715  0.128942  0.075 0.940624
competitorwerewolf                  NA         NA       NA      NA
tray                                  0.080043  0.181857  0.440 0.664129
positionB                            0.135836  0.349657  0.388 0.701392
positionC                            0.087976  0.489456  0.180 0.859000
conditioncompetition:competitororg11 NA         NA       NA      NA
conditioncompetition:competitorwerewolf NA         NA       NA      NA
tray:positionB                      -0.068462  0.219991 -0.311 0.758577
tray:positionC                      -0.234194  0.311365 -0.752 0.459932
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(335288.7) family taken to be 0.2063679)

Null deviance: 10.3160  on 29  degrees of freedom
Residual deviance: 4.5512  on 22  degrees of freedom
AIC: 110.29

Number of Fisher Scoring iterations: 4

```

```

Call:
glm(formula = output + 1 ~ condition * competitor + tray * position,
     family = negative.binomial(theta = 486628.2411), data = branches[which(branches$metric_ID ==
      "CII"), ])

Coefficients: (3 not defined because of singularities)
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    2.148e+00  2.767e-01   7.765 9.65e-08 ***
conditioncompetition -2.013e+00  1.541e-01  -13.062 7.67e-12 ***
competitororg11 -6.628e-03  1.953e-01  -0.034  0.9732
competitorwerewolf NA          NA          NA          NA
tray           -2.368e-17  1.734e-01   0.000  1.0000
positionB      -7.782e-01  3.370e-01  -2.309  0.0307 *
positionC      -1.313e-01  6.218e-01  -0.211  0.8347
conditioncompetition:competitororg11 NA          NA          NA          NA
conditioncompetition:competitorwerewolf NA          NA          NA          NA
tray:positionB  3.751e-01  2.071e-01   1.811  0.0838 .
tray:positionC  2.027e-16  3.878e-01   0.000  1.0000
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(486628.2) family taken to be 0.1804468)

Null deviance: 91.9062 on 29 degrees of freedom
Residual deviance: 4.4002 on 22 degrees of freedom
AIC: 98.763

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output + 1 ~ condition * competitor + tray * position,
     family = negative.binomial(theta = 614068.8399), data = branches[which(branches$metric_ID ==
      "Total"), ])

Coefficients: (3 not defined because of singularities)
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    2.56579  0.21724  11.811 5.39e-11 ***
conditioncompetition -1.34231  0.09774 -13.733 2.86e-12 ***
competitororg11  0.02970  0.11796   0.252  0.804
competitorwerewolf NA          NA          NA          NA
tray           0.10920  0.13329   0.819  0.421
positionB      -0.15785  0.25547  -0.618  0.543
positionC      0.06595  0.41639   0.158  0.876
conditioncompetition:competitororg11 NA          NA          NA          NA
conditioncompetition:competitorwerewolf NA          NA          NA          NA
tray:positionB  0.07959  0.15739   0.506  0.618
tray:positionC -0.21456  0.26303  -0.816  0.423
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(614068.8) family taken to be 0.2435574)

Null deviance: 115.80 on 29 degrees of freedom
Residual deviance:  5.42 on 22 degrees of freedom
AIC: 130.38

Number of Fisher Scoring iterations: 4

```

Figure 3.1.10 C

```

Call:
glm(formula = siliques ~ condition * competitor + tray * position,
     family = negative.binomial(theta = 54.02527075), data = data)

Coefficients: (3 not defined because of singularities)
                                         Estimate Std. Error t value Pr(>|t|)
(Intercept)                         4.52282   0.31392 14.407 1.10e-12 ***
conditioncompetition                 -1.86904   0.12607 -14.825 6.22e-13 ***
competitororgl1                      0.08857   0.14016  0.632  0.5340
competitorwerewolf                   NA        NA      NA      NA
tray                                    0.44353   0.18968  2.338  0.0289 *
positionB                            0.91116   0.36367  2.505  0.0201 *
positionC                            0.68850   0.51630  1.334  0.1960
conditioncompetition:competitororgl1    NA        NA      NA      NA
conditioncompetition:competitorwerewolf NA        NA      NA      NA
tray:positionB                       -0.53740   0.22549 -2.383  0.0262 *
tray:positionC                       -0.57700   0.32339 -1.784  0.0882 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(54.0253) family taken to be 1.735188)

Null deviance: 850.668 on 29 degrees of freedom
Residual deviance: 37.649 on 22 degrees of freedom
AIC: 251.5

Number of Fisher Scoring iterations: 4

```

Figure 3.1.10 D

```

Call:
glm(formula = output + 1 ~ condition * genotype_comp + tray,
     family = negative.binomial(theta = 164265.0321), data = branches[which(branches$metric_ID ==
"RI"), ])

Coefficients: (3 not defined because of singularities)
                                         Estimate Std. Error t value Pr(>|t|)
(Intercept)                         0.48103   0.25206  1.908 0.067437 .
conditioncompetition                 -0.83141   0.19384 -4.289 0.000219 ***
genotype_compCol-0                  0.02125   0.22488  0.094 0.925454
genotype_compcpc-2                  NA        NA      NA      NA
tray                                  0.21556   0.15712  1.372 0.181794
conditioncompetition:genotype_compCol-0 NA        NA      NA      NA
conditioncompetition:genotype_compcpc-2 NA        NA      NA      NA
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(164265) family taken to be 0.2516871)

Null deviance: 13.3250 on 29 degrees of freedom
Residual deviance: 6.4223 on 26 degrees of freedom
AIC: 80.061

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output ~ condition * genotype_comp + tray, family = negative.binomial(theta = 374705.2069),
     data = branches[which(branches$metric_ID == "CI"), ])

Coefficients: (3 not defined because of singularities)
                                         Estimate Std. Error t value Pr(>|t|)
(Intercept)                         1.28566   0.13427  9.575 5.19e-10 ***
conditioncompetition                 -0.60009   0.10431 -5.753 4.66e-06 ***
genotype_compCol-0                  0.09448   0.11455  0.825  0.417
genotype_compcpc-2                  NA        NA      NA      NA
tray                                 0.03514   0.08478  0.414  0.682
conditioncompetition:genotype_compCol-0 NA        NA      NA      NA
conditioncompetition:genotype_compcpc-2 NA        NA      NA      NA
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(374705.2) family taken to be 0.1432664)

Null deviance: 9.7858 on 29 degrees of freedom
Residual deviance: 3.7316 on 26 degrees of freedom
AIC: 97.275

Number of Fisher Scoring iterations: 4

```

```

Call:
glm(formula = output ~ condition * genotype_comp + tray, family = negative.binomial(theta = 23),
     data = branches[which(branches$metric_ID == "CII"), ])

Coefficients: (3 not defined because of singularities)
              Estimate Std. Error t value Pr(>|t|)
(Intercept)      0.21072   0.44308   0.476   0.638
conditioncompetition -21.47908 3720.33146 -0.006   0.995
genotype_compcol-0    0.03028 5260.11978   0.000   1.000
genotype_compcpc-2        NA       NA       NA       NA
tray            0.30010   0.28580   1.050   0.303
conditioncompetition:genotype_compcol-0    NA       NA       NA       NA
conditioncompetition:genotype_compcpc-2    NA       NA       NA       NA

(Dispersion parameter for Negative Binomial(23) family taken to be 0.3563238)

Null deviance: 53.647 on 29 degrees of freedom
Residual deviance: 12.519 on 26 degrees of freedom
AIC: 42.43

Number of Fisher Scoring iterations: 19

Call:
glm(formula = output ~ condition * genotype_comp + tray, family = negative.binomial(theta = 210922.0069),
     data = branches[which(branches$metric_ID == "Total"), ])

Coefficients: (3 not defined because of singularities)
              Estimate Std. Error t value Pr(>|t|)
(Intercept)      1.7095    0.1946   8.783 2.94e-09 ***
conditioncompetition -1.2208    0.1640  -7.445 6.62e-08 ***
genotype_compcol-0    0.1065    0.1967   0.541   0.593
genotype_compcpc-2        NA       NA       NA       NA
tray            0.1565    0.1239   1.263   0.218
conditioncompetition:genotype_compcol-0    NA       NA       NA       NA
conditioncompetition:genotype_compcpc-2    NA       NA       NA       NA
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(210922) family taken to be 0.4231079)

Null deviance: 48.575 on 29 degrees of freedom
Residual deviance: 11.596 on 26 degrees of freedom
AIC: 110.35

Number of Fisher Scoring iterations: 4

```

Figure 3.1.10 E

```

Call:
glm(formula = Siliques_19.02 ~ condition * genotype_comp + tray,
     family = negative.binomial(theta = 36.20223544), data = data)

Coefficients: (3 not defined because of singularities)
              Estimate Std. Error t value Pr(>|t|)
(Intercept)      4.51489   0.14283 31.610 < 2e-16 ***
conditioncompetition -1.49885   0.11114 -13.486 3.02e-13 ***
genotype_compcol-0    0.02828   0.12558   0.225   0.824
genotype_compcpc-2        NA       NA       NA       NA
tray            0.05183   0.09096   0.570   0.574
conditioncompetition:genotype_compcol-0    NA       NA       NA       NA
conditioncompetition:genotype_compcpc-2    NA       NA       NA       NA
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(36.2022) family taken to be 1.086436)

Null deviance: 343.348 on 29 degrees of freedom
Residual deviance: 28.181 on 26 degrees of freedom
AIC: 221.37

Number of Fisher Scoring iterations: 4

```

Figure 3.1.11 D

```

Call:
glm(formula = metric_output ~ condition * soil * heat_treatment,
     family = negative.binomial(theta = 8.9), data = siliques)

```

```

Estimate Std. Error t value Pr(>|t|)
(Intercept) 4.6613405 0.1240089 37.5887432 1.971348e-58
conditioncompetition -1.2906023 0.1790222 -7.2091758 1.402634e-10
soilVM-roots -1.6436293 0.1890448 -8.6943909 1.094290e-13
soilVM-roots+heat 0.1084964 0.1706112 0.6359275 5.263689e-01
soilVM+heat 0.7784765 0.1692265 4.6002033 1.316400e-05
soilVM+roots -1.6656082 0.1960543 -8.4956490 2.883322e-13
soilVM+roots+heat -0.5816866 0.1836795 -3.1668568 2.078256e-03
conditioncompetition:soilVM-roots -0.3725632 0.3240648 -1.1496567 2.532020e-01
conditioncompetition:soilVM-roots+heat -0.2126273 0.2545153 -0.8354206 4.055994e-01
conditioncompetition:soilVM+heat -0.4754488 0.2468974 -1.9256936 5.716488e-02
conditioncompetition:soilVM+roots 0.5386146 0.3009329 1.7898162 7.670352e-02
conditioncompetition:soilVM+roots+heat 0.5386787 0.2673233 2.0150831 4.675205e-02

```

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(8.9) family taken to be 1.136197)

Null deviance: 908.57 on 105 degrees of freedom
Residual deviance: 113.39 on 94 degrees of freedom
(11 Beobachtungen als fehlend gelöscht)
AIC: 883.44

Number of Fisher Scoring iterations: 4

Figure 3.1.11 E

```

Call:
glm(formula = metric_output + 1 ~ condition * soil * heat_treatment,
family = negative.binomial(theta = 184378.2253), data = branches[which(branches$metric_ID ==
"RI"), ])

```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.89381788	0.09968524	8.96640108	2.897230e-14
conditioncompetition	-0.89381788	0.17832285	-5.01235755	2.521820e-06
soilVM-roots	-0.69314718	0.17265977	-4.01452634	1.197250e-04
soilVM-roots+heat	-0.01834914	0.13800583	-0.13295913	8.945099e-01
soilVM+heat	0.17089286	0.13219601	1.29272326	1.992753e-01
soilVM+roots	-0.89381788	0.19304018	-4.63021676	1.170189e-05
soilVM+roots+heat	-0.67067432	0.17832287	-3.76101131	2.940626e-04
conditioncompetition:soilVM-roots	0.69314718	0.28107054	2.46609687	1.547213e-02
conditioncompetition:soilVM-roots+heat	0.01834914	0.25533995	0.07186159	9.428647e-01
conditioncompetition:soilVM+heat	-0.17089286	0.24738546	-0.69079589	4.913962e-01
conditioncompetition:soilVM+roots	0.89381788	0.30059553	2.97349023	3.740475e-03
conditioncompetition:soilVM+roots+heat	0.67067432	0.28458443	2.35667960	2.051461e-02

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(184378.2) family taken to be 0.2186177)

Null deviance: 51.356 on 105 degrees of freedom
Residual deviance: 19.937 on 94 degrees of freedom
(11 Beobachtungen als fehlend gelöscht)
AIC: 279.68

Number of Fisher Scoring iterations: 4

```

Call:
glm(formula = metric_output + 1 ~ condition * soil * heat_treatment,
family = negative.binomial(theta = 374968.1266), data = branches[which(branches$metric_ID ==
"RII"), ])

```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-5.695458e-16	0.1072284	-5.11521e-15	1.000000e+00
conditioncompetition	2.437787e-15	0.1478041	1.649336e-14	1.000000e+00
soilVM-roots	3.236876e-16	0.1516438	2.134525e-15	1.000000e+00
soilVM-roots+heat	9.531018e-02	0.1445867	6.591904e-01	5.113852e-01
soilVM+heat	7.884574e-01	0.1272856	6.194393e+00	1.532762e-08
soilVM+roots	1.685523e-16	0.1563109	1.078314e-15	1.000000e+00
soilVM+roots+heat	5.916891e-17	0.1563109	3.785335e-16	1.000000e+00
conditioncompetition:soilVM-roots	-1.395747e-15	0.2151259	-6.488050e-15	1.000000e+00
conditioncompetition:soilVM-roots+heat	-9.531018e-02	0.2067641	-4.609611e-01	6.458913e-01
conditioncompetition:soilVM+heat	-7.884574e-01	0.1920883	-4.104662e+00	8.623431e-05
conditioncompetition:soilVM+roots	-1.013784e-15	0.2226303	-4.553667e-15	1.000000e+00
conditioncompetition:soilVM+roots+heat	-7.778408e-16	0.2184408	-3.560877e-15	1.000000e+00

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(374968.1) family taken to be 0.103481)

Null deviance: 18.3803 on 105 degrees of freedom
Residual deviance: 9.1243 on 94 degrees of freedom
(11 Beobachtungen als fehlend gelöscht)
AIC: 251.08

Number of Fisher Scoring iterations: 5

```

Call:
glm(formula = metric_output ~ condition * soil * heat_treatment,
     family = negative.binomial(theta = 41158.21988), data = branches[which(branches$metric_ID ==
      "CI"), ])

              Estimate Std. Error   t value   Pr(>|t|)
(Intercept) 1.44036158 0.1254215 11.4841697 1.355489e-19
conditioncompetition -0.52407085 0.1990979 -2.6322267 9.916103e-03
soilVM-roots -1.15267951 0.2560083 -4.5025078 1.925462e-05
soilVM-roots+heat -0.07938503 0.1762317 -0.4504582 6.534174e-01
soilVM+heat 0.04124296 0.1712194 0.2408778 8.101744e-01
soilVM+roots -1.44036158 0.3007296 -4.7895570 6.219602e-06
soilVM+roots+heat -0.05406722 0.1855006 -0.2914666 7.713367e-01
conditioncompetition:soilVM-roots -0.74444047 0.5372935 -1.3855378 1.691669e-01
conditioncompetition:soilVM-roots+heat -0.14375852 0.2969414 -0.4841309 6.294190e-01
conditioncompetition:soilVM+heat 0.07208573 0.2730813 0.2639717 7.923796e-01
conditioncompetition:soilVM+roots -0.72869212 0.6428048 -1.1336133 2.598397e-01
conditioncompetition:soilVM+roots+heat -0.63907996 0.3436437 -1.8597167 6.605309e-02

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(41158.22) family taken to be 0.5976995)

Null deviance: 169.628 on 105 degrees of freedom
Residual deviance: 68.783 on 94 degrees of freedom
(11 Beobachtungen als fehlend gelöscht)
AIC: 336.33

Number of Fisher Scoring iterations: 5

Call:
glm(formula = metric_output + 1 ~ condition * soil * heat_treatment,
     family = negative.binomial(theta = 115023.4054), data = branches[which(branches$metric_ID ==
      "CII"), ])

              Estimate Std. Error   t value   Pr(>|t|)
(Intercept) 1.7540191 0.08820207 19.886372 1.902981e-35
conditioncompetition -1.7540191 0.21961755 -7.986698 3.404655e-12
soilVM-roots -1.7540191 0.22962266 -7.638702 1.815748e-11
soilVM-roots+heat -0.9211100 0.15927254 -5.783232 9.539265e-08
soilVM+heat 0.3378449 0.11302221 2.989191 3.569515e-03
soilVM+roots -1.7540191 0.24154697 -7.261607 1.094488e-10
soilVM+roots+heat -1.4355654 0.21107939 -6.801068 9.511663e-10
conditioncompetition:soilVM-roots 1.7540191 0.37913607 4.626358 1.188066e-05
conditioncompetition:soilVM-roots+heat 0.9211100 0.33281672 2.767619 6.800919e-03
conditioncompetition:soilVM+heat -0.3378449 0.30606952 -1.103818 2.724900e-01
conditioncompetition:soilVM+roots 1.7540191 0.39570968 4.432591 2.520519e-05
conditioncompetition:soilVM+roots+heat 1.4355654 0.36820118 3.898862 1.812170e-04

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(115023.4) family taken to be 0.4045191)

Null deviance: 226.595 on 105 degrees of freedom
Residual deviance: 37.766 on 94 degrees of freedom
(11 Beobachtungen als fehlend gelöscht)
AIC: 312.33

Number of Fisher Scoring iterations: 5

Call:
glm(formula = metric_output + 1 ~ condition * soil * heat_treatment,
     family = negative.binomial(theta = 29894.84923), data = branches[which(branches$metric_ID ==
      "Total"), ])

              Estimate Std. Error   t value   Pr(>|t|)
(Intercept) 2.4375044 0.07559474 32.244365 1.282985e-52
conditioncompetition -1.1847414 0.15009079 -7.893499 5.337546e-12
soilVM-roots -1.4992348 0.17691317 -8.474410 3.197431e-13
soilVM-roots+heat -0.3962841 0.11557580 -3.428781 9.017154e-04
soilVM+heat 0.3225055 0.09716185 3.319261 1.285337e-03
soilVM+roots -1.7443572 0.20613214 -8.462325 3.391155e-13
soilVM+roots+heat -0.7102835 0.13708400 -5.181374 1.253865e-06
conditioncompetition:soilVM-roots 0.5649255 0.31875075 1.772311 7.958283e-02
conditioncompetition:soilVM-roots+heat 0.2421334 0.22795679 1.062190 2.908708e-01
conditioncompetition:soilVM+heat -0.2402674 0.20430033 -1.176050 2.425447e-01
conditioncompetition:soilVM+roots 0.7429087 0.35310189 2.103950 3.805237e-02
conditioncompetition:soilVM+roots+heat 0.2684507 0.26133247 1.027238 3.069444e-01

```

```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(29894.85) family taken to be 0.5883749)

Null deviance: 391.676 on 105 degrees of freedom
Residual deviance: 57.353 on 94 degrees of freedom
(11 Beobachtungen als fehlend gelöscht)
AIC: 419.09

Number of Fisher Scoring iterations: 5

```

FIGURE 3.2.1 A

```

Call:
glm(formula = output + 1 ~ comp * genotype, family = negative.binomial(theta = 162351.5109),
     data = data[which(data$metric_ID == "R1"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept)      1.56219   0.06595 23.688 < 2e-16 ***
compcompetition -1.33904   0.14942 -8.962 8.07e-12 ***
genotypepephyB-9 -0.17589   0.09404 -1.870 0.0675 .
compcompetition:genotypepephyB-9  0.10690   0.21466  0.498  0.6208
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(162351.5) family taken to be 0.2696381)

Null deviance: 61.183 on 51 degrees of freedom
Residual deviance: 12.050 on 48 degrees of freedom
(4 Beobachtungen als fehlend gelöscht)
AIC: 163.6

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output + 1 ~ comp * genotype, family = negative.binomial(theta = 13),
     data = data[which(data$metric_ID == "RII"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept)      1.5459    0.1477 10.468 1.22e-13 ***
compcompetition -1.0864    0.2820 -3.852 0.000368 ***
genotypepephyB-9 -0.1935    0.2090 -0.926 0.359382
compcompetition:genotypepephyB-9 -0.2660    0.4673 -0.569 0.572034
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(13) family taken to be 0.9776032)

Null deviance: 70.206 on 48 degrees of freedom
Residual deviance: 37.098 on 45 degrees of freedom
(7 Beobachtungen als fehlend gelöscht)
AIC: 188.27

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output + 1 ~ comp * genotype, family = negative.binomial(theta = 489961.0966),
     data = data[which(data$metric_ID == "CI"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept)      1.71172   0.05011 34.161 < 2e-16 ***
compcompetition -0.24538   0.07738 -3.171 0.00273 **
genotypepephyB-9 -0.32542   0.07432 -4.379 7.04e-05 ***
compcompetition:genotypepephyB-9 -0.04230   0.12528 -0.338 0.73719
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(489961.1) family taken to be 0.1807675)

Null deviance: 16.7797 on 48 degrees of freedom
Residual deviance: 8.2491 on 45 degrees of freedom
(7 Beobachtungen als fehlend gelöscht)
AIC: 177.95

Number of Fisher Scoring iterations: 4

```

```

Call:
glm(formula = output + 1 ~ comp * genotype, family = negative.binomial(theta = 92334.65475),
     data = data[which(data$metric_ID == "CII"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.17998 0.07888 27.636 < 2e-16 ***
compcompetition -2.02583 0.23944 -8.461 7.43e-11 ***
genotypepephyB-9 -0.28286 0.11566 -2.446 0.018438 *
compcompetition:genotypepephyB-9 1.15036 0.30513 3.770 0.000473 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(92334.65) family taken to be 0.7155052)

Null deviance: 129.507 on 48 degrees of freedom
Residual deviance: 29.215 on 45 degrees of freedom
(7 Beobachtungen als fehlend gelöscht)
AIC: 194.33

Number of Fisher Scoring iterations: 5

Call:
glm(formula = output + 1 ~ comp * genotype, family = negative.binomial(theta = 3995.644422),
     data = data[which(data$metric_ID == "Total"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 3.03717 0.06467 46.963 < 2e-16 ***
compcompetition -1.36319 0.14773 -9.228 6.06e-12 ***
genotypepephyB-9 -0.29418 0.09508 -3.094 0.00339 **
compcompetition:genotypepephyB-9 0.18418 0.23008 0.801 0.42762
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(3995.644) family taken to be 1.12755)

Null deviance: 235.671 on 48 degrees of freedom
Residual deviance: 46.514 on 45 degrees of freedom
(7 Beobachtungen als fehlend gelöscht)
AIC: 257.99

Number of Fisher Scoring iterations: 4

```

Figure 3.2.1 B

```

Call:
glm(formula = output + 1 ~ condition * genotype, family = negative.binomial(theta = 243749.0624),
     data = branches[which(branches$ID == "RI"), ])

Coefficients:
                                         Estimate Std. Error t value Pr(>|t|)
(Intercept)                         1.22378   0.05381 22.743 < 2e-16 ***
conditioncompetition      -0.88730   0.09963 -8.906 9.43e-13 ***
genotypepephyB                  -0.08880   0.09038 -0.982 0.329647
genotypepephyAphyB                -0.63599   0.10535 -6.037 9.19e-08 ***
conditioncompetition:genotypepephyB  0.54078   0.14803  3.653 0.000529 ***
conditioncompetition:genotypepephyAphyB 0.29952   0.18138  1.651 0.103642
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(243749.1) family taken to be 0.1476643)

Null deviance: 34.3645 on 68 degrees of freedom
Residual deviance: 8.9551 on 63 degrees of freedom
(1 Beobachtung als fehlend gelöscht)
AIC: 199.48

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output + 1 ~ condition * genotype, family = negative.binomial(theta = 24246.10007),
     data = branches[which(branches$ID == "RII"), ])

Coefficients:
                                         Estimate Std. Error t value Pr(>|t|)
(Intercept)                         1.4028    0.1027 13.663 < 2e-16 ***
conditioncompetition      -1.4028    0.2311 -6.070 8.05e-08 ***
genotypepephyB                  0.3889    0.1498  2.596 0.01173 *
genotypepephyAphyB                -1.1405    0.2449 -4.656 1.71e-05 ***
conditioncompetition:genotypepephyB  -0.3889    0.3600 -1.080 0.28410
conditioncompetition:genotypepephyAphyB  1.1405    0.4088  2.789 0.00697 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(24246.1) family taken to be 0.6429019)

Null deviance: 131.607 on 68 degrees of freedom
Residual deviance: 40.385 on 63 degrees of freedom
(1 Beobachtung als fehlend gelöscht)
AIC: 221.26

Number of Fisher Scoring iterations: 5

Call:
glm(formula = output + 1 ~ condition * genotype, family = negative.binomial(theta = 333661.2506),
     data = branches[which(branches$ID == "CI"), ])

Coefficients:
                                         Estimate Std. Error t value Pr(>|t|)
(Intercept)                         1.450833   0.054779 26.485 < 2e-16 ***
conditioncompetition      -0.151550   0.080575 -1.881 0.064617 .
genotypepephyB                  -0.315853   0.099295 -3.181 0.002278 **
genotypepephyAphyB                0.007782   0.086411  0.090 0.928525
conditioncompetition:genotypepephyB  0.081281   0.141327  0.575 0.567255
conditioncompetition:genotypepephyAphyB -0.518608   0.140313 -3.696 0.000461 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(333661.3) family taken to be 0.1920419)

Null deviance: 24.471 on 68 degrees of freedom
Residual deviance: 13.231 on 63 degrees of freedom
(1 Beobachtung als fehlend gelöscht)
AIC: 238.03

Number of Fisher Scoring iterations: 4

```

```

Call:
glm(formula = output + 1 ~ condition * genotype, family = negative.binomial(theta = 108723.4766),
     data = branches[which(branches$ID == "CII"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.94591   0.07320 26.582 < 2e-16 ***
conditioncompetition -1.25276   0.15528 -8.068 2.72e-11 ***
genotypepephyB -0.38193   0.13581 -2.812 0.00655 **
genotypepephyAphyB -0.46431   0.13471 -3.447 0.00102 **
conditioncompetition:genotypepephyB 0.88271   0.23291  3.790 0.00034 ***
conditioncompetition:genotypepephyAphyB -0.04652   0.28946 -0.161 0.87283
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(108723.5) family taken to be 0.5626355)

Null deviance: 110.662 on 68 degrees of freedom
Residual deviance: 34.955 on 63 degrees of freedom
(1 Beobachtung als fehlend gelöscht)
AIC: 255.16

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output + 1 ~ condition * genotype, family = negative.binomial(theta = 191735.3158),
     data = branches[which(branches$ID == "Total"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.86410   0.05122 55.919 < 2e-16 ***
conditioncompetition -1.24142   0.10817 -11.476 < 2e-16 ***
genotypepephyB -0.14867   0.08773 -1.695 0.0951 .
genotypepephyAphyB -0.66688   0.10144 -6.574 1.1e-08 ***
conditioncompetition:genotypepephyB 0.38229   0.16599  2.303 0.0246 *
conditioncompetition:genotypepephyAphyB -0.08034   0.21934 -0.366 0.7154
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(191735.3) family taken to be 0.6898824)

Null deviance: 276.599 on 68 degrees of freedom
Residual deviance: 44.914 on 63 degrees of freedom
(1 Beobachtung als fehlend gelöscht)
AIC: 323.25

Number of Fisher Scoring iterations: 4

```

Figure 3.2.1 C

```

Call:
glm(formula = output ~ condition * genotype, family = negative.binomial(theta = 14.02459585),
     data = siliques)

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 5.302641   0.070904 74.786 < 2e-16 ***
conditioncompetition -1.494498   0.105778 -14.129 < 2e-16 ***
genotypepephyB -0.109067   0.116058 -0.940 0.35093
genotypepephyAphyB -0.074210   0.112278 -0.661 0.51106
conditioncompetition:genotypepephyB 0.499629   0.167822  2.977 0.00413 **
conditioncompetition:genotypepephyAphyB -0.008239   0.167926 -0.049 0.96102
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(14.0246) family taken to be 0.9885839)

Null deviance: 448.106 on 68 degrees of freedom
Residual deviance: 76.661 on 63 degrees of freedom
(1 Beobachtung als fehlend gelöscht)
AIC: 669.48

Number of Fisher Scoring iterations: 4

```

Figure 3.2.1 D

```
Call:  
glm(formula = dry_weight ~ genotype, family = negative.binomial(theta = 57.29418409),  
    data = data)  
  
Coefficients:  
            Estimate Std. Error t value Pr(>|t|)  
(Intercept)      5.56324   0.03870 143.758 <2e-16 ***  
genotypepephyB   -0.10792   0.06156 -1.753   0.0892 .  
genotypepephyBPhyB  0.05353   0.06102  0.877   0.3869  
---  
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1  
  
(Dispersion parameter for Negative Binomial(57.2942) family taken to be 1.05513)  
  
Null deviance: 41.563 on 34 degrees of freedom  
Residual deviance: 35.247 on 32 degrees of freedom  
AIC: 358.77  
  
Number of Fisher Scoring iterations: 4
```

Figure 3.2.2 A

```
Call:  
glm(formula = output + 1 ~ condition * genotype + tray, family = negative.binomial(theta = 8),  
    data = branches[which(branches$metric_ID == "RI"), ])  
  
Coefficients:  
            Estimate Std. Error t value Pr(>|t|)  
(Intercept)      1.0836   0.2879  3.764 0.000551 ***  
conditioncompetition -0.4930   0.2667 -1.848 0.072143 .  
genotypecry2-1     -0.7447   0.2709 -2.749 0.009002 **  
tray                 0.2996   0.1265  2.368 0.022918 *  
conditioncompetition:genotypecry2-1  0.2587   0.3999  0.647 0.521477  
---  
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1  
  
(Dispersion parameter for Negative Binomial(8) family taken to be 0.9249409)  
  
Null deviance: 51.943 on 43 degrees of freedom  
Residual deviance: 38.021 on 39 degrees of freedom  
AIC: 185.44  
  
Number of Fisher Scoring iterations: 7  
  
Call:  
glm(formula = output + 1 ~ condition * genotype + tray, family = negative.binomial(theta = 1.785470473),  
    data = branches[which(branches$metric_ID == "RII"), ])  
  
Coefficients:  
            Estimate Std. Error t value Pr(>|t|)  
(Intercept)      1.0009   0.4321  2.316 0.02589 *  
conditioncompetition -1.3266   0.4229 -3.137 0.00324 **  
genotypecry2-1     -1.2634   0.4077 -3.099 0.00359 **  
tray                 0.5890   0.1917  3.072 0.00386 **  
conditioncompetition:genotypecry2-1  1.0209   0.6017  1.697 0.09774 .  
---  
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1  
  
(Dispersion parameter for Negative Binomial(1.7855) family taken to be 1.025091)  
  
Null deviance: 54.906 on 43 degrees of freedom  
Residual deviance: 37.107 on 39 degrees of freedom  
AIC: 204.74  
  
Number of Fisher Scoring iterations: 9
```

```

Call:
glm(formula = output + 1 ~ condition * genotype + tray, family = negative.binomial(theta = 225976.5505),
     data = branches[which(branches$metric_ID == "CI"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.67187 0.13998 11.943 1.33e-14 ***
conditioncompetition -0.02480 0.14718 -0.168 0.86706
genotypecry2-1 0.44429 0.13366 3.324 0.00194 **
tray -0.10048 0.05811 -1.729 0.09168 .
conditioncompetition:genotypecry2-1 -0.21301 0.19021 -1.120 0.26961
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(225976.6) family taken to be 0.4730022)

Null deviance: 26.328 on 43 degrees of freedom
Residual deviance: 18.135 on 39 degrees of freedom
AIC: 181.29

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output + 1 ~ condition * genotype + tray, family = negative.binomial(theta = 4.11425227),
     data = branches[which(branches$metric_ID == "CII"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.85209 0.29778 6.220 2.57e-07 ***
conditioncompetition -0.29159 0.30078 -0.969 0.3383
genotypecry2-1 0.59758 0.27809 2.149 0.0379 *
tray -0.02727 0.12761 -0.214 0.8319
conditioncompetition:genotypecry2-1 -0.73890 0.40948 -1.805 0.0789 .
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(4.1143) family taken to be 1.030403)

Null deviance: 66.085 on 43 degrees of freedom
Residual deviance: 46.592 on 39 degrees of freedom
AIC: 244.48

Number of Fisher Scoring iterations: 5

Call:
glm(formula = output + 1 ~ condition * genotype + tray, family = negative.binomial(theta = 4.766491523),
     data = branches[which(branches$metric_ID == "Total"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.75458 0.24572 11.210 9.14e-14 ***
conditioncompetition -0.52025 0.24378 -2.134 0.0392 *
genotypecry2-1 0.02726 0.23406 0.116 0.9079
tray 0.11300 0.10549 1.071 0.2907
conditioncompetition:genotypecry2-1 -0.14239 0.33566 -0.424 0.6737
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(4.7665) family taken to be 1.055498)

Null deviance: 60.180 on 43 degrees of freedom
Residual deviance: 45.297 on 39 degrees of freedom
AIC: 308.85

Number of Fisher Scoring iterations: 7

```

Figure 3.2.2 B

```

Call:
glm(formula = output ~ condition * genotype + tray, family = negative.binomial(theta = 2.151925644),
     data = data[which(data$metric_ID == "Siliques"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 5.0930 0.3073 16.573 <2e-16 ***
conditioncompetition -0.7408 0.3021 -2.452 0.0188 *
genotypecry2-1 -0.1307 0.2991 -0.437 0.6646
tray 0.1531 0.1307 1.172 0.2484
conditioncompetition:genotypecry2-1 -0.1115 0.4156 -0.268 0.7900
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(2.1519) family taken to be 0.9596618)

Null deviance: 61.752 on 43 degrees of freedom
Residual deviance: 47.379 on 39 degrees of freedom
AIC: 519.9

Number of Fisher Scoring iterations: 11

```

Figure 3.2.2 C

```
Call:  
glm(formula = output + 1 ~ condition * genotype + tray, family = negative.binomial(theta = 182983.2253),  
  data = branches[which(branches$metric_ID == "RI"), ])  
  
Coefficients:  
Estimate Std. Error t value Pr(>|t|)  
(Intercept) 1.41606 0.09787 14.469 < 2e-16 ***  
conditioncompetition -1.36110 0.16621 -8.189 6.44e-10 ***  
genotypecry1-304 -0.00523 0.10244 -0.051 0.960  
tray2 -0.07894 0.10651 -0.741 0.463  
tray3 -0.08019 0.10823 -0.741 0.463  
conditioncompetition:genotypecry1-304 0.35091 0.21294 1.648 0.108  
---  
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
  
(Dispersion parameter for Negative Binomial(182983.2) family taken to be 0.2189285)  
  
Null deviance: 40.8151 on 43 degrees of freedom  
Residual deviance: 7.4834 on 38 degrees of freedom  
AIC: 137.03  
  
Number of Fisher Scoring iterations: 4  
  
Call:  
glm(formula = output + 1 ~ condition * genotype + tray, family = negative.binomial(theta = 72799.37896),  
  data = branches[which(branches$metric_ID == "RII"), ])  
  
Coefficients:  
Estimate Std. Error t value Pr(>|t|)  
(Intercept) 1.1122 0.1856 5.994 5.81e-07 ***  
conditioncompetition -0.8987 0.2908 -3.090 0.00373 **  
genotypecry1-304 0.5093 0.1913 2.662 0.01131 *  
tray2 -0.4100 0.1931 -2.123 0.04033 *  
tray3 -0.2140 0.1884 -1.136 0.26319  
conditioncompetition:genotypecry1-304 -0.5290 0.3835 -1.379 0.17588  
---  
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
  
(Dispersion parameter for Negative Binomial(72799.38) family taken to be 0.6014129)  
  
Null deviance: 63.618 on 43 degrees of freedom  
Residual deviance: 24.359 on 38 degrees of freedom  
AIC: 144.34  
  
Number of Fisher Scoring iterations: 5
```

```

Call:
glm(formula = output + 1 ~ condition * genotype + tray, family = negative.binomial(theta = 1124922.229),
     data = branches[which(branches$metric_ID == "CI"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.333295 0.053387 24.974 < 2e-16 ***
conditioncompetition 0.058810 0.062323 0.944 0.35132
genotypecry1-304 0.196655 0.058183 3.380 0.00169 **
tray2 -0.072011 0.049007 -1.469 0.14995
tray3 -0.009568 0.049442 -0.194 0.84757
conditioncompetition:genotypecry1-304 -0.115154 0.081962 -1.405 0.16815
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(1124922) family taken to be 0.07327874)

Null deviance: 4.0485 on 43 degrees of freedom
Residual deviance: 2.8447 on 38 degrees of freedom
AIC: 159.26

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output + 1 ~ condition * genotype + tray, family = negative.binomial(theta = 87092.64806),
     data = branches[which(branches$metric_ID == "CII"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.92409 0.14935 12.883 1.93e-15 ***
conditioncompetition -1.45483 0.27202 -5.348 4.45e-06 ***
genotypecry1-304 0.08653 0.15777 0.548 0.5866
tray2 -0.14484 0.15817 -0.916 0.3656
tray3 -0.02659 0.15567 -0.171 0.8653
conditioncompetition:genotypecry1-304 0.96573 0.31979 3.020 0.0045 **
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(87092.65) family taken to be 0.8987157)

Null deviance: 83.745 on 43 degrees of freedom
Residual deviance: 34.634 on 38 degrees of freedom
AIC: 188.78

Number of Fisher Scoring iterations: 5

Call:
glm(formula = output + 1 ~ condition * genotype + tray, family = negative.binomial(theta = 206555.717),
     data = branches[which(branches$metric_ID == "Total"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.69799 0.09925 27.184 < 2e-16 ***
conditioncompetition -1.11723 0.16120 -6.931 3.05e-08 ***
genotypecry1-304 0.20234 0.10402 1.945 0.0592 .
tray2 -0.19686 0.10391 -1.894 0.0658 .
tray3 -0.07947 0.10276 -0.773 0.4441
conditioncompetition:genotypecry1-304 0.38521 0.19850 1.941 0.0598 .
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(206555.7) family taken to be 0.8601783)

Null deviance: 134.679 on 43 degrees of freedom
Residual deviance: 32.686 on 38 degrees of freedom
AIC: 224.08

Number of Fisher Scoring iterations: 4

```

Figure 3.2.2 D

```

Call:
glm(formula = output ~ condition * genotype + tray, family = negative.binomial(theta = 16.87212487),
     data = cry1[which(cry1$metric_ID == "Siliques"), ])

Coefficients:
                                         Estimate Std. Error t value Pr(>|t|)
(Intercept)                         5.08169   0.11162  45.528 < 2e-16 ***
conditioncompetition      -1.29197   0.13500  -9.570 1.14e-11 ***
genotypecry1-304                  0.08715   0.12224   0.713   0.4803
tray2                               -0.02314   0.10828  -0.214   0.8319
tray3                               0.06386   0.11013   0.580   0.5655
conditioncompetition:genotypecry1-304 0.32597   0.18077   1.803   0.0793 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(16.8721) family taken to be 1.231703)

Null deviance: 239.782 on 43 degrees of freedom
Residual deviance: 44.858 on 38 degrees of freedom
AIC: 422.52

Number of Fisher Scoring iterations: 4

```

Figure 3.2.2 F

```

Call:
glm(formula = Siliques ~ condition * genotype * comp_spec * Soil_volume *
     partition, family = negative.binomial(theta = 11.78374636),
     data = siliques)

                                         Estimate Std. Error      t value      Pr(>|t|)
(Intercept)                         6.232202407  0.1105481  56.37547968 1.571645e-68
conditionsingle_s                   -1.087369521  0.2301994  -4.72359849 9.192242e-06
conditioncompetition      -1.718599414  0.1603360  -10.71873811 2.147416e-17
genotypecry1-304                  0.403744149  0.1560445   2.58736533 1.139216e-02
comp_specA.thaliana                0.312708742  0.1629702   1.91880943 5.840475e-02
Soil_volumes                        -0.362563087  0.1662755  -2.18049631 3.201756e-02
conditionsingle_s:genotypecry1-304 -0.391784949  0.3241891  -1.20850730 2.302433e-01
conditioncompetition:genotypecry1-304 -0.298520629  0.2262064  -1.31968270 1.905264e-01
genotypecry1-304:comp_specA.thaliana 0.293539150  0.2293327  1.27997075 2.040791e-01
genotypecry1-304:Soil_volumes       0.136641327  0.2338051   0.58442397 5.605015e-01
comp_specA.thaliana:Soil_volumes   0.056680309  0.2328011   0.24347102 8.082341e-01
genotypecry1-304:comp_specA.thaliana:Soil_volumes -0.005175986  0.3267430  -0.01584116 9.873987e-01

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(11.7837) family taken to be 1.125988)

Null deviance: 779.374 on 95 degrees of freedom
Residual deviance: 99.564 on 84 degrees of freedom
AIC: 1022.9

Number of Fisher Scoring iterations: 4

```

Figure 3.2.2 G

```

Call:
glm(formula = response_comp.sg ~ genotype * comp_spec * Soil_volume *
     partition, family = negative.binomial(theta = 150194.5267),
     data = responses)

Coefficients: (8 not defined because of singularities)
                                         Estimate Std. Error t value Pr(>|t|)
(Intercept)                         -1.405891  0.160826 -8.742 4.73e-12 ***
genotypecry1-304                   -0.004981  0.227726 -0.022   0.983
comp_specL.perenne                  -0.312709  0.247438 -1.264   0.212
Soil_volumeS                        1.144050  0.184672  6.195 7.31e-08 ***
partitionw/                         NA         NA       NA      NA
genotypecry1-304:comp_specL.perenne -0.293539  0.367261 -0.799   0.428
genotypecry1-304:Soil_volumes      0.386609  0.256364  1.508   0.137
comp_specL.perenne:Soil_volumes    -0.056680  0.285279 -0.199   0.843
genotypecry1-304:partitionw/       NA         NA       NA      NA
comp_specL.perenne:partitionw/     NA         NA       NA      NA
Soil_volumes:partitionw/           NA         NA       NA      NA
genotypecry1-304:comp_specL.perenne:Soil_volumes 0.005176  0.414153  0.012   0.990
genotypecry1-304:comp_specL.perenne:partitionw/   NA         NA       NA      NA
genotypecry1-304:Soil_volumes:partitionw/          NA         NA       NA      NA
comp_specL.perenne:Soil_volumes:partitionw/        NA         NA       NA      NA
genotypecry1-304:comp_specL.perenne:Soil_volumes:partitionw/ NA         NA       NA      NA
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(150194.5) family taken to be 0.05072604)

Null deviance: 48.748  on 63  degrees of freedom
Residual deviance: 35.252  on 56  degrees of freedom
AIC: 100.6

```

Figure 3.2.3 A

```

Call:
glm(formula = output + 1 ~ condition * genotype, family = negative.binomial(theta = 162725.8727),
     data = branches[which(branches$ID == "RI"), ])

Coefficients:
                                         Estimate Std. Error t value Pr(>|t|)
(Intercept)                         0.75769  0.09599  7.893 1.16e-10 ***
conditioncompetition                -0.75769  0.16992 -4.459 4.01e-05 ***
genotypehy5-51                      0.44629  0.12293  3.630 0.000514 ***
conditioncompetition:genotypehy5-51 -0.44629  0.23330 -1.913 0.060872 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(162725.9) family taken to be 0.2948672)

Null deviance: 46.338  on 59  degrees of freedom
Residual deviance: 17.259  on 56  degrees of freedom
AIC: 168.58

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output + 1 ~ condition * genotype, family = negative.binomial(theta = 165979.9319),
     data = branches[which(branches$ID == "RII"), ])

Coefficients:
                                         Estimate Std. Error t value Pr(>|t|)
(Intercept)                         0.12516  0.09386  1.334  0.1878
conditioncompetition                -0.12516  0.13709 -0.913  0.3652
genotypehy5-51                      0.21131  0.12626  1.674  0.0998 .
conditioncompetition:genotypehy5-51 -0.21131  0.18950 -1.115  0.2696
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(165979.9) family taken to be 0.1497632)

Null deviance: 8.2979  on 59  degrees of freedom
Residual deviance: 6.9327  on 56  degrees of freedom
AIC: 139.14

Number of Fisher Scoring iterations: 4

```

```

Call:
glm(formula = output + 1 ~ condition * genotype, family = negative.binomial(theta = 699534.0987),
     data = branches[which(branches$ID == "CI"), ])

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)      1.59601   0.03963 40.275 < 2e-16 ***
conditioncompetition -0.43286   0.06318 -6.852 6.08e-09 ***
genotypehy5-51    -0.02740   0.05643 -0.486 0.62919
conditioncompetition:genotypehy5-51  0.26707   0.08666  3.082  0.00319 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(699534.1) family taken to be 0.1162052)

Null deviance: 13.6626  on 59  degrees of freedom
Residual deviance: 6.6935  on 56  degrees of freedom
AIC: 212.61

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output + 1 ~ condition * genotype, family = negative.binomial(theta = 47237.75205),
     data = branches[which(branches$ID == "CII"), ])

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)      1.5546   0.1060 14.661 < 2e-16 ***
conditioncompetition -1.3182   0.2308 -5.712 4.45e-07 ***
genotypehy5-51    0.4558   0.1355  3.363  0.0014 **
conditioncompetition:genotypehy5-51 -0.1814   0.3038 -0.597  0.5529
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(47237.75) family taken to be 0.7982563)

Null deviance: 149.361  on 59  degrees of freedom
Residual deviance: 47.842  on 56  degrees of freedom
AIC: 228.41

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output + 1 ~ condition * genotype, family = negative.binomial(theta = 149913.3726),
     data = branches[which(branches$ID == "Total"), ])

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)      2.29590   0.06982 32.885 < 2e-16 ***
conditioncompetition -1.05270   0.13726 -7.669 2.71e-10 ***
genotypehy5-51    0.34316   0.09128  3.759 0.000409 ***
conditioncompetition:genotypehy5-51 -0.03173   0.18035 -0.176 0.861002
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(149913.4) family taken to be 0.7261999)

Null deviance: 178.007  on 59  degrees of freedom
Residual deviance: 43.973  on 56  degrees of freedom
AIC: 277.22

Number of Fisher Scoring iterations: 4

```

Figure 3.2.3 B

```

Call:
glm(formula = Siliques ~ condition * genotype, family = negative.binomial(theta = 18.32503105),
     data = siliques)

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)      3.25810   0.07186 45.337 < 2e-16 ***
conditionsingle    1.41536   0.09334 15.164 < 2e-16 ***
genotypehy5-51    0.70841   0.09615  7.368 8.54e-10 ***
conditionsingle:genotypehy5-51 -0.32308   0.12718 -2.540  0.0139 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(18.325) family taken to be 0.8326749)

Null deviance: 426.527  on 59  degrees of freedom
Residual deviance: 59.441  on 56  degrees of freedom
AIC: 525.63

Number of Fisher Scoring iterations: 4

```

Figure 3.2.3 C

```

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 574311.185),
  data = branches[which(branches$ID == "RI"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.38629  0.07179 19.311 < 2e-16 ***
Conditioncompetition -1.38629  0.16052 -8.636 5.01e-11 ***
Genotypepepif4 pif5  0.22314  0.08494  2.627  0.0118 *
GenotypepepifQ  0.18232  0.08544  2.134  0.0385 *
Conditioncompetition:Genotypepepif4 pif5 -0.12783  0.19286 -0.663  0.5109
Conditioncompetition:GenotypepepifQ  -0.18232  0.19550 -0.933  0.3561
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(574311.2) family taken to be 0.103064)

Null deviance: 68.9895 on 49 degrees of freedom
Residual deviance: 4.5539 on 44 degrees of freedom
AIC: 152.31

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 12.29785105),
  data = branches[which(branches$ID == "RII"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.2809   0.2124   6.032 3.03e-07 ***
Conditioncompetition -1.2809   0.4253  -3.011 0.004296 **
Genotypepepif4 pif5  1.0799   0.2369   4.558 4.09e-05 ***
GenotypepepifQ  0.8473   0.2402   3.528 0.000994 ***
Conditioncompetition:Genotypepepif4 pif5 -1.0799   0.5098  -2.118 0.039820 *
Conditioncompetition:GenotypepepifQ  -0.8473   0.5113  -1.657 0.104597
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(12.2979) family taken to be 0.6280336)

Null deviance: 174.520 on 49 degrees of freedom
Residual deviance: 35.659 on 44 degrees of freedom
AIC: 204.98

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 312616.2911),
  data = branches[which(branches$ID == "CI"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.64866  0.09435 17.475 < 2e-16 ***
Conditioncompetition -0.16705  0.13936 -1.199 0.237041
Genotypepepif4 pif5  -0.45474  0.12615 -3.605 0.000792 ***
GenotypepepifQ  -0.34033  0.12311 -2.764 0.008298 **
Conditioncompetition:Genotypepepif4 pif5 0.13628  0.18348  0.743 0.461573
Conditioncompetition:GenotypepepifQ  0.13966  0.17917  0.779 0.439895
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(312616.3) family taken to be 0.231422)

Null deviance: 15.156 on 49 degrees of freedom
Residual deviance: 10.656 on 44 degrees of freedom
AIC: 180.45

Number of Fisher Scoring iterations: 4

```

```

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 49271.32652),
     data = branches[which(branches$ID == "CII"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.1041 0.1545 13.620 < 2e-16 ***
Conditioncompetition -1.9218 0.4323 -4.445 5.88e-05 ***
Genotypepepf4 pif5 -0.2796 0.1991 -1.404 0.1673
GenotypepepfQ -0.2020 0.1961 -1.030 0.3086
Conditioncompetition:Genotypepepf4 pif5 1.0528 0.4902 2.147 0.0373 *
Conditioncompetition:GenotypepepfQ 0.8526 0.4940 1.726 0.0914 .
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(49271.33) family taken to be 0.9783135)

Null deviance: 110.585 on 49 degrees of freedom
Residual deviance: 43.572 on 44 degrees of freedom
AIC: 211.14

Number of Fisher Scoring iterations: 5

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 87255.25136),
     data = branches[which(branches$ID == "Total"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.8904 0.1053 27.457 < 2e-16 ***
Conditioncompetition -1.3643 0.2333 -5.847 5.65e-07 ***
Genotypepepf4 pif5 0.2877 0.1234 2.331 0.0244 *
GenotypepepfQ 0.2231 0.1246 1.792 0.0801 .
Conditioncompetition:Genotypepepf4 pif5 -0.2245 0.2810 -0.799 0.4286
Conditioncompetition:GenotypepepfQ -0.1600 0.2815 -0.568 0.5727
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(87255.25) family taken to be 0.9971273)

Null deviance: 350.499 on 49 degrees of freedom
Residual deviance: 42.878 on 44 degrees of freedom
AIC: 262.08

Number of Fisher Scoring iterations: 4

```

Figure 3.2.3 D

```

Call:
glm(formula = Siliques ~ Condition * Genotype, family = negative.binomial(theta = 12.45380587),
     data = data)

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 5.52545 0.14272 38.715 < 2e-16 ***
Conditioncompetition -2.00499 0.21662 -9.256 6.87e-12 ***
Genotypepepf4 pif5 0.12598 0.17463 0.721 0.474
GenotypepepfQ 0.02867 0.17476 0.164 0.870
Conditioncompetition:Genotypepepf4 pif5 0.01455 0.26432 0.055 0.956
Conditioncompetition:GenotypepepfQ 0.03161 0.26489 0.119 0.906
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(12.4538) family taken to be 1.208407)

Null deviance: 530.278 on 49 degrees of freedom
Residual deviance: 54.968 on 44 degrees of freedom
AIC: 496.72

Number of Fisher Scoring iterations: 4

```

Figure 3.2.4 A

```

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 390150.7871),
     data = branches[which(branches$ID == "RI"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.38629  0.07545 18.373 < 2e-16 ***
Conditioncompetition -1.38629  0.16872 -8.217 2.8e-10 ***
Genotypepeaxr4-1 0.37156  0.08750  4.246 0.000118 ***
Genotypetir1-1 afb2-3 afb4-8 -0.05129  0.09322 -0.550 0.585066
Conditioncompetition:Genotypepeaxr4-1 0.07027  0.19637  0.358 0.722260
Conditioncompetition:Genotypetir1-1 afb2-3 afb4-8  0.05129  0.21003  0.244 0.808255
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(390150.8) family taken to be 0.113865)

Null deviance: 61.4099 on 47 degrees of freedom
Residual deviance: 4.6159 on 42 degrees of freedom
AIC: 149.96

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 26.18810375),
     data = branches[which(branches$ID == "RII"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.28093  0.21933  5.840 6.74e-07 ***
Conditioncompetition -1.28093  0.45406 -2.821 0.007279 **
Genotypepeaxr4-1 0.87083  0.24467  3.559 0.000939 ***
Genotypetir1-1 afb2-3 afb4-8  0.05407  0.26654  0.203 0.840235
Conditioncompetition:Genotypepeaxr4-1 -0.76547  0.54524 -1.404 0.167696
Conditioncompetition:Genotypetir1-1 afb2-3 afb4-8 -0.05407  0.56296 -0.096 0.923945
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(26.1881) family taken to be 0.7612548)

Null deviance: 126.157 on 47 degrees of freedom
Residual deviance: 31.454 on 42 degrees of freedom
AIC: 179.83

Number of Fisher Scoring iterations: 5

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 625858.1978),
     data = branches[which(branches$ID == "CI"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.64866  0.06950 23.722 < 2e-16 ***
Conditioncompetition -0.16705  0.10266 -1.627 0.11134
Genotypepeaxr4-1 -0.28768  0.08972 -3.206 0.00261 **
Genotypetir1-1 afb2-3 afb4-8 -0.14458  0.08730 -1.656 0.10532
Conditioncompetition:Genotypepeaxr4-1 0.16420  0.13171  1.247 0.21958
Conditioncompetition:Genotypetir1-1 afb2-3 afb4-8 -0.08426  0.13347 -0.631 0.53135
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(625858.2) family taken to be 0.1255869)

Null deviance: 7.9010 on 46 degrees of freedom
Residual deviance: 5.1459 on 41 degrees of freedom
AIC: 171.37

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 102073.7303),
     data = branches[which(branches$ID == "CII"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.10413  0.11945 17.615 < 2e-16 ***
Conditioncompetition -1.92181  0.33432 -5.748 9.86e-07 ***
Genotypepeaxr4-1 -0.26359  0.15348 -1.717 0.0935 .
Genotypetir1-1 afb2-3 afb4-8  0.03593  0.14544  0.247 0.8061
Conditioncompetition:Genotypepeaxr4-1 0.52310  0.40354  1.296 0.2021
Conditioncompetition:Genotypetir1-1 afb2-3 afb4-8  0.00489  0.42090  0.012 0.9908
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(102073.7) family taken to be 0.5849956)

Null deviance: 136.76 on 46 degrees of freedom
Residual deviance: 23.53 on 41 degrees of freedom
AIC: 179.08

Number of Fisher Scoring iterations: 5

```

```

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 312245.9632),
     data = branches[which(branches$ID == "Total"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept)          2.89037  0.07746 37.317 < 2e-16 ***
Conditioncompetition -1.36432  0.17168 -7.947 7.85e-10 ***
Genotypepeaxr4-1      0.18232  0.09219  1.978  0.0547 .
Genotypetir1-1 afb2-3 afb4-8 -0.01117  0.09504 -0.118  0.9070
Conditioncompetition:Genotypepeaxr4-1 -0.07696  0.20907 -0.368  0.7147
Conditioncompetition:Genotypetir1-1 afb2-3 afb4-8 -0.19313  0.22473 -0.859  0.3951
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(312246) family taken to be 0.5399051)

Null deviance: 256.911 on 46 degrees of freedom
Residual deviance: 20.694 on 41 degrees of freedom
AIC: 225.74

Number of Fisher Scoring iterations: 4

```

Figure 3.2.4 B

```

Call:
glm(formula = Siliques ~ Condition * Genotype, family = negative.binomial(theta = 23.29175161),
     data = data)

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept)          5.52545  0.11305 48.878 < 2e-16 ***
Conditioncompetition -2.00499  0.18037 -11.116 6.01e-14 ***
Genotypepeaxr4-1      -0.15064  0.13877 -1.086  0.284
Genotypetir1-1 afb2-3 afb4-8 -0.20440  0.13890 -1.472  0.149
Conditioncompetition:Genotypepeaxr4-1 0.34915  0.22176  1.574  0.123
Conditioncompetition:Genotypetir1-1 afb2-3 afb4-8 -0.02023  0.22948 -0.088  0.930
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Negative Binomial(23.2918) family taken to be 1.361893)

Null deviance: 698.651 on 46 degrees of freedom
Residual deviance: 53.814 on 41 degrees of freedom
(3 Beobachtungen als fehlend gelöscht)
AIC: 440.26

Number of Fisher Scoring iterations: 4

```

Figure 3.2.4 C

```

Call:
glm(formula = avg_TR_leaf ~ group * condition, family = negative.binomial(theta = 3.748910983),
     data = data)

Coefficients: (1 not defined because of singularities)
              Estimate Std. Error t value Pr(>|t|)
(Intercept)      1.11048   0.34200   3.247  0.00404 **
groupDR5::GUS w/o -0.17176   0.49603  -0.346  0.73276
groupDR5::GUS auxin  3.15052   0.41481   7.595 2.58e-07 ***
conditioncompetition -0.01265   0.48452  -0.026  0.97943
groupDR5::GUS w/o:conditioncompetition  0.37804   0.68514   0.552  0.58722
groupDR5::GUS auxin:conditioncompetition    NA        NA        NA        NA
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(3.7489) family taken to be 0.981024)

Null deviance: 171.998 on 24 degrees of freedom
Residual deviance: 21.354 on 20 degrees of freedom
AIC: 142.17

Number of Fisher Scoring iterations: 5

```

Figure 3.2.4 D

```

Call:
glm(formula = avg_TR_bud ~ group * condition, family = negative.binomial(theta = 6.3877305),
     data = data)

Coefficients: (1 not defined because of singularities)
              Estimate Std. Error t value Pr(>|t|)
(Intercept)      4.4270   0.2187  20.246 8.55e-15 ***
groupDR5::GUS w/o  1.5354   0.3049   5.036 6.33e-05 ***
groupDR5::GUS auxin  5.5085   0.3037  18.136 6.93e-14 ***
conditioncompetition  0.5858   0.3068   1.909  0.0707 .
groupDR5::GUS w/o:conditioncompetition  0.1162   0.4290   0.271  0.7893
groupDR5::GUS auxin:conditioncompetition    NA        NA        NA        NA
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(6.3877) family taken to be 1.418857)

Null deviance: 657.460 on 24 degrees of freedom
Residual deviance: 25.671 on 20 degrees of freedom
AIC: 352.61

Number of Fisher Scoring iterations: 5

```

Figure 3.2.5 A

```

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 411864.3593),
     data = branches[which(branches$ID == "RI"), ])

Coefficients:
                                         Estimate Std. Error t value Pr(>|t|)
(Intercept)                         1.13943   0.04799 23.741 < 2e-16 ***
Conditioncompetition                 -1.11696   0.10612 -10.525 < 2e-16 ***
Genotypeamp1-1                      0.85527   0.07103 12.040 < 2e-16 ***
Conditioncompetition:Genotypeamp1-1 -0.76651   0.18767 -4.084 7.59e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(411864.4) family taken to be 0.4031081)

Null deviance: 249.432 on 136 degrees of freedom
Residual deviance: 57.621 on 133 degrees of freedom
AIC: 427.72

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 11.9029663),
     data = branches[which(branches$ID == "RII"), ])

Coefficients:
                                         Estimate Std. Error t value Pr(>|t|)
(Intercept)                         0.93048   0.08294 11.218 < 2e-16 ***
Conditioncompetition                 -0.93048   0.16346 -5.692 7.66e-08 ***
Genotypeamp1-1                      1.36206   0.11971 11.378 < 2e-16 ***
Conditioncompetition:Genotypeamp1-1 -1.36206   0.29244 -4.658 7.66e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(11.903) family taken to be 0.8053363)

Null deviance: 331.213 on 136 degrees of freedom
Residual deviance: 94.204 on 133 degrees of freedom
AIC: 475.35

Number of Fisher Scoring iterations: 5

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 190293.3479),
     data = branches[which(branches$ID == "CI"), ])

Coefficients:
                                         Estimate Std. Error t value Pr(>|t|)
(Intercept)                         1.54299   0.04484 34.414 < 2e-16 ***
Conditioncompetition                 -0.34358   0.07495 -4.584 1.04e-05 ***
Genotypeamp1-1                      -0.05009   0.08904 -0.563   0.575
Conditioncompetition:Genotypeamp1-1 -0.19835   0.15332 -1.294   0.198
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(190293.3) family taken to be 0.5266859)

Null deviance: 101.435 on 136 degrees of freedom
Residual deviance: 79.315 on 133 degrees of freedom
AIC: 518.77

Number of Fisher Scoring iterations: 4

```

```

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 26235.92088),
     data = branches[which(branches$ID == "CII"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.62010 0.06916 23.426 < 2e-16 ***
Conditioncompetition -1.43399 0.17412 -8.236 1.47e-13 ***
Genotypeamp1-1 -0.01066 0.13534 -0.079 0.937
Conditioncompetition:Genotypeamp1-1 0.16940 0.31661 0.535 0.594
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(26235.92) family taken to be 1.353281)

Null deviance: 350.05 on 136 degrees of freedom
Residual deviance: 189.27 on 133 degrees of freedom
AIC: 571.79

Number of Fisher Scoring iterations: 5

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 12.32878308),
     data = branches[which(branches$ID == "Total"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.51856 0.05707 44.132 < 2e-16 ***
Conditioncompetition -1.25289 0.11210 -11.176 < 2e-16 ***
Genotypeamp1-1 0.88762 0.09850 9.011 1.91e-15 ***
Conditioncompetition:Genotypeamp1-1 -0.97917 0.21190 -4.621 8.93e-06 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(12.3288) family taken to be 1.128011)

Null deviance: 643.68 on 136 degrees of freedom
Residual deviance: 176.87 on 133 degrees of freedom
AIC: 781.22

Number of Fisher Scoring iterations: 4

```

Figure 3.2.5 B

```

Call:
glm(formula = Siliques ~ Condition * Genotype, family = negative.binomial(theta = 7.633529039),
     data = data)

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 5.28574 0.05582 94.700 < 2e-16 ***
Conditioncompetition -1.50973 0.08662 -17.428 < 2e-16 ***
Genotypeamp1-1 0.60784 0.11499 5.286 4.27e-07 ***
Conditioncompetition:Genotypeamp1-1 -0.95557 0.17927 -5.330 3.48e-07 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(7.6335) family taken to be 1.51115)

Null deviance: 1080.4 on 155 degrees of freedom
Residual deviance: 304.4 on 152 degrees of freedom
(327 Beobachtungen als fehlend gelöscht)
AIC: 1710.2

Number of Fisher Scoring iterations: 4

```

Figure 3.2.6 A

```

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 250855.2976),
     data = branches[which(branches$ID == "RI"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.5686 0.1137 13.802 < 2e-16 ***
Conditioncompetition -1.4733 0.2632 -5.597 3.72e-07 ***
Genotypemax1-1 0.8473 0.1358 6.237 2.72e-08 ***
Genotypemax2-1 1.1461 0.1305 8.784 5.27e-13 ***
Genotypemax3-9 0.9963 0.1330 7.492 1.36e-10 ***
Conditioncompetition:Genotypemax1-1 0.8979 0.2910 3.086 0.002878 **
Conditioncompetition:Genotypemax2-1 0.9558 0.2833 3.374 0.001198 **
Conditioncompetition:Genotypemax3-9 1.1384 0.2841 4.007 0.000148 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(250855.3) family taken to be 0.6200013)

Null deviance: 251.346 on 79 degrees of freedom
Residual deviance: 52.591 on 72 degrees of freedom
AIC: 370.53

Number of Fisher Scoring iterations: 5

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 36.58028729),
     data = branches[which(branches$ID == "RII"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.5261 0.1946 7.843 3.01e-11 ***
Conditioncompetition -1.5261 0.4436 -3.440 0.000971 ***
Genotypemax1-1 1.9944 0.2160 9.232 7.73e-14 ***
Genotypemax2-1 2.0519 0.2154 9.525 2.22e-14 ***
Genotypemax3-9 1.9112 0.2169 8.810 4.73e-13 ***
Conditioncompetition:Genotypemax1-1 -0.3652 0.4901 -0.745 0.458614
Conditioncompetition:Genotypemax2-1 -0.7710 0.5025 -1.534 0.129381
Conditioncompetition:Genotypemax3-9 -0.1533 0.4867 -0.315 0.753710
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(36.5803) family taken to be 1.54703)

Null deviance: 919.14 on 79 degrees of freedom
Residual deviance: 106.78 on 72 degrees of freedom
AIC: 453.18

Number of Fisher Scoring iterations: 5

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 3.36026777),
     data = branches[which(branches$ID == "RIII"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) -8.462e-16 3.327e-01 0.000 1.00000
Conditioncompetition 2.820e-15 4.705e-01 0.000 1.00000
Genotypemax1-1 1.504e+00 3.937e-01 3.820 0.00028 ***
Genotypemax2-1 2.665e-16 4.705e-01 0.000 1.00000
Genotypemax3-9 1.361e+00 3.974e-01 3.425 0.00102 **
Conditioncompetition:Genotypemax1-1 -1.504e+00 6.135e-01 -2.452 0.01664 *
Conditioncompetition:Genotypemax2-1 -8.077e-16 6.653e-01 0.000 1.00000
Conditioncompetition:Genotypemax3-9 -1.361e+00 6.158e-01 -2.210 0.03028 *
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(3.3603) family taken to be 0.8528452)

Null deviance: 88.399 on 79 degrees of freedom
Residual deviance: 43.751 on 72 degrees of freedom
AIC: 263.88

Number of Fisher Scoring iterations: 4

```

```

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 373988.5004),
     data = branches[which(branches$ID == "CI"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.60944 0.06889 23.362 < 2e-16 ***
Conditioncompetition -0.15082 0.10131 -1.489 0.14094
Genotypemax1-1 -0.12783 0.10069 -1.270 0.20834
Genotypemax2-1 -0.06188 0.09897 -0.625 0.53382
Genotypemax3-9 -0.30111 0.10564 -2.850 0.00569 **
Conditioncompetition:Genotypemax1-1 0.08021 0.14644 0.548 0.58560
Conditioncompetition:Genotypemax2-1 0.27097 0.14068 1.926 0.05804 .
Conditioncompetition:Genotypemax3-9 0.25348 0.14989 1.691 0.09514 .
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(373988.5) family taken to be 0.2372947)

Null deviance: 21.550 on 79 degrees of freedom
Residual deviance: 17.266 on 72 degrees of freedom
AIC: 300.41

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 131527.9132),
     data = branches[which(branches$ID == "CII"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.14007 0.09345 22.901 < 2e-16 ***
Conditioncompetition -1.73460 0.24127 -7.189 4.94e-10 ***
Genotypemax1-1 0.11123 0.12863 0.865 0.390086
Genotypemax2-1 0.10064 0.12895 0.780 0.437681
Genotypemax3-9 -0.06062 0.13421 -0.452 0.652822
Conditioncompetition:Genotypemax1-1 1.32386 0.27894 4.746 1.02e-05 ***
Conditioncompetition:Genotypemax2-1 1.04145 0.28618 3.639 0.000511 ***
Conditioncompetition:Genotypemax3-9 1.58668 0.27973 5.672 2.75e-07 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(131527.9) family taken to be 0.7422315)

Null deviance: 147.90 on 79 degrees of freedom
Residual deviance: 55.27 on 72 degrees of freedom
AIC: 360.16

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 263.7739707),
     data = branches[which(branches$ID == "Total"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.99072 0.08099 36.928 < 2e-16 ***
Conditioncompetition -1.40148 0.17829 -7.861 2.79e-11 ***
Genotypemax1-1 1.12506 0.09486 11.860 < 2e-16 ***
Genotypemax2-1 1.14124 0.09470 12.052 < 2e-16 ***
Genotypemax3-9 1.07145 0.09544 11.227 < 2e-16 ***
Conditioncompetition:Genotypemax1-1 0.21956 0.20284 1.082 0.2827
Conditioncompetition:Genotypemax2-1 0.24505 0.20211 1.212 0.2293
Conditioncompetition:Genotypemax3-9 0.47915 0.20013 2.394 0.0193 *
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(263.774) family taken to be 1.213701)

Null deviance: 1127.427 on 79 degrees of freedom
Residual deviance: 93.033 on 72 degrees of freedom
AIC: 522.86

Number of Fisher Scoring iterations: 4

```

Figure 3.2.6 B

```
Call:  
glm(formula = Siliques ~ Condition * Genotype, family = negative.binomial(theta = 11.82757853),  
    data = data)  
  
Coefficients:  
Estimate Std. Error t value Pr(>|t|)  
(Intercept) 5.70145 0.09466 60.229 < 2e-16 ***  
Conditioncompetition -1.70508 0.13948 -12.224 < 2e-16 ***  
Genotypemax1-1 0.38851 0.13346 2.911 0.004792 **  
Genotypemax2-1 0.17461 0.13367 1.306 0.195618  
Genotypemax3-9 0.47525 0.13339 3.563 0.000655 ***  
Conditioncompetition:Genotypemax1-1 0.28234 0.19464 1.451 0.151248  
Conditioncompetition:Genotypemax2-1 0.46473 0.19486 2.385 0.019718 *  
Conditioncompetition:Genotypemax3-9 0.60043 0.19377 3.099 0.002772 **  
---  
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
  
(Dispersion parameter for Negative Binomial(11.8276) family taken to be 1.019569)  
  
Null deviance: 521.479 on 79 degrees of freedom  
Residual deviance: 85.776 on 72 degrees of freedom  
AIC: 895.32  
  
Number of Fisher Scoring iterations: 4
```

Figure 3.2.6 D

```
Call:  
glm(formula = Siliques_25.03 ~ condition * genotype * comp_spec *  
    partition, family = negative.binomial(theta = 13.27202625),  
    data = siliques)  
  
Coefficients:  
Estimate Std. Error t value Pr(>|t|)  
(Intercept) 6.10456999 0.08925588 68.3940381 2.315754e-91  
conditionsingle_s -2.00192663 0.13191403 -15.1759944 1.220983e-28  
conditioncompetition -2.08279612 0.13245482 -15.7245779 8.474446e-30  
genotypemax2-1 0.04199716 0.12964539 0.3239387 7.466052e-01  
comp_specA.thaliana 0.12294690 0.13763149 0.8933050 3.736619e-01  
partitionw/ 0.36274965 0.13636508 2.6601359 8.989596e-03  
conditionsingle_S:genotypemax2-1 -0.07049867 0.18901428 -0.3729807 7.098872e-01  
conditioncompetition:genotypemax2-1 0.16452150 0.18873227 0.8717190 3.852777e-01  
genotypemax2-1:comp_specA.thaliana 0.36400740 0.18986019 1.9172392 5.782524e-02  
genotypemax2-1:partitionw/ -0.23049458 0.19203789 -1.2002558 2.326421e-01  
comp_specA.thaliana:partitionw/ -0.10408265 0.19009580 -0.5475274 5.851359e-01  
genotypemax2-1:comp_specA.thaliana:partitionw/ -0.22598798 0.26673607 -0.8472344 3.987209e-01  
---  
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
  
(Dispersion parameter for Negative Binomial(13.272) family taken to be 1.026902)  
  
Null deviance: 1069.57 on 120 degrees of freedom  
Residual deviance: 127.46 on 109 degrees of freedom  
(1 Beobachtung als fehlend gelöscht)  
AIC: 1180.4  
  
Number of Fisher Scoring iterations: 4
```

Figure 3.2.6 F

```
Call:  
glm(formula = response.siliques ~ genotype * comp_spec * partition,  
    family = negative.binomial(theta = 175943.0981), data = responses)  
  
Coefficients:  
Estimate Std. Error t value Pr(>|t|)  
(Intercept) -1.9598 0.1929 -10.159 1.12e-15 ***  
genotypemax2-1 0.5285 0.2391 2.211 0.0302 *  
comp_specL.perenne -0.1229 0.2816 -0.437 0.6637  
partitionw/ 2.2606 0.2019 11.199 < 2e-16 ***  
genotypemax2-1:comp_specL.perenne -0.3640 0.3674 -0.991 0.3250  
genotypemax2-1:partitionw/ -0.3860 0.2531 -1.525 0.1315  
comp_specL.perenne:partitionw/ 0.1041 0.2946 0.353 0.7249  
genotypemax2-1:comp_specL.perenne:partitionw/ 0.2260 0.3870 0.584 0.5610  
---  
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
  
(Dispersion parameter for Negative Binomial(175943.1) family taken to be 0.05243556)  
  
Null deviance: 73.181 on 81 degrees of freedom  
Residual deviance: 27.123 on 74 degrees of freedom  
AIC: 143.33  
  
Number of Fisher Scoring iterations: 4
```

Figure 3.2.6 G

```

Call:
glm(formula = response_ri ~ genotype * comp_spec * partition,
     family = negative.binomial(theta = 17442.21107), data = responses)

Coefficients:
                                         Estimate Std. Error t value Pr(>|t|)
(Intercept)                               -2.3224    0.6657  -3.489 0.000822 ***
genotypemax2-1                            1.3666    0.7389   1.850 0.068368 .
comp_specL.perenne                      -0.2231    0.9986  -0.223 0.823793
partitionw/                                2.5948    0.6879   3.772 0.000324 ***
genotypemax2-1:comp_specL.perenne        0.3750    1.0941   0.343 0.732776
genotypemax2-1:partitionw/                -2.1296    0.8043  -2.648 0.009900 **
comp_specL.perenne:partitionw/           0.1514    1.0309   0.147 0.883643
genotypemax2-1:comp_specL.perenne:partitionw/ -0.1635    1.1812  -0.138 0.890315
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Dispersion parameter for Negative Binomial(17442.21) family taken to be 0.434493)

Null deviance: 93.037 on 81 degrees of freedom
 Residual deviance: 65.874 on 74 degrees of freedom
 AIC: 153.2

Number of Fisher Scoring iterations: 5

Figure 3.2.7 B

```

Call:
glm(formula = output + 1 ~ condition * competitor2, family = negative.binomial(theta = 379332.2857),
     data = branches[which(branches$ID == "RI"), ])
```

```

Coefficients: (3 not defined because of singularities)
                                         Estimate Std. Error t value Pr(>|t|)
(Intercept)                           9.163e-01  7.097e-02 12.911 4.57e-13 ***
conditioncompetition      -9.163e-01  1.328e-01 -6.901 2.05e-07 ***
competitor2max3-9                  1.583e-16  1.587e-01   0.000      1
competitor2wt                         NA         NA         NA         NA
conditioncompetition:competitor2max3-9  NA         NA         NA         NA
conditioncompetition:competitor2wt    NA         NA         NA         NA
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Dispersion parameter for Negative Binomial(379332.3) family taken to be 0.1259256)

Null deviance: 13.1020 on 29 degrees of freedom
 Residual deviance: 3.7793 on 27 degrees of freedom
 AIC: 77.232

Number of Fisher Scoring iterations: 4

```

Call:
glm(formula = output + 1 ~ condition * competitor2, family = negative.binomial(theta = 472091.9508),
     data = branches[which(branches$ID == "CI"), ])
```

```

Coefficients: (3 not defined because of singularities)
                                         Estimate Std. Error t value Pr(>|t|)
(Intercept)                           1.52606   0.05276 28.925 < 2e-16 ***
conditioncompetition      -0.49644   0.08577 -5.788 3.71e-06 ***
competitor2max3-9                  0.10178   0.09329  1.091   0.285
competitor2wt                         NA         NA         NA         NA
conditioncompetition:competitor2max3-9  NA         NA         NA         NA
conditioncompetition:competitor2wt    NA         NA         NA         NA
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Dispersion parameter for Negative Binomial(472092) family taken to be 0.1280445)

Null deviance: 8.9471 on 29 degrees of freedom
 Residual deviance: 3.8245 on 27 degrees of freedom
 AIC: 102.68

Number of Fisher Scoring iterations: 4

```

Call:
glm(formula = output + 1 ~ condition * competitor2, family = negative.binomial(theta = 654.2061252),
     data = branches[which(branches$ID == "CII"), ])

Coefficients: (3 not defined because of singularities)
              Estimate Std. Error t value Pr(>|t|)
(Intercept)      1.224e+00  1.320e-01   9.270 7.04e-10 ***
conditioncompetition -1.224e+00  2.765e-01  -4.425 0.000143 ***
competitor2max3-9 -6.211e-17  3.436e-01   0.000 1.000000
competitor2wt        NA         NA         NA         NA
conditioncompetition:competitor2max3-9       NA         NA         NA         NA
conditioncompetition:competitor2wt       NA         NA         NA         NA
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(654.2061) family taken to be 0.5895288)

Null deviance: 35.028 on 29 degrees of freedom
Residual deviance: 15.351 on 27 degrees of freedom
AIC: 90.308

Number of Fisher Scoring iterations: 5

Call:
glm(formula = output + 1 ~ condition * competitor2, family = negative.binomial(theta = 186191.6736),
     data = branches[which(branches$ID == "Total"), ])

Coefficients: (3 not defined because of singularities)
              Estimate Std. Error t value Pr(>|t|)
(Intercept)      2.14007  0.07825 27.348 < 2e-16 ***
conditioncompetition -1.11045  0.15720 -7.064 1.35e-07 ***
competitor2max3-9  0.10178  0.18809  0.541  0.593
competitor2wt        NA         NA         NA         NA
conditioncompetition:competitor2max3-9       NA         NA         NA         NA
conditioncompetition:competitor2wt       NA         NA         NA         NA
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(186191.7) family taken to be 0.5204668)

Null deviance: 54.270 on 29 degrees of freedom
Residual deviance: 14.416 on 27 degrees of freedom
AIC: 118.65

Number of Fisher Scoring iterations: 4

```

Figure 3.2.7 C

```

Call:
glm(formula = output + 1 ~ condition * competitor2, family = negative.binomial(theta = 186191.6736),
     data = branches[which(branches$ID == "Total"), ])

Coefficients: (3 not defined because of singularities)
              Estimate Std. Error t value Pr(>|t|)
(Intercept)      2.14007  0.07825 27.348 < 2e-16 ***
conditioncompetition -1.11045  0.15720 -7.064 1.35e-07 ***
competitor2max3-9  0.10178  0.18809  0.541  0.593
competitor2wt        NA         NA         NA         NA
conditioncompetition:competitor2max3-9       NA         NA         NA         NA
conditioncompetition:competitor2wt       NA         NA         NA         NA
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(186191.7) family taken to be 0.5204668)

Null deviance: 54.270 on 29 degrees of freedom
Residual deviance: 14.416 on 27 degrees of freedom
AIC: 118.65

```

Number of Fisher Scoring iterations: 4

Figure 3.2.7 D

```

Call:
glm(formula = weight_focal_mg ~ group, family = negative.binomial(theta = 9.291698944),
     data = data)

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)      4.7123   0.1151   40.93 < 2e-16 ***
groupcompetition wt -1.9510   0.1808  -10.79 2.69e-11 ***
groupcompetition max3-9 -1.9657   0.1811  -10.86 2.36e-11 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(9.2917) family taken to be 1.136726)

Null deviance: 236.193 on 29 degrees of freedom
Residual deviance: 31.612 on 27 degrees of freedom
AIC: 237.26

Number of Fisher Scoring iterations: 4

```

Figure 3.2.7 E

Welch Two Sample t-test

```
data: data$weight_comp_mg by data$competitor2
t = 1.3688, df = 17.773, p-value = 0.1881
alternative hypothesis: true difference in means between group max3-9 and group wt is not equal to 0
95 percent confidence interval:
-14.59165 69.01165
sample estimates:
mean in group max3-9      mean in group wt
169.07                      141.86
```

Figure 3.2.8 A

```
Call:
glm(formula = output + 1 ~ Condition * Genotype + tray * position,
family = negative.binomial(theta = 286513.6539), data = branches[which(branches$ID ==
"RI"), ])
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	1.1630	0.2803	4.149	0.000253 ***
Conditioncompetition	-1.2357	0.1984	-6.228	7.38e-07 ***
Genotypebrc1-2	0.8422	0.1155	7.289	4.08e-08 ***
tray	0.1832	0.1465	1.250	0.220863
positionB	0.1593	0.3146	0.506	0.616317
positionC	-0.2182	0.4115	-0.530	0.599821
Conditioncompetition:Genotypebrc1-2	-0.1834	0.2509	-0.731	0.470419
tray:positionB	-0.3024	0.1917	-1.578	0.125134
tray:positionC	0.1087	0.2403	0.452	0.654314

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(286513.7) family taken to be 0.249992)

Null deviance: 105.1882 on 38 degrees of freedom
Residual deviance: 8.0971 on 30 degrees of freedom
AIC: 139.09

Number of Fisher Scoring iterations: 4

```
Call:
glm(formula = output + 1 ~ Condition * Genotype + tray * position,
family = negative.binomial(theta = 275597.2277), data = branches[which(branches$ID ==
"RII"), ])
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.63351	0.21533	2.942	0.00623 **
Conditioncompetition	-0.54860	0.19170	-2.862	0.00761 **
Genotypebrc1-2	2.16621	0.12707	17.048	< 2e-16 ***
tray	0.05351	0.10272	0.521	0.60624
positionB	-0.62124	0.24744	-2.511	0.01767 *
positionC	0.28256	0.27995	1.009	0.32089
Conditioncompetition:Genotypebrc1-2	-2.03275	0.25593	-7.943	7.27e-09 ***
tray:positionB	0.17473	0.15675	1.115	0.27383
tray:positionC	-0.33075	0.17128	-1.931	0.06298 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(275597.2) family taken to be 0.2006789)

Null deviance: 261.0943 on 38 degrees of freedom
Residual deviance: 5.6543 on 30 degrees of freedom
AIC: 129.82

Number of Fisher Scoring iterations: 4

```

Call:
glm(formula = output + 1 ~ Condition * Genotype + tray * position,
     family = negative.binomial(theta = 497830.9185), data = branches[which(branches$ID ==
      "CI"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.45881 0.28785 5.068 1.92e-05 ***
Conditioncompetition -0.42912 0.12339 -3.478 0.00157 **
Genotypebrc1-2 0.07257 0.10338 0.702 0.48812
tray 0.05387 0.15933 0.338 0.73765
positionB 0.14355 0.30348 0.473 0.63964
positionC 0.32801 0.39036 0.840 0.40739
Conditioncompetition:Genotypebrc1-2 0.50002 0.16588 3.014 0.00520 **
tray:positionB -0.05850 0.18157 -0.322 0.74955
tray:positionC -0.12836 0.24062 -0.533 0.59766
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(497830.9) family taken to be 0.2138131)

Null deviance: 13.427 on 38 degrees of freedom
Residual deviance: 6.663 on 30 degrees of freedom
AIC: 157.41

Number of Fisher Scoring iterations: 4

Call:
glm(formula = output + 1 ~ Condition * Genotype + tray * position,
     family = negative.binomial(theta = 87757.0772), data = branches[which(branches$ID ==
      "CII"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.3491 0.5647 2.389 0.0234 *
Conditioncompetition -1.7539 0.3704 -4.736 4.91e-05 ***
Genotypebrc1-2 0.3694 0.1941 1.903 0.0667 .
tray 0.2917 0.2986 0.977 0.3364
positionB 0.9903 0.6059 1.635 0.1126
positionC 0.3008 0.8262 0.364 0.7184
Conditioncompetition:Genotypebrc1-2 0.4704 0.4654 1.011 0.3202
tray:positionB -0.7066 0.3603 -1.961 0.0592 .
tray:positionC -0.2150 0.4840 -0.444 0.6601
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(87757.08) family taken to be 0.9570136)

Null deviance: 119.74 on 38 degrees of freedom
Residual deviance: 28.38 on 30 degrees of freedom
AIC: 162.74

Number of Fisher Scoring iterations: 5

Call:
glm(formula = output + 1 ~ Condition * Genotype + tray * position,
     family = negative.binomial(theta = 331027.1462), data = branches[which(branches$ID ==
      "Total"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.47959 0.25190 9.844 6.60e-11 ***
Conditioncompetition -1.37558 0.18831 -7.305 3.91e-08 ***
Genotypebrc1-2 0.93534 0.10542 8.873 6.86e-10 ***
tray 0.14402 0.13265 1.086 0.286
positionB 0.17832 0.28092 0.635 0.530
positionC 0.21143 0.36283 0.583 0.564
Conditioncompetition:Genotypebrc1-2 -0.01465 0.23363 -0.063 0.950
tray:positionB -0.26344 0.17257 -1.527 0.137
tray:positionC -0.18409 0.21624 -0.851 0.401
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(331027.1) family taken to be 0.7904631)

Null deviance: 397.858 on 38 degrees of freedom
Residual deviance: 25.012 on 30 degrees of freedom
AIC: 205.55

Number of Fisher Scoring iterations: 4

```

Figure 3.2.8 B

```
Call:  
glm(formula = output + 1 ~ Condition * Genotype + tray * position,  
    family = negative.binomial(theta = 331027.1462), data = branches[which(branches$ID ==  
    "Total"), ])  
  
Coefficients:  
Estimate Std. Error t value Pr(>|t|)  
(Intercept) 2.47959 0.25190 9.844 6.60e-11 ***  
Conditioncompetition -1.37558 0.18831 -7.305 3.91e-08 ***  
Genotypebrc1-2 0.93534 0.10542 8.873 6.86e-10 ***  
tray 0.14402 0.13265 1.086 0.286  
positionB 0.17832 0.28092 0.635 0.530  
positionC 0.21143 0.36283 0.583 0.564  
Conditioncompetition:Genotypebrc1-2 -0.01465 0.23363 -0.063 0.950  
tray:positionB -0.26344 0.17257 -1.527 0.137  
tray:positionC -0.18409 0.21624 -0.851 0.401  
---  
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
  
(Dispersion parameter for Negative Binomial(331027.1) family taken to be 0.7904631)  
  
Null deviance: 397.858 on 38 degrees of freedom  
Residual deviance: 25.012 on 30 degrees of freedom  
AIC: 205.55  
  
Number of Fisher Scoring iterations: 4
```

Figure 3.2.8 C

```
Call:  
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 274707.7433),  
    data = branches[which(branches$ID == "RI"), ])  
  
Coefficients:  
Estimate Std. Error t value Pr(>|t|)  
(Intercept) 1.4351 0.1015 14.140 < 2e-16 ***  
Conditioncompetition -1.4351 0.2416 -5.940 6.88e-07 ***  
Genotypebrc1brc2 1.1860 0.1137 10.433 1.04e-12 ***  
Conditioncompetition:Genotypebrc1brc2 0.2874 0.2646 1.086 0.284  
---  
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
  
(Dispersion parameter for Negative Binomial(274707.7) family taken to be 0.432605)  
  
Null deviance: 173.301 on 41 degrees of freedom  
Residual deviance: 16.989 on 38 degrees of freedom  
AIC: 165.22  
  
Number of Fisher Scoring iterations: 4  
  
Call:  
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 6.262593799),  
    data = branches[which(branches$ID == "RII"), ])  
  
Coefficients:  
Estimate Std. Error t value Pr(>|t|)  
(Intercept) 0.09531 0.21119 0.451 0.654  
Conditioncompetition -0.09531 0.31364 -0.304 0.763  
Genotypebrc1brc2 3.09654 0.22711 13.634 3.25e-16 ***  
Conditioncompetition:Genotypebrc1brc2 -2.92948 0.37882 -7.733 2.56e-09 ***  
---  
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
  
(Dispersion parameter for Negative Binomial(6.2626) family taken to be 0.4172958)  
  
Null deviance: 271.110 on 41 degrees of freedom  
Residual deviance: 20.789 on 38 degrees of freedom  
AIC: 171.97  
  
Number of Fisher Scoring iterations: 4  
  
Call:  
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 1076521.371),  
    data = branches[which(branches$ID == "CI"), ])  
  
Coefficients:  
Estimate Std. Error t value Pr(>|t|)  
(Intercept) 1.68640 0.04108 41.054 < 2e-16 ***  
Conditioncompetition -0.32828 0.06550 -5.012 1.28e-05 ***  
Genotypebrc1brc2 -0.02817 0.05598 -0.503 0.618  
Conditioncompetition:Genotypebrc1brc2 0.52065 0.08390 6.206 2.97e-07 ***  
---  
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
  
(Dispersion parameter for Negative Binomial(1076521) family taken to be 0.09111624)  
  
Null deviance: 9.3856 on 41 degrees of freedom  
Residual deviance: 3.4286 on 38 degrees of freedom  
AIC: 159.01  
  
Number of Fisher Scoring iterations: 4
```

```

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 249.3258323),
     data = branches[which(branches$ID == "CII"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.15176 0.12562 17.129 < 2e-16 ***
Conditioncompetition -2.04640 0.38413 -5.327 4.76e-06 ***
Genotypebrc1brc2 -0.07232 0.17287 -0.418 0.6781
Conditioncompetition:Genotypebrc1brc2 1.06557 0.44933 2.371 0.0229 *
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(249.3258) family taken to be 1.311917)

Null deviance: 132.621 on 41 degrees of freedom
Residual deviance: 45.564 on 38 degrees of freedom
AIC: 187.84

Number of Fisher Scoring iterations: 5

Call:
glm(formula = output + 1 ~ Condition * Genotype, family = negative.binomial(theta = 19.72850306),
     data = branches[which(branches$ID == "Total"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.791165 0.098578 28.314 < 2e-16 ***
Conditioncompetition -1.404871 0.196712 -7.142 1.58e-08 ***
Genotypebrc1brc2 1.086956 0.121970 8.912 7.59e-11 ***
Conditioncompetition:Genotypebrc1brc2 0.004051 0.233394 0.017 0.986
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(19.7285) family taken to be 0.8673529)

Null deviance: 306.970 on 41 degrees of freedom
Residual deviance: 34.886 on 38 degrees of freedom
AIC: 260.53

Number of Fisher Scoring iterations: 4

```

Figure 3.2.8 D

```

Call:
glm(formula = Siliques ~ Condition * Genotype, family = negative.binomial(theta = 19.16747567),
     data = data)

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 5.23484 0.07669 68.259 < 2e-16 ***
Conditioncompetition -1.44060 0.11987 -12.018 1.63e-14 ***
Genotypebrc1brc2 0.28994 0.10329 2.807 0.00784 **
Conditioncompetition:Genotypebrc1brc2 -0.30621 0.16166 -1.894 0.06583 .
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(19.1675) family taken to be 1.022878)

Null deviance: 440.607 on 41 degrees of freedom
Residual deviance: 41.088 on 38 degrees of freedom
AIC: 398.22

Number of Fisher Scoring iterations: 4

```

Figure 3.2.9 A

Welch Two Sample t-test

```

data: norm by Condition
t = 2.165, df = 5.9855, p-value = 0.07368
alternative hypothesis: true difference in means between group single and group competition is not equal to 0
95 percent confidence interval:
-0.6017196 9.7953259
sample estimates:
mean in group single mean in group competition
16.41851 11.82171

```

Figure 3.2.9 B

```
Welch Two Sample t-test

data: deltaC by Condition
t = 0.93848, df = 4.6133, p-value = 0.3945
alternative hypothesis: true difference in means between group single and group competition is not equal to 0
95 percent confidence interval:
-0.3686103 0.7759994
sample estimates:
mean in group single mean in group competition
2.502499 2.298804

Welch Two Sample t-test

data: deltaC by Condition
t = 1.3371, df = 5.8111, p-value = 0.2311
alternative hypothesis: true difference in means between group single and group competition is not equal to 0
95 percent confidence interval:
-0.2803333 0.9442508
sample estimates:
mean in group single mean in group competition
3.101935 2.769976

Welch Two Sample t-test

data: deltaC by Condition
t = 0.7027, df = 5.7009, p-value = 0.5099
alternative hypothesis: true difference in means between group single and group competition is not equal to 0
95 percent confidence interval:
-0.5394207 0.9663584
sample estimates:
mean in group single mean in group competition
3.590412 3.376943
```

Figure 3.2.11 A

```
Call:
glm(formula = response ~ genotype, family = negative.binomial(theta = 59714.44176),
     data = competition_data[which(competition_data$verification_round ==
      "A"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.5743 0.2520 -6.246 8.42e-08 ***
genotypeM3-11 -0.5238 0.5759 -0.910 0.3673
genotypeM3-12 -0.1612 0.4613 -0.349 0.7282
genotypeM3-14-1 0.2329 0.4809 0.484 0.6303
genotypeM3-14-2 0.6107 0.3478 1.756 0.0851 .
genotypeM3-17-1 0.2975 0.3973 0.749 0.4574
genotypeM3-19-1 0.2184 0.4070 0.537 0.5939
genotypeM3-20 0.4606 0.4046 1.138 0.2603
genotypeM3-22 -0.5674 0.6610 -0.858 0.3947
genotypeM3-25-1 1.4310 0.3186 4.492 4.07e-05 ***
genotypeM3-26 -0.1655 0.5598 -0.296 0.7687
genotypeM3-28 0.3323 0.3932 0.845 0.4021
genotypeM3-37 -0.0416 0.4427 -0.094 0.9255
genotypeM3-5 -0.1215 0.5501 -0.221 0.8261
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(59714.44) family taken to be 0.1315837)

Null deviance: 50.066 on 64 degrees of freedom
Residual deviance: 45.068 on 51 degrees of freedom
  (10 Beobachtungen als fehlend gelöscht)
AIC: 96.042

Number of Fisher Scoring iterations: 5

Call:
glm(formula = response ~ genotype, family = negative.binomial(theta = 32724.34669),
     data = competition_data[which(competition_data$verification_round ==
      "B"), ])

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.6099 0.2138 -7.530 1.59e-07 ***
genotypeM3-14 -0.1842 0.3945 -0.467 0.645
genotypeM3-55 -1.0717 0.5092 -2.105 0.047 *
genotypeM3-66 0.2497 0.3205 0.779 0.444
genotypeM3-69 -0.3265 0.3835 -0.851 0.404
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(32724.35) family taken to be 0.07310574)

Null deviance: 16.298 on 26 degrees of freedom
Residual deviance: 15.654 on 22 degrees of freedom
AIC: 31.189

Number of Fisher Scoring iterations: 5
```

```

Call:
glm(formula = response ~ genotype, family = negative.binomial(theta = 52650.36436),
     data = response_C)

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.3116    0.4117  -3.186  0.00344 ***
genotypeM3-16 -0.1927    0.6530  -0.295  0.77003
genotypeM3-17-2 -0.1810    0.6507  -0.278  0.78286
genotypeM3-19-2 -0.8029    0.7402  -1.085  0.28700
genotypeM3-2-2   2.1853    0.4397  4.970  2.76e-05 ***
genotypeM3-40   -1.1556    0.8414  -1.373  0.18013
genotypeM3-74   -0.8254    0.7460  -1.106  0.27762
genotypeM3-98   -0.1174    0.6001  -0.196  0.84632
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(52650.36) family taken to be 0.2283414)

Null deviance: 51.642 on 36 degrees of freedom
Residual deviance: 27.413 on 29 degrees of freedom
AIC: 59.154

Number of Fisher Scoring iterations: 5

```