Statistical modeling for phenotypic traits

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5. Linear models with Soil variable with Plant_type

UCL_StatisticalAnalysis

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Statistical modeling for phenotypic traits

The explanatory variable (X) refers to the genotype, which is a categorical variable. The response variables (Y) are the phenotypic data of the variables dataframe.

In this case, the variables are:

And the genotypes are:

```
print(variables)
```

```
## [1] "DW_shoot_g" "FW_shoot_g" "DW_root_g"  "FW_root_g"
```

```
unique(endpoint$Genotype)
```

```
##  [1] EPPN14_H EPPN3_L  EPPN12_H EPPN10_H Local    EPPN6_H  EPPN15_L EPPN13_H
##  [9] EPPN9_L  EPPN20_T EPPN4_H  EPPN1_H  EPPN1_L  EPPN11_H EPPN14_L EPPN5_H
## [17] EPPN2_H  EPPN6_L  EPPN8_H  EPPN4_L  EPPN5_L  EPPN11_L EPPN7_L  EPPN8_L
## [25] EPPN7_H  EPPN3_H  EPPN15_H EPPN12_L EPPN2_L  EPPN10_L EPPN9_H  EPPN13_L
## 32 Levels: EPPN1_H EPPN1_L EPPN10_H EPPN10_L EPPN11_H EPPN11_L ... Local
```

1. First linear models

Firstly, we model the Y = X + r + c + e Where - Y is the phenotypic trait; - X the genotype (fixed effect); - r the row effect (fixed or random); - c the column effect (fixed or random);

```r
fit_models_fixed <- function(data, trait_name) {
  fixed_formula <- as.formula(paste(trait_name, "~ Genotype + Row + Column"))
  fixed_model <- lm(fixed_formula, data)
  print(paste("Summary for fixed effects model of", trait_name))
  print(summary(fixed_model))
  print(anova(fixed_model))
}

fit_models_random <- function(data, trait_name)  {
  random_formula <- as.formula(paste(trait_name, "~ Genotype + (1|Row) + (1|Column)"))
  random_model <- lmer(random_formula, data)
  print(paste("Summary for random effects model of", trait_name))
  print(summary(random_model))
  print(anova(random_model))
  print(ranova(random_model))
}

for (trait in variables) {
  fit_models_fixed(endpoint_clean, trait)
}
```

```
## [1] "Summary for fixed effects model of DW_shoot_g"
##
## Call:
## lm(formula = fixed_formula, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.16351 -0.03817  0.00349  0.03984  0.17040
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.3100392  0.0319584   9.701  < 2e-16 ***
## GenotypeEPPN1_L  -0.0468561  0.0212118  -2.209 0.027688 *
## GenotypeEPPN10_H -0.0319144  0.0205056  -1.556 0.120334
## GenotypeEPPN10_L -0.1639319  0.0276737  -5.924 6.32e-09 ***
## GenotypeEPPN11_H  0.0206734  0.0203767   1.015 0.310870
## GenotypeEPPN11_L -0.1510864  0.0219025  -6.898 1.83e-11 ***
## GenotypeEPPN12_H -0.0469736  0.0208342  -2.255 0.024644 *
## GenotypeEPPN12_L -0.1364992  0.0247408  -5.517 5.87e-08 ***
## GenotypeEPPN13_H  0.0418462  0.0233651   1.791 0.073980 .
## GenotypeEPPN13_L -0.1299123  0.0365470  -3.555 0.000419 ***
## GenotypeEPPN14_H  0.0420186  0.0236309   1.778 0.076070 .
## GenotypeEPPN14_L -0.1954248  0.0363329  -5.379 1.22e-07 ***
## GenotypeEPPN15_H -0.0620797  0.0208125  -2.983 0.003014 **
## GenotypeEPPN15_L -0.1240663  0.0234728  -5.286 1.97e-07 ***
## GenotypeEPPN2_H  -0.0483828  0.0210499  -2.298 0.021999 *
## GenotypeEPPN2_L  -0.0927946  0.0247224  -3.753 0.000198 ***
## GenotypeEPPN20_T -0.1206553  0.0198031  -6.093 2.41e-09 ***
## GenotypeEPPN3_H  -0.0532887  0.0232780  -2.289 0.022536 *
## GenotypeEPPN3_L  -0.0536726  0.0221086  -2.428 0.015593 *
## GenotypeEPPN4_H  -0.0918857  0.0226486  -4.057 5.87e-05 ***
## GenotypeEPPN4_L  -0.1126110  0.0229076  -4.916 1.25e-06 ***
## GenotypeEPPN5_H  -0.0037836  0.0229427  -0.165 0.869087
## GenotypeEPPN5_L  -0.0765401  0.0330318  -2.317 0.020950 *
## GenotypeEPPN6_H   0.0180329  0.0207485   0.869 0.385252
## GenotypeEPPN6_L  -0.0905992  0.0250730  -3.613 0.000337 ***
## GenotypeEPPN7_H  -0.0647614  0.0341803  -1.895 0.058783 .
## GenotypeEPPN7_L  -0.0925214  0.0245580  -3.767 0.000187 ***
## GenotypeEPPN8_H   0.0486047  0.0222968   2.180 0.029791 *
## GenotypeEPPN8_L  -0.0919858  0.0227462  -4.044 6.20e-05 ***
## GenotypeEPPN9_H   0.0148376  0.0205938   0.720 0.471604
## GenotypeEPPN9_L  -0.0370621  0.0213751  -1.734 0.083633 .
## GenotypeLocal    -0.0383952  0.0181406  -2.117 0.034857 *
## Row2             0.0310245  0.0379588   0.817 0.414184
## Row3            -0.0556898  0.0390413  -1.426 0.154448
## Row4             0.0330091  0.0406342   0.812 0.417028
## Row5             0.0464051  0.0390464   1.188 0.235289
## Row6             0.0117962  0.0446895   0.264 0.791934
## Row7            -0.0248066  0.0403645  -0.615 0.539158
## Row8             0.0052285  0.0393376   0.133 0.894323
## Row9            -0.0310842  0.0393934  -0.789 0.430492
## Row10           -0.0203908  0.0362553  -0.562 0.574112
## Row11           -0.0025699  0.0377421  -0.068 0.945745
## Row12           -0.0125319  0.0420920  -0.298 0.766052
## Row13            0.0027616  0.0380467   0.073 0.942169
```

```
## Row14        -0.0379824  0.0387509  -0.980 0.327538
## Row15        -0.0377407  0.0378929  -0.996 0.319803
## Row16        -0.0542250  0.0406686  -1.333 0.183106
## Row17        -0.0100134  0.0381697  -0.262 0.793181
## Row18         0.0017936  0.0452021   0.040 0.968367
## Row19        -0.0014885  0.0389980  -0.038 0.969571
## Row20        -0.0053037  0.0368356  -0.144 0.885578
## Row21         0.0155377  0.0381799   0.407 0.684235
## Row22         0.0001205  0.0374643   0.003 0.997435
## Row23         0.0043695  0.0425018   0.103 0.918163
## Row24         0.0237300  0.0422903   0.561 0.574998
## Row25        -0.0151538  0.0376942  -0.402 0.687864
## Row26        -0.0422593  0.0460817  -0.917 0.359615
## Row27         0.0071620  0.0427243   0.168 0.866948
## Row28        -0.0029803  0.0377029  -0.079 0.937032
## Row29        -0.0015674  0.0390745  -0.040 0.968020
## Row30        -0.0033774  0.0405262  -0.083 0.933620
## Row31        -0.0152828  0.0387458  -0.394 0.693447
## Row32         0.0343860  0.0402977   0.853 0.393955
## Row33        -0.0466555  0.0430252  -1.084 0.278787
## Row34        -0.0124809  0.0369737  -0.338 0.735853
## Row35         0.0228231  0.0390931   0.584 0.559643
## Row36        -0.0017360  0.0376448  -0.046 0.963239
## Row37        -0.0569811  0.0381658  -1.493 0.136153
## Row38         0.0442887  0.0394091   1.124 0.261698
## Row39         0.0046026  0.0379241   0.121 0.903458
## Row40        -0.0278645  0.0376320  -0.740 0.459421
## Row41        -0.0368844  0.0390597  -0.944 0.345526
## Row42        -0.0046947  0.0402659  -0.117 0.907235
## Row43         0.0140200  0.0386895   0.362 0.717247
## Row44         0.0081032  0.0365312   0.222 0.824560
## Row45         0.0095268  0.0404549   0.235 0.813936
## Row46         0.0197277  0.0505744   0.390 0.696670
## Row47         0.0033527  0.0390498   0.086 0.931618
## Row48        -0.0160613  0.0381851  -0.421 0.674239
## Row49        -0.0069346  0.0393645  -0.176 0.860245
## Row50        -0.0120869  0.0425962  -0.284 0.776730
## Row51        -0.0359168  0.0454728  -0.790 0.430038
## Row52        -0.0364745  0.0422546  -0.863 0.388491
## Row53        -0.0700042  0.0455267  -1.538 0.124848
## Row54         0.0127054  0.0379935   0.334 0.738228
## Row55        -0.0027981  0.0405156  -0.069 0.944972
## Row56         0.0070337  0.0493685   0.142 0.886770
## Row57        -0.0162580  0.0386492  -0.421 0.674211
## Row58         0.0002008  0.0426809   0.005 0.996249
## Row59        -0.0120630  0.0387990  -0.311 0.756016
## Row60        -0.0174948  0.0381140  -0.459 0.646450
## Row61        -0.0482912  0.0452580  -1.067 0.286543
## Row62        -0.0147416  0.0384160  -0.384 0.701359
## Row63        -0.0250974  0.0391440  -0.641 0.521753
## Row64         0.0558682  0.0391278   1.428 0.154043
## Row65        -0.0062082  0.0460678  -0.135 0.892860
## Row66         0.0251330  0.0428113   0.587 0.557460
## Row67        -0.0147575  0.0424416  -0.348 0.728221
## Row68         0.0183702  0.0407229   0.451 0.652136
## Row69        -0.0786975  0.0440805  -1.785 0.074894 .
```

```
## Row70             -0.0333088  0.0453189  -0.735 0.462736
## Row71              0.0181767  0.0501057   0.363 0.716952
## Row72              0.0065298  0.0495402   0.132 0.895195
## Row73             -0.0171884  0.0391166  -0.439 0.660576
## Row74             -0.0140158  0.0426890  -0.328 0.742822
## Row75             -0.0394037  0.0426317  -0.924 0.355843
## Row76             -0.0732097  0.0494013  -1.482 0.139068
## Row77              0.0153411  0.0454623   0.337 0.735939
## Row78             -0.0116358  0.0576091  -0.202 0.840027
## Row79             -0.0349751  0.0422897  -0.827 0.408662
## Row80             -0.0659949  0.0496045  -1.330 0.184064
## Row81             -0.0367278  0.0379713  -0.967 0.333947
## Row82             -0.0222029  0.0422420  -0.526 0.599421
## Row83             -0.0225662  0.0421025  -0.536 0.592239
## Row84             -0.0687160  0.0454831  -1.511 0.131551
## Row85             -0.0340303  0.0404614  -0.841 0.400770
## Row86              0.0212482  0.0498801   0.426 0.670326
## Row87              0.0275434  0.0427708   0.644 0.519925
## Row88             -0.0038460  0.0454205  -0.085 0.932558
## Row89             -0.0030590  0.0423636  -0.072 0.942469
## Row90             -0.0312875  0.0405082  -0.772 0.440304
## Row91              0.0139417  0.0455151   0.306 0.759512
## Row92              0.0063690  0.0402418   0.158 0.874318
## Row93              0.0184519  0.0572887   0.322 0.747539
## Row94              0.0001783  0.0501728   0.004 0.997165
## Row95             -0.0249105  0.0375973  -0.663 0.507956
## Row96             -0.0460787  0.0453258  -1.017 0.309894
## Row97              0.0236995  0.0502746   0.471 0.637586
## Row98             -0.0011359  0.0574669  -0.020 0.984239
## Row99             -0.0185219  0.0389603  -0.475 0.634734
## Column2            0.0122573  0.0139995   0.876 0.381747
## Column3            0.0046898  0.0136207   0.344 0.730773
## Column4            0.0055116  0.0138327   0.398 0.690490
## Column5           -0.0308478  0.0130073  -2.372 0.018139 *
## Column6           -0.0028140  0.0137245  -0.205 0.837638
## Column7            0.0302328  0.0141543   2.136 0.033232 *
## Column8           -0.0038262  0.0135295  -0.283 0.777457
## Column9           -0.0080644  0.0133769  -0.603 0.546911
## Column10          -0.0245646  0.0132209  -1.858 0.063829 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06813 on 443 degrees of freedom
##   (39 observations effacées parce que manquantes)
## Multiple R-squared:  0.5283, Adjusted R-squared:  0.3814
## F-statistic: 3.595 on 138 and 443 DF,  p-value: < 2.2e-16
##
## Analysis of Variance Table
##
## Response: DW_shoot_g
##            Df  Sum Sq  Mean Sq F value    Pr(>F)
## Genotype   31 1.76482 0.056930 12.2651 < 2.2e-16 ***
## Row        98 0.39454 0.004026  0.8673 0.8032209
## Column      9 0.14363 0.015959  3.4383 0.0004143 ***
## Residuals 443 2.05624 0.004642
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Summary for fixed effects model of FW_shoot_g"
##
## Call:
## lm(formula = fixed_formula, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.85297 -0.59056  0.06683  0.60993  3.12202
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       4.348956   0.521526    8.339 9.32e-16 ***
## GenotypeEPPN1_L  -1.105731   0.345028   -3.205 0.001448 **
## GenotypeEPPN10_H -0.537219   0.331019   -1.623 0.105310
## GenotypeEPPN10_L -2.507442   0.451752   -5.550 4.89e-08 ***
## GenotypeEPPN11_H  0.150257   0.329555    0.456 0.648655
## GenotypeEPPN11_L -2.802217   0.357801   -7.832 3.52e-14 ***
## GenotypeEPPN12_H -0.901255   0.334170   -2.697 0.007261 **
## GenotypeEPPN12_L -2.480643   0.402140   -6.169 1.54e-09 ***
## GenotypeEPPN13_H  0.571808   0.380670    1.502 0.133773
## GenotypeEPPN13_L -1.996234   0.557385   -3.581 0.000379 ***
## GenotypeEPPN14_H  0.782309   0.406685    1.924 0.055035 .
## GenotypeEPPN14_L -3.185594   0.592576   -5.376 1.23e-07 ***
## GenotypeEPPN15_H -0.842782   0.339818   -2.480 0.013501 *
## GenotypeEPPN15_L -2.216787   0.389657   -5.689 2.31e-08 ***
## GenotypeEPPN2_H  -1.059901   0.344395   -3.078 0.002215 **
## GenotypeEPPN2_L  -1.825187   0.412143   -4.429 1.19e-05 ***
## GenotypeEPPN20_T -2.059717   0.325817   -6.322 6.26e-10 ***
## GenotypeEPPN3_H  -0.530639   0.394152   -1.346 0.178894
## GenotypeEPPN3_L  -1.175765   0.354886   -3.313 0.000998 ***
## GenotypeEPPN4_H  -1.791307   0.363561   -4.927 1.18e-06 ***
## GenotypeEPPN4_L  -1.989734   0.360710   -5.516 5.87e-08 ***
## GenotypeEPPN5_H  -0.128998   0.374823   -0.344 0.730890
## GenotypeEPPN5_L  -2.552314   0.497405   -5.131 4.30e-07 ***
## GenotypeEPPN6_H   0.452259   0.338421    1.336 0.182104
## GenotypeEPPN6_L  -1.674546   0.389233   -4.302 2.08e-05 ***
## GenotypeEPPN7_H  -1.209966   0.553923   -2.184 0.029454 *
## GenotypeEPPN7_L  -1.595932   0.391810   -4.073 5.48e-05 ***
## GenotypeEPPN8_H   0.594590   0.363814    1.634 0.102893
## GenotypeEPPN8_L  -2.038065   0.371224   -5.490 6.74e-08 ***
## GenotypeEPPN9_H   0.458648   0.337752    1.358 0.175166
## GenotypeEPPN9_L  -0.484223   0.352593   -1.373 0.170340
## GenotypeLocal    -0.848264   0.294192   -2.883 0.004124 **
## Row2              0.691489   0.605083    1.143 0.253731
## Row3             -0.626579   0.637669   -0.983 0.326330
## Row4              0.747718   0.662928    1.128 0.259965
## Row5              0.764697   0.637745    1.199 0.231136
## Row6              0.265037   0.729297    0.363 0.716467
## Row7             -0.115923   0.659265   -0.176 0.860502
## Row8              0.375086   0.642050    0.584 0.559380
## Row9             -0.083270   0.641626   -0.130 0.896799
## Row10             0.070628   0.608065    0.116 0.907584
## Row11             0.306383   0.616257    0.497 0.619315
## Row12             0.231177   0.687706    0.336 0.736910
## Row13             0.584631   0.621296    0.941 0.347219
```

```
## Row14         -0.124679   0.632877   -0.197 0.843914
## Row15         -0.244861   0.618702   -0.396 0.692466
## Row16         -0.535333   0.662964   -0.807 0.419816
## Row17          0.121445   0.623462    0.195 0.845644
## Row18          0.571454   0.737998    0.774 0.439144
## Row19          0.403021   0.637096    0.633 0.527324
## Row20          0.457537   0.601792    0.760 0.447480
## Row21          0.759803   0.623326    1.219 0.223505
## Row22          0.404143   0.596882    0.677 0.498697
## Row23          0.207513   0.662951    0.313 0.754416
## Row24          0.990238   0.690487    1.434 0.152237
## Row25          0.125606   0.615849    0.204 0.838480
## Row26         -0.042311   0.751959   -0.056 0.955154
## Row27          0.202231   0.666365    0.303 0.761662
## Row28          0.199547   0.636877    0.313 0.754183
## Row29          0.372038   0.638179    0.583 0.560208
## Row30          0.349353   0.661613    0.528 0.597739
## Row31          0.150464   0.632231    0.238 0.811998
## Row32          0.734404   0.658827    1.115 0.265570
## Row33         -0.454387   0.701612   -0.648 0.517554
## Row34          0.197000   0.603816    0.326 0.744382
## Row35          0.593550   0.638225    0.930 0.352872
## Row36          0.342900   0.614437    0.558 0.577074
## Row37         -0.150416   0.622666   -0.242 0.809226
## Row38          1.170357   0.643304    1.819 0.069535 .
## Row39          0.420675   0.619379    0.679 0.497369
## Row40          0.146071   0.614715    0.238 0.812282
## Row41         -0.343955   0.638008   -0.539 0.590080
## Row42          0.065040   0.657851    0.099 0.921288
## Row43          0.423073   0.632100    0.669 0.503641
## Row44          0.372007   0.596206    0.624 0.532974
## Row45          0.373771   0.660513    0.566 0.571759
## Row46          1.135543   0.751020    1.512 0.131239
## Row47          0.143829   0.619096    0.232 0.816394
## Row48          0.011204   0.623115    0.018 0.985662
## Row49          0.319706   0.643138    0.497 0.619359
## Row50         -0.258145   0.693181   -0.372 0.709766
## Row51         -0.441885   0.742211   -0.595 0.551901
## Row52         -0.257948   0.690183   -0.374 0.708775
## Row53         -0.674353   0.743062   -0.908 0.364613
## Row54         -0.121485   0.636637   -0.191 0.848751
## Row55          0.344667   0.661609    0.521 0.602657
## Row56          0.473861   0.806373    0.588 0.557067
## Row57         -0.014330   0.630476   -0.023 0.981877
## Row58          0.078423   0.696956    0.113 0.910460
## Row59         -0.037389   0.632942   -0.059 0.952922
## Row60          0.029074   0.622479    0.047 0.962768
## Row61         -0.614117   0.688607   -0.892 0.372965
## Row62          0.002782   0.626802    0.004 0.996460
## Row63         -0.591874   0.638991   -0.926 0.354808
## Row64          1.116987   0.638723    1.749 0.081014 .
## Row65          0.343351   0.751846    0.457 0.648124
## Row66          0.458278   0.698126    0.656 0.511877
## Row67         -0.019806   0.693294   -0.029 0.977222
## Row68          0.529612   0.664583    0.797 0.425926
## Row69         -1.138073   0.647638   -1.757 0.079555 .
```

```
## Row70             -0.224334    0.739478   -0.303 0.761751
## Row71             -0.281618    0.817305   -0.345 0.730580
## Row72              0.588461    0.808804    0.728 0.467257
## Row73             -0.471560    0.635897   -0.742 0.458739
## Row74              0.182555    0.696930    0.262 0.793487
## Row75             -0.272700    0.695793   -0.392 0.695298
## Row76             -0.606288    0.806534   -0.752 0.452614
## Row77              0.792191    0.742450    1.067 0.286548
## Row78             -0.962910    0.811550   -1.187 0.236051
## Row79              0.063913    0.690454    0.093 0.926289
## Row80             -0.947643    0.809866   -1.170 0.242574
## Row81             -0.331855    0.620104   -0.535 0.592804
## Row82              0.096944    0.689927    0.141 0.888317
## Row83             -0.704339    0.731606   -0.963 0.336202
## Row84             -0.915201    0.742252   -1.233 0.218220
## Row85             -0.306333    0.660434   -0.464 0.642991
## Row86              0.370469    0.814698    0.455 0.649522
## Row87              0.416461    0.744771    0.559 0.576318
## Row88              0.177227    0.741957    0.239 0.811320
## Row89              0.352860    0.691399    0.510 0.610053
## Row90             -0.262948    0.661673   -0.397 0.691262
## Row91              0.940391    0.811124    1.159 0.246924
## Row92              0.345541    0.656800    0.526 0.599081
## Row93              0.661874    0.935767    0.707 0.479744
## Row94              0.830055    0.753086    1.102 0.270964
## Row95             -0.138448    0.614026   -0.225 0.821712
## Row96              0.026760    0.808258    0.033 0.973603
## Row97              0.619551    0.819850    0.756 0.450234
## Row98             -0.744286    0.812848   -0.916 0.360342
## Row99             -0.184734    0.636436   -0.290 0.771749
## Column2            0.227406    0.226981    1.002 0.316945
## Column3            0.164975    0.219537    0.751 0.452766
## Column4            0.086248    0.227433    0.379 0.704702
## Column5           -0.487560    0.210173   -2.320 0.020800 *
## Column6            0.209418    0.221137    0.947 0.344146
## Column7            0.682185    0.224327    3.041 0.002496 **
## Column8            0.275760    0.219404    1.257 0.209459
## Column9            0.131529    0.214814    0.612 0.540654
## Column10          -0.200589    0.211769   -0.947 0.344044
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.112 on 448 degrees of freedom
##   (34 observations effacées parce que manquantes)
## Multiple R-squared:  0.5749, Adjusted R-squared:  0.444
## F-statistic: 4.391 on 138 and 448 DF,  p-value: < 2.2e-16
##
## Analysis of Variance Table
##
## Response: FW_shoot_g
##            Df Sum Sq Mean Sq F value    Pr(>F)
## Genotype   31 582.15 18.7792 15.1770 < 2.2e-16 ***
## Row        98 120.57  1.2303  0.9943    0.5009
## Column      9  47.01  5.2237  4.2217 2.913e-05 ***
## Residuals 448 554.33  1.2373
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Summary for fixed effects model of DW_root_g"
##
## Call:
## lm(formula = fixed_formula, data = data)
##
## Residuals:
##       Min       1Q   Median       3Q      Max
## -0.123726 -0.018320  0.001036  0.018254  0.096287
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.259e-01  1.618e-02   7.779 4.92e-14 ***
## GenotypeEPPN1_L  -2.065e-02  1.103e-02  -1.871  0.06194 .
## GenotypeEPPN10_H -3.334e-02  1.026e-02  -3.249  0.00124 **
## GenotypeEPPN10_L -7.756e-02  1.403e-02  -5.529 5.42e-08 ***
## GenotypeEPPN11_H  7.330e-03  1.033e-02   0.710  0.47812
## GenotypeEPPN11_L -6.232e-02  1.110e-02  -5.615 3.42e-08 ***
## GenotypeEPPN12_H -2.267e-02  1.065e-02  -2.129  0.03382 *
## GenotypeEPPN12_L -6.325e-02  1.281e-02  -4.938 1.11e-06 ***
## GenotypeEPPN13_H  4.831e-02  1.184e-02   4.081 5.29e-05 ***
## GenotypeEPPN13_L -4.491e-02  1.729e-02  -2.598  0.00968 **
## GenotypeEPPN14_H  5.571e-03  1.229e-02   0.453  0.65064
## GenotypeEPPN14_L -1.168e-01  2.021e-02  -5.779 1.39e-08 ***
## GenotypeEPPN15_H -3.039e-03  1.055e-02  -0.288  0.77334
## GenotypeEPPN15_L -4.924e-02  1.153e-02  -4.270 2.38e-05 ***
## GenotypeEPPN2_H  -8.251e-03  1.038e-02  -0.795  0.42725
## GenotypeEPPN2_L  -3.225e-02  1.194e-02  -2.700  0.00719 **
## GenotypeEPPN20_T -4.281e-02  1.009e-02  -4.241 2.70e-05 ***
## GenotypeEPPN3_H  -2.012e-02  1.124e-02  -1.790  0.07404 .
## GenotypeEPPN3_L  -2.895e-02  1.103e-02  -2.623  0.00900 **
## GenotypeEPPN4_H  -2.893e-02  1.107e-02  -2.614  0.00924 **
## GenotypeEPPN4_L  -4.390e-02  1.119e-02  -3.924  0.00010 ***
## GenotypeEPPN5_H   8.370e-03  1.233e-02   0.679  0.49746
## GenotypeEPPN5_L  -3.730e-02  1.545e-02  -2.414  0.01616 *
## GenotypeEPPN6_H   3.082e-02  1.053e-02   2.927  0.00359 **
## GenotypeEPPN6_L  -2.782e-02  1.237e-02  -2.249  0.02500 *
## GenotypeEPPN7_H  -9.085e-03  1.731e-02  -0.525  0.60000
## GenotypeEPPN7_L  -2.898e-02  1.248e-02  -2.322  0.02066 *
## GenotypeEPPN8_H  -4.654e-03  1.081e-02  -0.431  0.66692
## GenotypeEPPN8_L  -5.250e-02  1.152e-02  -4.558 6.64e-06 ***
## GenotypeEPPN9_H   1.872e-02  1.042e-02   1.797  0.07304 .
## GenotypeEPPN9_L  -2.806e-02  1.069e-02  -2.625  0.00894 **
## GenotypeLocal    -4.227e-02  9.144e-03  -4.623 4.93e-06 ***
## Row2             1.486e-02  1.972e-02   0.753  0.45164
## Row3            -1.434e-02  1.974e-02  -0.727  0.46779
## Row4             2.742e-02  2.053e-02   1.336  0.18228
## Row5             2.774e-02  1.975e-02   1.405  0.16079
## Row6             7.125e-04  2.260e-02   0.032  0.97487
## Row7            -4.514e-03  2.043e-02  -0.221  0.82522
## Row8             6.238e-03  1.989e-02   0.314  0.75401
## Row9            -2.291e-03  1.989e-02  -0.115  0.90835
## Row10            3.094e-04  1.833e-02   0.017  0.98654
## Row11            2.771e-03  1.865e-02   0.149  0.88199
## Row12           -5.737e-03  2.131e-02  -0.269  0.78787
## Row13            2.539e-03  1.926e-02   0.132  0.89516
```

```
## Row14          -5.274e-03  1.961e-02  -0.269  0.78810
## Row15          -1.167e-02  1.917e-02  -0.609  0.54296
## Row16          -1.979e-02  2.054e-02  -0.963  0.33603
## Row17           1.203e-02  1.881e-02   0.640  0.52279
## Row18           1.732e-02  2.284e-02   0.758  0.44884
## Row19           7.825e-03  1.974e-02   0.396  0.69195
## Row20          -3.713e-04  1.863e-02  -0.020  0.98411
## Row21           2.764e-02  1.929e-02   1.433  0.15261
## Row22           2.075e-02  1.890e-02   1.098  0.27284
## Row23           8.846e-03  2.055e-02   0.431  0.66702
## Row24           1.039e-02  2.039e-02   0.510  0.61061
## Row25           5.619e-03  1.908e-02   0.294  0.76852
## Row26           1.144e-02  2.330e-02   0.491  0.62385
## Row27           9.709e-03  2.061e-02   0.471  0.63779
## Row28           3.040e-02  1.973e-02   1.541  0.12397
## Row29           1.840e-02  1.981e-02   0.929  0.35332
## Row30           2.164e-02  2.049e-02   1.056  0.29146
## Row31           1.825e-02  2.031e-02   0.899  0.36923
## Row32           1.875e-04  2.039e-02   0.009  0.99267
## Row33          -1.001e-02  2.173e-02  -0.461  0.64520
## Row34           3.942e-03  1.870e-02   0.211  0.83319
## Row35           3.634e-02  1.976e-02   1.839  0.06659 .
## Row36           1.550e-02  1.903e-02   0.815  0.41577
## Row37          -9.240e-03  1.929e-02  -0.479  0.63206
## Row38           1.972e-02  1.993e-02   0.990  0.32293
## Row39           4.307e-03  1.918e-02   0.225  0.82239
## Row40          -1.272e-02  1.904e-02  -0.668  0.50431
## Row41           1.721e-04  1.974e-02   0.009  0.99305
## Row42          -1.494e-03  2.039e-02  -0.073  0.94162
## Row43           1.737e-02  1.958e-02   0.887  0.37542
## Row44           1.831e-02  1.848e-02   0.991  0.32237
## Row45           2.302e-02  1.918e-02   1.200  0.23063
## Row46           2.261e-03  2.560e-02   0.088  0.92965
## Row47           9.737e-03  1.915e-02   0.508  0.61145
## Row48           2.852e-02  1.934e-02   1.475  0.14098
## Row49          -9.709e-05  1.989e-02  -0.005  0.99611
## Row50           4.634e-03  2.047e-02   0.226  0.82104
## Row51          -8.871e-03  2.304e-02  -0.385  0.70042
## Row52           5.899e-03  2.137e-02   0.276  0.78267
## Row53          -1.033e-02  2.303e-02  -0.448  0.65413
## Row54           1.098e-02  1.921e-02   0.572  0.56774
## Row55           1.023e-02  2.150e-02   0.476  0.63447
## Row56          -5.967e-03  2.279e-02  -0.262  0.79356
## Row57           1.459e-02  2.023e-02   0.721  0.47119
## Row58          -2.266e-02  2.527e-02  -0.897  0.37044
## Row59           9.282e-03  1.962e-02   0.473  0.63632
## Row60           8.874e-03  1.926e-02   0.461  0.64514
## Row61          -1.299e-02  2.134e-02  -0.609  0.54303
## Row62           1.278e-02  1.943e-02   0.658  0.51081
## Row63           1.482e-04  1.983e-02   0.007  0.99404
## Row64           4.458e-02  1.979e-02   2.253  0.02476 *
## Row65          -1.030e-02  2.171e-02  -0.474  0.63551
## Row66           1.553e-02  2.162e-02   0.718  0.47292
## Row67           1.217e-02  2.148e-02   0.566  0.57141
## Row68           3.727e-02  2.059e-02   1.810  0.07091 .
## Row69          -2.290e-02  2.007e-02  -1.141  0.25440
```

```
## Row70                -2.129e-02  2.153e-02  -0.989  0.32336
## Row71                 1.611e-02  2.532e-02   0.636  0.52480
## Row72                -1.095e-02  2.506e-02  -0.437  0.66247
## Row73                 3.196e-03  1.917e-02   0.167  0.86764
## Row74                 1.122e-02  2.161e-02   0.519  0.60371
## Row75                 1.185e-02  2.157e-02   0.549  0.58312
## Row76                -1.625e-02  2.499e-02  -0.650  0.51588
## Row77                 3.322e-02  2.301e-02   1.444  0.14939
## Row78                -2.455e-02  2.516e-02  -0.976  0.32978
## Row79                -4.538e-03  2.140e-02  -0.212  0.83218
## Row80                -4.280e-02  2.508e-02  -1.707  0.08859 .
## Row81                -5.391e-04  1.919e-02  -0.028  0.97760
## Row82                -7.111e-03  2.040e-02  -0.349  0.72753
## Row83                -1.733e-02  2.268e-02  -0.764  0.44504
## Row84                -2.790e-02  2.299e-02  -1.214  0.22551
## Row85                 4.069e-04  2.046e-02   0.020  0.98414
## Row86                 1.934e-02  2.519e-02   0.768  0.44299
## Row87                 2.163e-02  2.164e-02   1.000  0.31804
## Row88                -2.039e-02  2.516e-02  -0.810  0.41813
## Row89                -2.732e-03  2.045e-02  -0.134  0.89381
## Row90                -1.829e-02  1.965e-02  -0.931  0.35242
## Row91                 7.491e-03  2.301e-02   0.326  0.74491
## Row92                 1.289e-02  2.034e-02   0.634  0.52648
## Row93                 1.294e-02  2.899e-02   0.446  0.65555
## Row94                 2.766e-02  2.330e-02   1.187  0.23581
## Row95                 1.318e-02  1.961e-02   0.672  0.50190
## Row96                -2.901e-02  2.154e-02  -1.347  0.17867
## Row97                 1.846e-02  2.538e-02   0.727  0.46745
## Row98                -2.360e-02  2.521e-02  -0.936  0.34981
## Row99                 5.065e-03  1.971e-02   0.257  0.79736
## Column2               -2.022e-03  6.960e-03  -0.290  0.77157
## Column3               -8.350e-04  6.761e-03  -0.124  0.90176
## Column4               -7.260e-03  6.921e-03  -1.049  0.29475
## Column5               -8.979e-03  6.416e-03  -1.400  0.16234
## Column6               -1.668e-02  6.853e-03  -2.435  0.01529 *
## Column7               -3.647e-03  6.886e-03  -0.530  0.59665
## Column8               -1.710e-02  6.767e-03  -2.527  0.01184 *
## Column9               -1.197e-02  6.617e-03  -1.808  0.07122 .
## Column10              -2.027e-02  6.548e-03  -3.096  0.00208 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.03448 on 456 degrees of freedom
##   (26 observations effacées parce que manquantes)
## Multiple R-squared:  0.5211, Adjusted R-squared:  0.3761
## F-statistic: 3.595 on 138 and 456 DF,  p-value: < 2.2e-16
##
## Analysis of Variance Table
##
## Response: DW_root_g
##            Df  Sum Sq   Mean Sq F value  Pr(>F)
## Genotype   31 0.43555 0.0140500 11.8152 < 2e-16 ***
## Row        98 0.12912 0.0013175  1.1080 0.24467
## Column      9 0.02529 0.0028105  2.3634 0.01288 *
## Residuals 456 0.54225 0.0011891
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Summary for fixed effects model of FW_root_g"
##
## Call:
## lm(formula = fixed_formula, data = data)
##
## Residuals:
##      Min      1Q   Median      3Q      Max
## -2.94440 -0.42454  0.05301  0.49390  2.79578
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        2.49770    0.41243   6.056 2.96e-09 ***
## GenotypeEPPN1_L   -0.99396    0.28513  -3.486 0.000539 ***
## GenotypeEPPN10_H  -0.71940    0.27768  -2.591 0.009889 **
## GenotypeEPPN10_L  -2.42450    0.36446  -6.652 8.43e-11 ***
## GenotypeEPPN11_H   0.67080    0.27863   2.408 0.016464 *
## GenotypeEPPN11_L  -2.01685    0.29748  -6.780 3.81e-11 ***
## GenotypeEPPN12_H  -0.29017    0.27502  -1.055 0.291955
## GenotypeEPPN12_L  -1.70449    0.33606  -5.072 5.78e-07 ***
## GenotypeEPPN13_H   1.69149    0.31514   5.367 1.28e-07 ***
## GenotypeEPPN13_L  -1.34014    0.44413  -3.017 0.002694 **
## GenotypeEPPN14_H   0.69928    0.33136   2.110 0.035383 *
## GenotypeEPPN14_L  -2.69373    0.46942  -5.738 1.76e-08 ***
## GenotypeEPPN15_H   0.32706    0.28014   1.168 0.243629
## GenotypeEPPN15_L  -1.28194    0.29858  -4.293 2.16e-05 ***
## GenotypeEPPN2_H    0.17548    0.28337   0.619 0.536052
## GenotypeEPPN2_L   -0.99309    0.32273  -3.077 0.002218 **
## GenotypeEPPN20_T  -1.32849    0.27651  -4.804 2.12e-06 ***
## GenotypeEPPN3_H   -0.02534    0.29983  -0.085 0.932693
## GenotypeEPPN3_L   -0.66829    0.29612  -2.257 0.024501 *
## GenotypeEPPN4_H   -0.47685    0.29535  -1.615 0.107120
## GenotypeEPPN4_L   -1.34407    0.29757  -4.517 8.04e-06 ***
## GenotypeEPPN5_H    0.85745    0.30548   2.807 0.005221 **
## GenotypeEPPN5_L   -0.98160    0.40295  -2.436 0.015238 *
## GenotypeEPPN6_H    0.96179    0.28276   3.401 0.000730 ***
## GenotypeEPPN6_L   -1.14465    0.31202  -3.669 0.000273 ***
## GenotypeEPPN7_H   -0.73862    0.41132  -1.796 0.073210 .
## GenotypeEPPN7_L   -0.82254    0.33277  -2.472 0.013816 *
## GenotypeEPPN8_H    0.10441    0.28780   0.363 0.716925
## GenotypeEPPN8_L   -1.65754    0.30370  -5.458 8.00e-08 ***
## GenotypeEPPN9_H    1.09088    0.27752   3.931 9.81e-05 ***
## GenotypeEPPN9_L   -0.56712    0.28393  -1.997 0.046392 *
## GenotypeLocal     -1.05953    0.24730  -4.284 2.24e-05 ***
## Row2               0.62643    0.47045   1.332 0.183684
## Row3              -0.20103    0.49525  -0.406 0.685005
## Row4               0.42907    0.49870   0.860 0.390045
## Row5               0.60690    0.49553   1.225 0.221318
## Row6               0.05640    0.56683   0.100 0.920783
## Row7               0.48260    0.53712   0.898 0.369404
## Row8               0.01727    0.51770   0.033 0.973396
## Row9               0.06751    0.49865   0.135 0.892361
## Row10              0.23998    0.47240   0.508 0.611707
## Row11              0.20394    0.47850   0.426 0.670161
## Row12              0.43659    0.53466   0.817 0.414600
## Row13              0.49795    0.48283   1.031 0.302944
```

```
## Row14      -0.02888    0.51029   -0.057 0.954893
## Row15       0.09453    0.48111    0.196 0.844328
## Row16      -0.17563    0.51533   -0.341 0.733397
## Row17       0.68644    0.47114    1.457 0.145822
## Row18       0.98993    0.57306    1.727 0.084781 .
## Row19       0.58277    0.49538    1.176 0.240058
## Row20       0.29892    0.46746    0.639 0.522850
## Row21       0.82128    0.48372    1.698 0.090234 .
## Row22       0.84551    0.46406    1.822 0.069122 .
## Row23       0.63508    0.51489    1.233 0.218060
## Row24       0.57228    0.51152    1.119 0.263825
## Row25       0.32854    0.47850    0.687 0.492691
## Row26       0.52193    0.58423    0.893 0.372141
## Row27       0.66781    0.54550    1.224 0.221514
## Row28       0.97619    0.49491    1.972 0.049170 *
## Row29       0.86766    0.49599    1.749 0.080918 .
## Row30       0.85671    0.51375    1.668 0.096097 .
## Row31       1.08337    0.49111    2.206 0.027894 *
## Row32       0.92882    0.49341    1.882 0.060425 .
## Row33       0.27865    0.54545    0.511 0.609691
## Row34       0.58152    0.46896    1.240 0.215615
## Row35       1.16895    0.49572    2.358 0.018797 *
## Row36       0.70206    0.49297    1.424 0.155103
## Row37       0.45139    0.48317    0.934 0.350689
## Row38       1.04063    0.50000    2.081 0.037976 *
## Row39       0.82259    0.48100    1.710 0.087932 .
## Row40       0.48657    0.49262    0.988 0.323817
## Row41       0.32719    0.49544    0.660 0.509343
## Row42       0.24618    0.51112    0.482 0.630295
## Row43       0.47534    0.49107    0.968 0.333581
## Row44       0.36643    0.47588    0.770 0.441694
## Row45       0.63361    0.48122    1.317 0.188621
## Row46       1.34565    0.58221    2.311 0.021269 *
## Row47       0.53194    0.48081    1.106 0.269175
## Row48       0.69815    0.48454    1.441 0.150329
## Row49       0.81914    0.49858    1.643 0.101098
## Row50       0.28364    0.51358    0.552 0.581030
## Row51       0.17508    0.57747    0.303 0.761892
## Row52       0.51219    0.53594    0.956 0.339751
## Row53       0.02788    0.57728    0.048 0.961505
## Row54       0.77581    0.48197    1.610 0.108180
## Row55       1.02607    0.53876    1.905 0.057485 .
## Row56       0.38567    0.57131    0.675 0.499988
## Row57       0.52796    0.50699    1.041 0.298268
## Row58       0.95910    0.54096    1.773 0.076917 .
## Row59       0.56619    0.51286    1.104 0.270198
## Row60       0.56285    0.48283    1.166 0.244345
## Row61      -0.08506    0.53515   -0.159 0.873785
## Row62       0.41881    0.48688    0.860 0.390140
## Row63       0.24326    0.51591    0.472 0.637500
## Row64       1.20153    0.49639    2.421 0.015895 *
## Row65       0.63760    0.58420    1.091 0.275684
## Row66       1.09275    0.54270    2.014 0.044654 *
## Row67       0.78721    0.53833    1.462 0.144357
## Row68       1.09038    0.51660    2.111 0.035353 *
## Row69      -0.20366    0.52489   -0.388 0.698203
```

```
## Row70               -0.21458      0.54028   -0.397 0.691428
## Row71                0.67221      0.63424    1.060 0.289777
## Row72                0.78927      0.62875    1.255 0.210023
## Row73                0.35186      0.48105    0.731 0.464893
## Row74                0.70984      0.54095    1.312 0.190123
## Row75                0.28577      0.54132    0.528 0.597825
## Row76               -0.11252      0.57282   -0.196 0.844358
## Row77                1.23508      0.57663    2.142 0.032741 *
## Row78                0.12704      0.73035    0.174 0.861985
## Row79                0.48733      0.53673    0.908 0.364386
## Row80               -0.82666      0.62953   -1.313 0.189809
## Row81                0.26952      0.48154    0.560 0.575957
## Row82                0.45386      0.53639    0.846 0.397920
## Row83               -0.44226      0.56844   -0.778 0.436967
## Row84               -0.72552      0.63893   -1.136 0.256761
## Row85                0.06722      0.51350    0.131 0.895915
## Row86                0.86896      0.63229    1.374 0.170036
## Row87                0.65335      0.57642    1.133 0.257633
## Row88                1.31591      0.63016    2.088 0.037343 *
## Row89                0.15095      0.51345    0.294 0.768908
## Row90                0.28960      0.54206    0.534 0.593421
## Row91                0.37649      0.57737    0.652 0.514683
## Row92                0.48562      0.51030    0.952 0.341799
## Row93                0.78874      0.72716    1.085 0.278641
## Row94                0.58102      0.58422    0.995 0.320505
## Row95                0.12559      0.47696    0.263 0.792425
## Row96               -0.48043      0.54024   -0.889 0.374329
## Row97                0.85817      0.63687    1.347 0.178508
## Row98               -0.51043      0.63204   -0.808 0.419753
## Row99                0.04611      0.49422    0.093 0.925702
## Column2              0.09927      0.17601    0.564 0.573019
## Column3              0.08650      0.16913    0.511 0.609285
## Column4             -0.03641      0.17439   -0.209 0.834723
## Column5             -0.24622      0.16273   -1.513 0.130962
## Column6              0.28291      0.17266    1.638 0.102020
## Column7              0.34079      0.17437    1.954 0.051267 .
## Column8              0.16145      0.17087    0.945 0.345245
## Column9              0.14782      0.16724    0.884 0.377237
## Column10            -0.13529      0.16710   -0.810 0.418595
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8641 on 448 degrees of freedom
##   (34 observations effacées parce que manquantes)
## Multiple R-squared:  0.6406, Adjusted R-squared:  0.5299
## F-statistic: 5.786 on 138 and 448 DF,  p-value: < 2.2e-16
##
## Analysis of Variance Table
##
## Response: FW_root_g
##           Df Sum Sq Mean Sq F value  Pr(>F)
## Genotype  31 488.62 15.7620 21.1116 < 2e-16 ***
## Row       98  91.16  0.9302  1.2459 0.07229 .
## Column     9  16.35  1.8167  2.4333 0.01043 *
## Residuals 448 334.48  0.7466
```

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

```r
for (trait in variables) {
  fit_models_random(endpoint_clean, trait)
}
```

```
## boundary (singular) fit: see help('isSingular')
```

```
## [1] "Summary for random effects model of DW_shoot_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: random_formula
##    Data: data
##
## REML criterion at convergence: -1309.1
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.9894 -0.5455  0.0518  0.6358  3.3001
##
## Random effects:
##  Groups   Name        Variance  Std.Dev.
##  Row      (Intercept) 0.0000000 0.00000
##  Column   (Intercept) 0.0002268 0.01506
##  Residual             0.0045033 0.06711
## Number of obs: 582, groups:  Row, 99; Column, 10
##
## Fixed effects:
##                   Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)        0.29736    0.01334 220.04703  22.286  < 2e-16 ***
## GenotypeEPPN1_L   -0.04833    0.01874 541.30540  -2.579 0.010185 *
## GenotypeEPPN10_H  -0.02630    0.01875 541.56937  -1.403 0.161302
## GenotypeEPPN10_L  -0.15192    0.02468 542.99000  -6.157 1.44e-09 ***
## GenotypeEPPN11_H   0.01636    0.01813 541.25913   0.903 0.367164
## GenotypeEPPN11_L  -0.13870    0.01925 541.94955  -7.205 1.96e-12 ***
## GenotypeEPPN12_H  -0.04602    0.01899 541.63735  -2.424 0.015680 *
## GenotypeEPPN12_L  -0.13330    0.02188 542.34033  -6.092 2.11e-09 ***
## GenotypeEPPN13_H   0.03974    0.02138 542.35916   1.858 0.063642 .
## GenotypeEPPN13_L  -0.14174    0.03259 543.19047  -4.349 1.64e-05 ***
## GenotypeEPPN14_H   0.04390    0.02139 542.56653   2.053 0.040582 *
## GenotypeEPPN14_L  -0.18510    0.03267 544.71160  -5.666 2.37e-08 ***
## GenotypeEPPN15_H  -0.05577    0.01853 541.58304  -3.010 0.002736 **
## GenotypeEPPN15_L  -0.12353    0.02092 541.84356  -5.905 6.23e-09 ***
## GenotypeEPPN2_H   -0.05283    0.01899 541.52821  -2.783 0.005575 **
## GenotypeEPPN2_L   -0.08491    0.02191 543.54894  -3.875 0.000120 ***
## GenotypeEPPN20_T  -0.12055    0.01795 541.38915  -6.714 4.79e-11 ***
## GenotypeEPPN3_H   -0.04930    0.02093 542.17224  -2.356 0.018852 *
## GenotypeEPPN3_L   -0.05364    0.02018 542.60728  -2.658 0.008081 **
## GenotypeEPPN4_H   -0.09211    0.02017 542.16543  -4.567 6.12e-06 ***
## GenotypeEPPN4_L   -0.11056    0.02094 542.51289  -5.280 1.87e-07 ***
## GenotypeEPPN5_H   -0.01102    0.02094 542.33284  -0.526 0.598885
## GenotypeEPPN5_L   -0.08922    0.02836 543.54740  -3.147 0.001742 **
## GenotypeEPPN6_H    0.01663    0.01876 541.79386   0.887 0.375713
## GenotypeEPPN6_L   -0.07685    0.02242 541.81572  -3.428 0.000655 ***
## GenotypeEPPN7_H   -0.06381    0.03021 543.79858  -2.112 0.035142 *
## GenotypeEPPN7_L   -0.09094    0.02187 542.16240  -4.157 3.74e-05 ***
## GenotypeEPPN8_H    0.04754    0.02016 541.86375   2.358 0.018720 *
## GenotypeEPPN8_L   -0.09317    0.02017 542.40421  -4.618 4.84e-06 ***
## GenotypeEPPN9_H    0.01369    0.01833 541.50325   0.747 0.455264
## GenotypeEPPN9_L   -0.03151    0.01927 542.47889  -1.636 0.102483
## GenotypeLocal     -0.03662    0.01621 541.40288  -2.259 0.024260 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Correlation matrix not shown by default, as p = 32 > 12.
## Use print(summary(random_model), correlation=TRUE)  or
##     vcov(summary(random_model))        if you need it
```

```
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
##
## Type III Analysis of Variance Table with Satterthwaite's method
##            Sum Sq  Mean Sq NumDF  DenDF F value    Pr(>F)
## Genotype 1.7683 0.057043    31 542.66  12.667 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## boundary (singular) fit: see help('isSingular')
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## DW_shoot_g ~ Genotype + (1 | Row) + (1 | Column)
##               npar logLik    AIC    LRT Df Pr(>Chisq)
## <none>          35 654.54 -1239.1
## (1 | Row)       34 654.54 -1241.1  0.000  1  1.0000000
## (1 | Column)    34 647.87 -1227.7 13.351  1  0.0002583 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## boundary (singular) fit: see help('isSingular')
```

```
## [1] "Summary for random effects model of FW_shoot_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: random_formula
##    Data: data
##
## REML criterion at convergence: 1792.5
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.2990 -0.5076  0.1056  0.5894  3.2957
##
## Random effects:
##  Groups   Name        Variance  Std.Dev.
##  Row      (Intercept) 3.700e-15 6.083e-08
##  Column   (Intercept) 7.466e-02 2.732e-01
##  Residual             1.228e+00 1.108e+00
## Number of obs: 587, groups:  Row, 99; Column, 10
##
## Fixed effects:
##                   Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)        4.55689    0.22323 190.55612  20.414  < 2e-16 ***
## GenotypeEPPN1_L   -1.14154    0.30952 546.42721  -3.688 0.000249 ***
## GenotypeEPPN10_H  -0.38983    0.30600 546.63391  -1.274 0.203229
## GenotypeEPPN10_L  -2.34956    0.40751 547.88045  -5.766 1.36e-08 ***
## GenotypeEPPN11_H   0.07997    0.29642 546.34873   0.270 0.787412
## GenotypeEPPN11_L  -2.60679    0.31792 546.99431  -8.200 1.73e-15 ***
## GenotypeEPPN12_H  -0.86454    0.30592 546.47578  -2.826 0.004886 **
## GenotypeEPPN12_L  -2.40006    0.36133 547.30548  -6.642 7.47e-11 ***
## GenotypeEPPN13_H   0.48937    0.35308 547.28883   1.386 0.166306
## GenotypeEPPN13_L  -2.04744    0.49821 547.64532  -4.110 4.57e-05 ***
## GenotypeEPPN14_H   0.83245    0.37091 547.82015   2.244 0.025209 *
## GenotypeEPPN14_L  -3.00507    0.53957 549.33563  -5.569 4.01e-08 ***
## GenotypeEPPN15_H  -0.79670    0.30601 546.64879  -2.604 0.009477 **
## GenotypeEPPN15_L  -2.30517    0.35287 546.94902  -6.533 1.48e-10 ***
## GenotypeEPPN2_H   -1.12656    0.31352 546.61812  -3.593 0.000356 ***
## GenotypeEPPN2_L   -1.73398    0.37084 547.81855  -4.676 3.69e-06 ***
## GenotypeEPPN20_T  -1.99562    0.29937 546.38695  -6.666 6.44e-11 ***
## GenotypeEPPN3_H   -0.33275    0.36115 547.09035  -0.921 0.357268
## GenotypeEPPN3_L   -1.20378    0.32751 547.02605  -3.676 0.000261 ***
## GenotypeEPPN4_H   -1.68420    0.32759 547.16950  -5.141 3.81e-07 ***
## GenotypeEPPN4_L   -2.06014    0.33303 547.19709  -6.186 1.21e-09 ***
## GenotypeEPPN5_H   -0.21801    0.34575 547.31496  -0.631 0.528613
## GenotypeEPPN5_L   -2.79938    0.44370 547.81455  -6.309 5.79e-10 ***
## GenotypeEPPN6_H    0.42744    0.30972 546.85210   1.380 0.168127
## GenotypeEPPN6_L   -1.46886    0.35314 547.47801  -4.159 3.70e-05 ***
## GenotypeEPPN7_H   -0.92676    0.49899 548.53554  -1.857 0.063805 .
## GenotypeEPPN7_L   -1.49576    0.35297 547.09432  -4.238 2.65e-05 ***
## GenotypeEPPN8_H    0.63847    0.33290 546.91209   1.918 0.055644 .
## GenotypeEPPN8_L   -2.04161    0.33316 547.38192  -6.128 1.70e-09 ***
## GenotypeEPPN9_H    0.42112    0.30610 546.85389   1.376 0.169456
## GenotypeEPPN9_L   -0.49847    0.32263 547.20870  -1.545 0.122921
## GenotypeLocal     -0.79272    0.26644 546.58333  -2.975 0.003057 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Correlation matrix not shown by default, as p = 32 > 12.
## Use print(summary(random_model), correlation=TRUE)  or
##     vcov(summary(random_model))        if you need it
```

```
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
##
## Type III Analysis of Variance Table with Satterthwaite's method
##          Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## Genotype  576.8  18.607    31 547.54  15.152 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## boundary (singular) fit: see help('isSingular')
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## FW_shoot_g ~ Genotype + (1 | Row) + (1 | Column)
##              npar  logLik    AIC    LRT Df Pr(>Chisq)
## <none>        35 -896.23 1862.5
## (1 | Row)     34 -896.23 1860.5  0.000  1          1
## (1 | Column)  34 -905.45 1878.9 18.441  1  1.752e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Summary for random effects model of DW_root_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: random_formula
##    Data: data
##
## REML criterion at convergence: -2084.7
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.3443 -0.5896 -0.0033  0.5715  3.5110
##
## Random effects:
##  Groups   Name        Variance  Std.Dev.
##  Row      (Intercept) 1.865e-05 0.004319
##  Column   (Intercept) 2.384e-05 0.004882
##  Residual             1.197e-03 0.034597
## Number of obs: 595, groups:  Row, 99; Column, 10
##
## Fixed effects:
##                   Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)       0.117991   0.006664 383.581184  17.707  < 2e-16 ***
## GenotypeEPPN1_L  -0.016450   0.009994 554.689414  -1.646 0.100323
## GenotypeEPPN10_H -0.027746   0.009601 541.301119  -2.890 0.004006 **
## GenotypeEPPN10_L -0.071638   0.012815 557.164839  -5.590 3.56e-08 ***
## GenotypeEPPN11_H  0.008793   0.009412 553.049111   0.934 0.350594
## GenotypeEPPN11_L -0.049845   0.010000 555.582300  -4.985 8.31e-07 ***
## GenotypeEPPN12_H -0.018987   0.009847 549.770811  -1.928 0.054348 .
## GenotypeEPPN12_L -0.059543   0.011648 555.899759  -5.112 4.40e-07 ***
## GenotypeEPPN13_H  0.050859   0.011077 545.299523   4.592 5.47e-06 ***
## GenotypeEPPN13_L -0.042487   0.015659 556.729842  -2.713 0.006868 **
## GenotypeEPPN14_H  0.013389   0.011350 554.018359   1.180 0.238649
## GenotypeEPPN14_L -0.102488   0.018662 558.925103  -5.492 6.05e-08 ***
## GenotypeEPPN15_H  0.003471   0.009617 552.970162   0.361 0.718297
## GenotypeEPPN15_L -0.045380   0.010642 550.528176  -4.264 2.36e-05 ***
## GenotypeEPPN2_H  -0.008303   0.009609 549.359787  -0.864 0.387914
## GenotypeEPPN2_L  -0.028473   0.010872 556.575775  -2.619 0.009061 **
## GenotypeEPPN20_T -0.041691   0.009398 544.381421  -4.436 1.11e-05 ***
## GenotypeEPPN3_H  -0.014743   0.010447 546.256754  -1.411 0.158735
## GenotypeEPPN3_L  -0.024905   0.010279 547.074059  -2.423 0.015721 *
## GenotypeEPPN4_H  -0.023382   0.010136 554.324936  -2.307 0.021428 *
## GenotypeEPPN4_L  -0.044489   0.010450 545.951689  -4.258 2.43e-05 ***
## GenotypeEPPN5_H   0.007508   0.011353 553.271191   0.661 0.508697
## GenotypeEPPN5_L  -0.035166   0.013976 551.111221  -2.516 0.012146 *
## GenotypeEPPN6_H   0.037835   0.009727 550.481581   3.890 0.000113 ***
```

```
## GenotypeEPPN6_L    -0.013919    0.011346 552.307649   -1.227 0.220444
## GenotypeEPPN7_H    -0.002822    0.015675 558.402072   -0.180 0.857212
## GenotypeEPPN7_L    -0.023825    0.011354 555.405531   -2.098 0.036331 *
## GenotypeEPPN8_H     0.001505    0.009979 550.175915    0.151 0.880150
## GenotypeEPPN8_L    -0.042596    0.010466 554.539103   -4.070 5.38e-05 ***
## GenotypeEPPN9_H     0.021880    0.009510 552.796541    2.301 0.021787 *
## GenotypeEPPN9_L    -0.022033    0.009860 553.975181   -2.235 0.025838 *
## GenotypeLocal      -0.038857    0.008370 551.083178   -4.642 4.31e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Correlation matrix not shown by default, as p = 32 > 12.
## Use print(summary(random_model), correlation=TRUE)  or
##     vcov(summary(random_model))        if you need it
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##             Sum Sq  Mean Sq NumDF  DenDF F value   Pr(>F)
## Genotype 0.43205 0.013937    31 551.35  11.644 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## DW_root_g ~ Genotype + (1 | Row) + (1 | Column)
##              npar logLik    AIC    LRT Df Pr(>Chisq)
## <none>         35 1042.3 -2014.7
## (1 | Row)      34 1042.2 -2016.3 0.3087  1    0.57846
## (1 | Column)   34 1040.7 -2013.3 3.3431  1    0.06749 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Summary for random effects model of FW_root_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: random_formula
##    Data: data
##
## REML criterion at convergence: 1529.9
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.3494 -0.5254  0.0077  0.5524  3.6527
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Row      (Intercept) 0.01318  0.1148
##  Column   (Intercept) 0.02693  0.1641
##  Residual             0.75712  0.8701
## Number of obs: 587, groups:  Row, 99; Column, 10
##
## Fixed effects:
##                   Estimate Std. Error       df t value Pr(>|t|)
## (Intercept)         2.9893     0.1946 366.6528  15.362  < 2e-16 ***
## GenotypeEPPN1_L    -0.9470     0.2619 546.2520  -3.617 0.000326 ***
## GenotypeEPPN10_H   -0.6538     0.2614 535.2384  -2.501 0.012688 *
## GenotypeEPPN10_L   -2.1838     0.3357 548.9591  -6.505 1.75e-10 ***
## GenotypeEPPN11_H    0.6510     0.2567 546.2932   2.536 0.011485 *
## GenotypeEPPN11_L   -1.7936     0.2715 547.5764  -6.607 9.30e-11 ***
## GenotypeEPPN12_H   -0.2644     0.2586 535.2333  -1.023 0.306996
## GenotypeEPPN12_L   -1.8006     0.3075 547.9957  -5.855 8.20e-09 ***
## GenotypeEPPN13_H    1.5859     0.2998 529.5884   5.289 1.80e-07 ***
## GenotypeEPPN13_L   -1.3988     0.4052 548.8553  -3.452 0.000598 ***
## GenotypeEPPN14_H    0.6934     0.3077 547.8860   2.253 0.024638 *
## GenotypeEPPN14_L   -2.4539     0.4362 547.7946  -5.626 2.95e-08 ***
## GenotypeEPPN15_H    0.4111     0.2592 544.6595   1.586 0.113374
## GenotypeEPPN15_L   -1.2217     0.2787 539.5068  -4.383 1.40e-05 ***
## GenotypeEPPN2_H     0.0712     0.2646 542.9662   0.269 0.787948
## GenotypeEPPN2_L    -0.9244     0.2947 549.1555  -3.137 0.001799 **
## GenotypeEPPN20_T   -1.1770     0.2566 544.0001  -4.587 5.57e-06 ***
## GenotypeEPPN3_H     0.1343     0.2830 532.2673   0.474 0.635351
## GenotypeEPPN3_L    -0.7197     0.2748 540.9639  -2.619 0.009076 **
```

```
## GenotypeEPPN4_H    -0.3051    0.2717 548.1187  -1.123 0.261938
## GenotypeEPPN4_L    -1.3782    0.2787 538.2942  -4.945 1.02e-06 ***
## GenotypeEPPN5_H     0.8626    0.2882 535.1159   2.993 0.002886 **
## GenotypeEPPN5_L    -0.9781    0.3640 540.7263  -2.687 0.007431 **
## GenotypeEPPN6_H     0.9919    0.2648 541.4096   3.746 0.000199 ***
## GenotypeEPPN6_L    -0.9349    0.2886 544.7117  -3.239 0.001272 **
## GenotypeEPPN7_H    -0.4476    0.3812 546.4826  -1.174 0.240871
## GenotypeEPPN7_L    -0.8267    0.3072 546.1904  -2.691 0.007337 **
## GenotypeEPPN8_H     0.2181    0.2676 543.9525   0.815 0.415511
## GenotypeEPPN8_L    -1.5612    0.2793 546.2587  -5.589 3.61e-08 ***
## GenotypeEPPN9_H     1.0711    0.2566 544.5263   4.175 3.47e-05 ***
## GenotypeEPPN9_L    -0.4957    0.2648 545.1092  -1.872 0.061761 .
## GenotypeLocal      -1.0266    0.2300 542.4190  -4.464 9.81e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Correlation matrix not shown by default, as p = 32 > 12.
## Use print(summary(random_model), correlation=TRUE)  or
##     vcov(summary(random_model))         if you need it
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##          Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## Genotype  482.7  15.571    31 542.77  20.566 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## FW_root_g ~ Genotype + (1 | Row) + (1 | Column)
##              npar  logLik    AIC    LRT Df Pr(>Chisq)
## <none>         35 -764.96 1599.9
## (1 | Row)      34 -765.12 1598.2 0.3318  1   0.564584
## (1 | Column)   34 -769.28 1606.6 8.6490  1   0.003272 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

2. Linear models with Plant_type

Model with X as Plant_type instead of Genotype, and row and column effects as random effects.
Plant_type is defined as H for Hybrid, L for pure Line and T for Tester.

```r
endpoint_clean$Plant_type <- as.factor(endpoint_clean$Plant_type)
endpoint_clean$Plant_type <- relevel(endpoint_clean$Plant_type, ref = "T") # T as base
level

fit_model_plant_type <- function(data, trait) {
  # Random effects model with Plant_type as a fixed effect
  model_formula <- as.formula(paste(trait, "~ Plant_type + (1|Row) + (1|Column)"))
  model <- lmer(model_formula, data)
  print(paste("Summary for mixed effects model of", trait))
  print(summary(model))
  print(anova(model))
  print(ranova(model))
}

for (trait in variables) {
  fit_model_plant_type(endpoint_clean, trait)
}
```

```
## boundary (singular) fit: see help('isSingular')
```

```
## [1] "Summary for mixed effects model of DW_shoot_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: model_formula
##     Data: data
##
## REML criterion at convergence: -1318.4
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.6498 -0.6468 -0.0255  0.7025  3.2543
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Row      (Intercept) 0.000000 0.00000
##  Column   (Intercept) 0.000194 0.01393
##  Residual             0.005701 0.07550
## Number of obs: 582, groups:  Row, 99; Column, 10
##
## Fixed effects:
##              Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)   0.17688    0.01519 322.57781  11.645  < 2e-16 ***
## Plant_typeH   0.10736    0.01518 569.78178   7.072 4.50e-12 ***
## Plant_typeI   0.08384    0.01864 569.98350   4.499 8.29e-06 ***
## Plant_typeL   0.02639    0.01543 570.25345   1.710   0.0877 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) Plnt_H Plnt_t
## Plant_typeH -0.916
## Plant_typeI -0.746  0.747
## Plant_typeL -0.902  0.902  0.735
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
##
## Type III Analysis of Variance Table with Satterthwaite's method
##            Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## Plant_type 0.96216 0.32072     3 570.47  56.259 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## boundary (singular) fit: see help('isSingular')
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## DW_shoot_g ~ Plant_type + (1 | Row) + (1 | Column)
##               npar logLik     AIC     LRT Df Pr(>Chisq)
## <none>           7 659.21 -1304.4
## (1 | Row)        6 659.21 -1306.4 0.0000  1   0.999999
## (1 | Column)     6 655.11 -1298.2 8.1939  1   0.004203 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## boundary (singular) fit: see help('isSingular')
```

```
## [1] "Summary for mixed effects model of FW_shoot_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: model_formula
##    Data: data
##
## REML criterion at convergence: 1949.7
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.3222 -0.6653  0.0055  0.6841  3.3998
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Row      (Intercept) 0.00000  0.0000
##  Column   (Intercept) 0.07251  0.2693
##  Residual             1.57650  1.2556
## Number of obs: 587, groups:  Row, 99; Column, 10
##
## Fixed effects:
##             Estimate Std. Error       df t value Pr(>|t|)
## (Intercept)   2.5639     0.2607 278.7791   9.835  < 2e-16 ***
## Plant_typeH   1.7631     0.2569 574.6962   6.864 1.74e-11 ***
## Plant_typeI   1.2013     0.3122 574.9913   3.848 0.000132 ***
## Plant_typeL   0.1913     0.2607 575.2697   0.734 0.463414
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) Plnt_H Plnt_t
## Plant_typeH -0.906
## Plant_typeI -0.746  0.757
## Plant_typeL -0.894  0.907  0.746
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
##
## Type III Analysis of Variance Table with Satterthwaite's method
##            Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## Plant_type 342.09  114.03     3 575.53  72.331 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## boundary (singular) fit: see help('isSingular')
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## FW_shoot_g ~ Plant_type + (1 | Row) + (1 | Column)
##             npar   logLik    AIC    LRT Df Pr(>Chisq)
## <none>         7 -974.86 1963.7
## (1 | Row)      6 -974.86 1961.7   0.00  1  1.0000000
## (1 | Column)   6 -981.54 1975.1  13.36  1  0.0002571 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Summary for mixed effects model of DW_root_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: model_formula
##    Data: data
##
## REML criterion at convergence: -2143.2
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.1196 -0.5896 -0.0156  0.5974  3.2946
##
## Random effects:
##  Groups   Name        Variance  Std.Dev.
##  Row      (Intercept) 1.777e-05 0.004216
##  Column   (Intercept) 1.222e-05 0.003495
##  Residual             1.485e-03 0.038533
## Number of obs: 595, groups:  Row, 99; Column, 10
##
## Fixed effects:
##              Estimate Std. Error        df t value Pr(>|t|)
## (Intercept) 7.635e-02  7.682e-03 5.089e+02   9.939  < 2e-16 ***
## Plant_typeH 4.416e-02  7.907e-03 5.733e+02   5.585 3.62e-08 ***
## Plant_typeI 2.673e-03  9.615e-03 5.710e+02   0.278    0.781
## Plant_typeL 4.914e-03  8.027e-03 5.743e+02   0.612    0.541
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) Plnt_H Plnt_t
## Plant_typeH -0.948
## Plant_typeI -0.780  0.757
## Plant_typeL -0.934  0.908  0.746
## Type III Analysis of Variance Table with Satterthwaite's method
##             Sum Sq  Mean Sq NumDF  DenDF F value    Pr(>F)
## Plant_type 0.23603 0.078677     3 579.11  52.989 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## DW_root_g ~ Plant_type + (1 | Row) + (1 | Column)
##             npar  logLik     AIC     LRT Df Pr(>Chisq)
## <none>         7 1071.6 -2129.2
```

```
## (1 | Row)          6 1071.5 -2131.0 0.20531  1      0.6505
## (1 | Column)       6 1071.2 -2130.4 0.79013  1      0.3741
```

```
## boundary (singular) fit: see help('isSingular')
```

```
## [1] "Summary for mixed effects model of FW_root_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: model_formula
##    Data: data
##
## REML criterion at convergence: 1680.2
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.2688 -0.6001 -0.0073  0.5866  3.9673
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  Row       (Intercept) 0.00000  0.0000
##  Column    (Intercept) 0.02094  0.1447
##  Residual              1.00081  1.0004
## Number of obs: 587, groups:  Row, 99; Column, 10
##
## Fixed effects:
##              Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)   1.81871    0.20534 429.80168   8.857  < 2e-16 ***
## Plant_typeH   1.50029    0.20847 575.15593   7.197 1.93e-12 ***
## Plant_typeI   0.14274    0.25172 575.22586   0.567    0.571
## Plant_typeL  -0.03538    0.21114 576.00198  -0.168    0.867
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) Plnt_H Plnt_t
## Plant_typeH -0.936
## Plant_typeI -0.775  0.763
## Plant_typeL -0.924  0.910  0.754
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
##
## Type III Analysis of Variance Table with Satterthwaite's method
##             Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## Plant_type 333.21  111.07     3 576.31  110.98 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## boundary (singular) fit: see help('isSingular')
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## FW_root_g ~ Plant_type + (1 | Row) + (1 | Column)
##              npar  logLik    AIC     LRT Df Pr(>Chisq)
## <none>          7 -840.11 1694.2
## (1 | Row)       6 -840.11 1692.2 0.0000  1    1.00000
## (1 | Column)    6 -842.16 1696.3 4.1022  1    0.04283 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

3. Linear models with asreml library

```
modasreml <- asreml(fixed = DW_shoot_g ~ Genotype,
                    random = ~ Row + Column,
                    residual = ~  NULL,
                    data = endpoint_clean)
```

```
## ASReml Version 4.2 09/06/2024 16:56:49
##           LogLik      Sigma2     DF     wall
## 1      1153.738  0.004225154    550  16:56:49
## 2      1158.344  0.004374624    550  16:56:49  (  1 restrained)
## 3      1159.875  0.004488579    550  16:56:49  (  1 restrained)
## 4      1159.954  0.004503463    550  16:56:49  (  1 restrained)
## 5      1159.958  0.004503295    550  16:56:49  (  1 restrained)
## 6      1159.958  0.004503324    550  16:56:49
```

```
plot(modasreml)
```
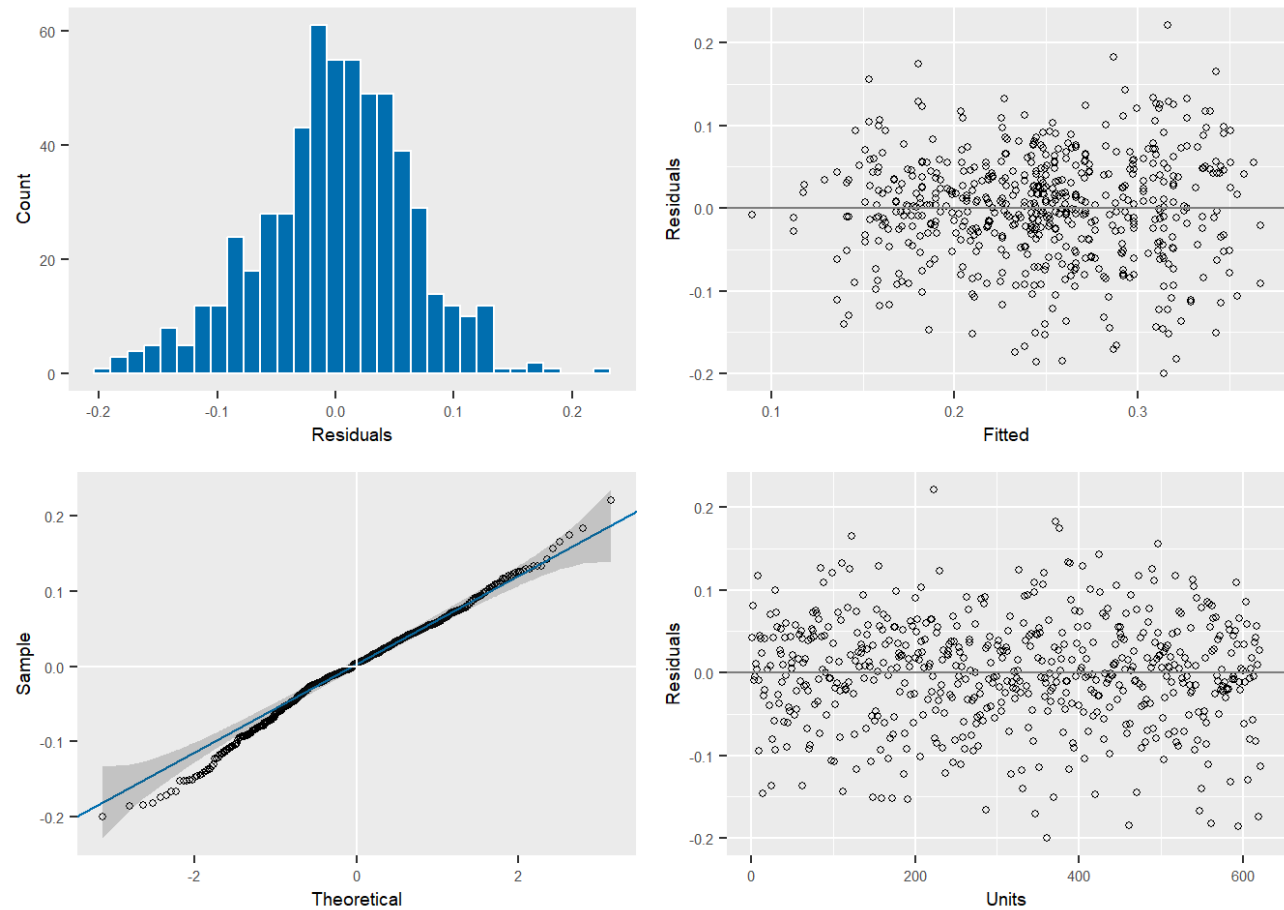
```
summary(modasreml)$varcomp
```

```
##            component    std.error   z.ratio bound %ch
## Column   2.268488e-04 0.0001442598 1.572503     P   0
## Row      2.400963e-09          NA        NA     B  NA
## units!R  4.503324e-03 0.0002738023 16.447356    P   0
```

4. Linear models with Soil variable

Model with Soil as explicative variable.

5. Linear models with Soil variable with Plant_type