

Three way ANOVA

Sources of variation = treatment:genotype:year

```
*****  
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*****  
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```

1. %Relative leaf water content

Shapiro-Wilk normality test

data: resRWC

W = 0.99582, p-value = 0.8398

summary(anovaRWC)

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
treatment	1	33696	33696	1088.91	< 2e-16	***
genotype	4	20656	5164	166.88	< 2e-16	***
year	1	5527	5527	178.59	< 2e-16	***
treatment:genotype	4	24349	6087	196.71	< 2e-16	***
treatment:year	1	3114	3114	100.64	< 2e-16	***
genotype:year	4	2078	519	16.79	8.44e-12	***
treatment:genotype:year	4	1310	327	10.58	9.24e-08	***
Residuals	190	5880	31			

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

> print(model.tables(anovaRWC,"means"),digits=3)

Tables of means

Grand mean

72.82724

treatment

treatment

control drought

85.5 60.2

genotype

genotype

Barke HOR10151 S42IL-141 S42IL-143 Scarlett

61.8 60.9 81.0 85.3 75.0

year

year

2018 2019

80.9 69.6

treatment:genotype

genotype

treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett

control 88.0 85.1 84.5 85.0 84.8

drought 35.5 36.8 77.5 85.7 65.3

```

treatment:year
  year
treatment 2018 2019
  control 87.5 84.7
  drought 74.4 54.5

```

```

genotype:year
  year
genotype 2018 2019
  Barke 72.9 57.3
  HOR10151 71.8 56.6
  S42IL-141 86.3 78.9
  S42IL-143 85.1 85.4
  Scarlett 88.6 69.6

```

```

treatment:genotype:year
, , year = 2018

```

```

      genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
  control 89.4 86.4 85.3 85.6 91.0
  drought 56.5 57.2 87.4 84.6 86.1

```

```

, , year = 2019

```

```

      genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
  control 87.5 84.6 84.2 84.7 82.4
  drought 27.1 28.6 73.6 86.2 56.9

```

```

*****
*****

```

2. Length of the Main Spike

Shapiro-Wilk normality test

```

data: resspikelength
W = 0.98852, p-value = 0.09021

```

```

summary(anovaspikelength)

```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
treatment	1	234.7	234.69	275.384	< 2e-16	***
genotype	4	846.9	211.73	248.448	< 2e-16	***
year	1	23.0	22.96	26.946	5.35e-07	***
treatment:genotype	4	15.0	3.75	4.399	0.00201	**
treatment:year	1	0.7	0.74	0.867	0.35286	
genotype:year	4	2.9	0.74	0.863	0.48750	
treatment:genotype:year	4	5.4	1.36	1.593	0.17782	
Residuals	190	161.9	0.85			

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

```
> print(model.tables(anovaspikelength,"means"),digits=3)
```

Tables of means

Grand mean

9.12381

treatment

treatment

control drought

10.18	8.07
-------	------

genotype

genotype

Barke	HOR10151	S42IL-141	S42IL-143	Scarlett
8.90	5.34	10.93	10.48	9.96

year

year

2018 2019

9.65	8.91
------	------

treatment:genotype

genotype

treatment	Barke	HOR10151	S42IL-141	S42IL-143	Scarlett
control	10.26	6.43	11.55	11.40	11.26
drought	7.55	4.25	10.30	9.56	8.67

treatment:year

year

treatment	2018	2019
control	10.61	10.01
drought	8.68	7.82

genotype:year

year

genotype	2018	2019
Barke	9.50	8.67
HOR10151	5.55	5.26
S42IL-141	11.70	10.62
S42IL-143	11.07	10.25
Scarlett	10.42	9.78

treatment:genotype:year

, , year = 2018

genotype

treatment	Barke	HOR10151	S42IL-141	S42IL-143	Scarlett
control	10.75	6.22	12.67	11.75	11.67
drought	8.25	4.88	10.73	10.38	9.17

, , year = 2019

```

      genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
  control 10.07  6.51    11.10    11.27    11.10
  drought  7.27  4.00    10.13     9.23     8.47
*****
*****

```

3. Wilting Score
Shapiro-Wilk normality test

```

data: resWS
W = 0.99198, p-value = 0.3041

```

```

summary(anovaWS)

```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
treatment	1	477.9	477.9	2683.797	< 2e-16	***
genotype	4	122.9	30.7	172.549	< 2e-16	***
year	1	0.1	0.1	0.782	0.37767	
treatment:genotype	4	114.0	28.5	160.014	< 2e-16	***
treatment:year	1	8.8	8.8	49.388	3.66e-11	***
genotype:year	4	2.3	0.6	3.171	0.01499	*
treatment:genotype:year	4	2.5	0.6	3.565	0.00788	**
Residuals	190	33.8	0.2			

```

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

```

```

> print(model.tables(anovaWS,"means"),digits=3)
Tables of means
Grand mean

```

1.705714

```

treatment
treatment
control drought
  0.20    3.21

```

```

genotype
genotype
  Barke  HOR10151  S42IL-141  S42IL-143  Scarlett
  2.214    2.883    1.050    0.790    1.590

```

```

year
year
2018 2019
1.665 1.722

```

```

treatment:genotype
genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
  control 0.24  0.22    0.20    0.13    0.20
  drought 4.19  5.55    1.90    1.45    2.98

```

```

treatment:year
  year
treatment 2018 2019
  control 0.48 0.08
  drought 2.85 3.36

```

```

genotype:year
  year
genotype 2018 2019
  Barke 1.917 2.333
  HOR10151 2.733 2.943
  S42IL-141 1.217 0.983
  S42IL-143 0.808 0.783
  Scarlett 1.650 1.567

```

```

treatment:genotype:year
, , year = 2018

```

```

      genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
  control 0.50 0.55 0.52 0.45 0.38
  drought 3.33 4.92 1.92 1.17 2.92

```

```

, , year = 2019

```

```

      genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
  control 0.13 0.09 0.07 0.00 0.13
  drought 4.53 5.80 1.90 1.57 3.00

```

```

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```

4. Grain weight/plant

Shapiro-Wilk normality test

```

data: resGrain_DW
W = 0.98853, p-value = 0.09076

```

```
summary(anovaGrain_DW)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
treatment	1	4751	4751	2205.606	< 2e-16 ***
genotype	4	415	104	48.179	< 2e-16 ***
year	1	1	1	0.418	0.51891
treatment:genotype	4	266	67	30.885	< 2e-16 ***
treatment:year	1	15	15	6.979	0.00894 **
genotype:year	4	12	3	1.430	0.22563
treatment:genotype:year	4	18	5	2.120	0.07984 .
Residuals	190	409	2		

```
---
```

```

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

```

```
> print(model.tables(anovaGrain_DW,"means"),digits=3)
```

```
Tables of means
```

```
Grand mean
```

```
8.135014
```

```
treatment
```

```
treatment
```

```
control drought
```

```
12.89 3.38
```

```
genotype
```

```
genotype
```

```
Barke HOR10151 S42IL-141 S42IL-143 Scarlett
```

```
7.32 6.00 8.99 10.11 8.26
```

```
year
```

```
year
```

```
2018 2019
```

```
8.24 8.09
```

```
treatment:genotype
```

```
genotype
```

```
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
```

```
control 13.91 10.40 12.95 13.53 13.67
```

```
drought 0.73 1.59 5.03 6.69 2.85
```

```
treatment:year
```

```
year
```

```
treatment 2018 2019
```

```
control 12.57 13.02
```

```
drought 3.90 3.17
```

```
genotype:year
```

```
year
```

```
genotype 2018 2019
```

```
Barke 7.54 7.23
```

```
HOR10151 6.32 5.87
```

```
S42IL-141 8.33 9.25
```

```
S42IL-143 10.38 10.00
```

```
Scarlett 8.62 8.12
```

```
treatment:genotype:year
```

```
, , year = 2018
```

```
genotype
```

```
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
```

```
control 13.68 9.83 11.33 14.01 14.01
```

```
drought 1.41 2.81 5.33 6.74 3.23
```

```
, , year = 2019
```

```
genotype
```

```
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
```

```

control 14.00 10.63    13.59    13.34    13.54
drought  0.46  1.10     4.90     6.67     2.70
*****
*****

```

5. Plant height
Shapiro-Wilk normality test

```

data: resplant_height
W = 0.99101, p-value = 0.2189
summary(anovaplant_height)

```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
treatment	1	27915	27915	892.913	< 2e-16	***
genotype	4	767	192	6.133	0.000116	***
year	1	640	640	20.476	1.06e-05	***
treatment:genotype	4	239	60	1.909	0.110498	
treatment:year	1	769	769	24.605	1.56e-06	***
genotype:year	4	124	31	0.989	0.414495	
treatment:genotype:year	4	301	75	2.407	0.050976	.
Residuals	190	5940	31			

```

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

```

```
> print(model.tables(anovaplant_height, "means"), digits=3)
```

Tables of means

Grand mean

81.6361

```

treatment
treatment
control drought
  93.2    70.1

```

```

genotype
genotype
  Barke  HOR10151  S42IL-141  S42IL-143  Scarlett
  84.0    81.9    80.0    83.3    79.0

```

```

year
year
2018 2019
84.4 80.5

```

```

treatment:genotype
  genotype
treatment Barke  HOR10151  S42IL-141  S42IL-143  Scarlett
  control  94.7   94.9    90.1    94.6    91.5
  drought  73.3   68.9    69.8    72.1    66.5

```

```

treatment:year
  year
treatment 2018 2019
  control  92.9 93.3

```

```

drought 75.9 67.8

genotype:year
  year
genotype 2018 2019
  Barke 84.6 83.8
  HOR10151 84.7 80.8
  S42IL-141 83.3 78.6
  S42IL-143 86.2 82.2
  Scarlett 83.3 77.3

treatment:genotype:year
, , year = 2018

      genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
  control 92.3 96.5 88.0 96.7 91.0
  drought 76.8 72.8 78.6 75.7 75.5

, , year = 2019

      genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
  control 95.7 94.3 91.0 93.7 91.7
  drought 71.9 67.4 66.2 70.6 62.9
*****
*****
6. Grain number per main spike
Shapiro-Wilk normality test

data: resgrainnumber_mainspike
W = 0.98342, p-value = 0.51436

summary(anovagrainnumber_mainspike)
      Df Sum Sq Mean Sq F value Pr(>F)
treatment 1 11470 11470 432.871 < 2e-16 ***
genotype 4 3316 829 31.282 < 2e-16 ***
year 1 122 122 4.601 0.0332 *
treatment:genotype 4 5208 1302 49.134 < 2e-16 ***
treatment:year 1 1186 1186 44.750 2.44e-10 ***
genotype:year 4 159 40 1.498 0.2045
treatment:genotype:year 4 1073 268 10.125 1.89e-07 ***
Residuals 190 5035 26
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
' ' 1
> print(model.tables(anovagrainnumber_mainspike,"means"),digits=3)
Tables of means
Grand mean

20.42857

treatment
treatment

```


control drought
27.82 13.04

genotype
genotype

Barke	HOR10151	S42IL-141	S42IL-143	Scarlett
13.10	23.24	23.79	22.64	19.38

year
year
2018 2019
21.63 19.95

treatment:genotype
genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
control 22.7 38.7 25.0 26.0 26.7
drought 3.5 7.8 22.6 19.3 12.0

treatment:year
year
treatment 2018 2019
control 25.27 28.84
drought 18.00 11.05

genotype:year
year
genotype 2018 2019
Barke 13.42 12.97
HOR10151 22.33 23.60
S42IL-141 25.08 23.27
S42IL-143 25.25 21.60
Scarlett 22.08 18.30

treatment:genotype:year
, , year = 2018

genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
control 20.5 27.3 26.5 26.3 25.7
drought 6.3 17.3 23.7 24.2 18.5

, , year = 2019

genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
control 23.6 43.2 24.4 25.9 27.1
drought 2.3 4.0 22.1 17.3 9.5

7. Tiller number
Shapiro-Wilk normality test

```
data: restiller_number
W = 0.98711, p-value = 0.05402
```

```
summary(anovatiller_number)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
treatment	1	3497	3497	1200.472	< 2e-16	***
genotype	4	195	49	16.732	9.13e-12	***
year	1	19	19	6.408	0.01217	*
treatment:genotype	4	104	26	8.894	1.33e-06	***
treatment:year	1	450	450	154.427	< 2e-16	***
genotype:year	4	56	14	4.809	0.00102	**
treatment:genotype:year	4	74	19	6.354	8.07e-05	***
Residuals	190	554	3			

```
---
```

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

```
> print(model.tables(anovatiller_number, "means"), digits=3)
```

```
Tables of means
```

```
Grand mean
```

```
16.20476
```

```
treatment
```

```
treatment
```

```
control drought
```

```
20.29 12.12
```

```
genotype
```

```
genotype
```

```
Barke HOR10151 S42IL-141 S42IL-143 Scarlett
```

```
16.14 14.88 16.64 17.74 15.62
```

```
year
```

```
year
```

```
2018 2019
```

```
15.73 16.39
```

```
treatment:genotype
```

```
genotype
```

```
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
```

```
control 20.95 19.48 20.05 20.81 20.14
```

```
drought 11.33 10.29 13.24 14.67 11.10
```

```
treatment:year
```

```
year
```

```
treatment 2018 2019
```

```
control 17.50 21.40
```

```
drought 13.97 11.39
```

```
genotype:year
```

```
year
```

```
genotype 2018 2019
```

```
Barke 16.67 15.93
```

```
HOR10151 15.08 14.80
```

```
S42IL-141 15.92 16.93
S42IL-143 15.92 18.47
Scarlett 15.08 15.83
```

```
treatment:genotype:year
, , year = 2018
```

```
      genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
control 18.83 16.17 17.17 18.33 17.00
drought 14.50 14.00 14.67 13.50 13.17
```

```
, , year = 2019
```

```
      genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
control 21.80 20.80 21.20 21.80 21.40
drought 10.07 8.80 12.67 15.13 10.27
```

```
*****
*****
```

8. Fresh weight
Shapiro-Wilk normality test

```
data: resfreshwght
W = 0.98965, p-value = 0.7246
```

```
summary(anovafreshwght)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
treatment	1	11970	11970	118.466	< 2e-16 ***
genotype	4	17116	4279	42.350	< 2e-16 ***
year	1	26198	26198	259.282	< 2e-16 ***
treatment:genotype	4	8053	2013	19.925	1.03e-13 ***
treatment:year	1	104	104	1.032	0.31094
genotype:year	4	3460	865	8.561	2.26e-06 ***
treatment:genotype:year	4	1482	371	3.667	0.00667 **
Residuals	190	19197	101		

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

```
> print(model.tables(anovafreshwght,"means"),digits=3)
```

```
Tables of means
Grand mean
```

```
34.91013
```

```
treatment
treatment
control drought
42.5 27.4
```

```
genotype
genotype
Barke HOR10151 S42IL-141 S42IL-143 Scarlett
```

48.5 21.5 39.5 30.3 34.8

year
year
2018 2019
52.6 27.8

treatment:genotype
genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
control 64.8 25.0 53.3 31.7 37.5
drought 32.3 17.9 25.7 28.9 32.0

treatment:year
year
treatment 2018 2019
control 59.0 35.8
drought 46.1 19.9

genotype:year
year
genotype 2018 2019
Barke 69.6 40.1
HOR10151 29.3 18.3
S42IL-141 52.4 34.3
S42IL-143 51.0 22.0
Scarlett 60.6 24.5

treatment:genotype:year
, , year = 2018

genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
control 80.1 28.6 62.8 56.8 66.8
drought 59.1 30.0 42.0 45.2 54.3

, , year = 2019

genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
control 58.7 23.6 49.5 21.7 25.8
drought 21.5 13.1 19.2 22.4 23.1

9. SPike Number
Shapiro-Wilk normality test

data: resspikenumber
W = 0.98547, p-value = 0.5103

summary(anovaspikenumber)
Df Sum Sq Mean Sq F value Pr(>F)

```

treatment          1   4781   4781 2133.861 < 2e-16 ***
genotype           4    146    37   16.296 1.71e-11 ***
year               1   2228   2228 994.360 < 2e-16 ***
treatment:genotype 4    154    39   17.187 4.76e-12 ***
treatment:year     1     29    29   12.967 0.000405 ***
genotype:year      4    136    34   15.154 9.03e-11 ***
treatment:genotype:year 4     29     7    3.254 0.013084 *
Residuals         190   426     2

```

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

```
> print(model.tables(anovaspikenummer, "means"), digits=3)
```

Tables of means

Grand mean

19.33333

```

treatment
treatment
control drought
  24.10  14.56

```

```

genotype
genotype
  Barke  HOR10151  S42IL-141  S42IL-143  Scarlett
  18.86   18.64   19.38   20.93   18.86

```

```

year
year
2018 2019
14.18 21.39

```

```

treatment:genotype
  genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
control 24.52 24.24 23.52 24.38 23.86
drought 13.19 13.05 15.24 17.48 13.86

```

```

treatment:year
  year
treatment 2018 2019
control 18.37 26.40
drought 10.00 16.39

```

```

genotype:year
  year
genotype 2018 2019
Barke 13.67 20.93
HOR10151 15.75 19.80
S42IL-141 13.00 21.93
S42IL-143 14.58 23.47
Scarlett 13.92 20.83

```

```
treatment:genotype:year
```

, , year = 2018

	genotype				
treatment	Barke	HOR10151	S42IL-141	S42IL-143	Scarlett
control	18.83	20.33	16.83	18.33	17.50
drought	8.50	11.17	9.17	10.83	10.33

, , year = 2019

	genotype				
treatment	Barke	HOR10151	S42IL-141	S42IL-143	Scarlett
control	26.80	25.80	26.20	26.80	26.40
drought	15.07	13.80	17.67	20.13	15.27

```
*****
*****
Gas exchange, 15 days after stress
*****
*****
```

10. Transpiration rate (E)

Shapiro-Wilk normality test

data: resE
W = 0.98116, p-value = 0.7441

summary(anovaE)

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
treatment	1	0.0003816	0.0003816	1892.22	< 2e-16	***
genotype	4	0.0000348	0.0000087	43.09	< 2e-16	***
year	1	0.0004534	0.0004534	2248.09	< 2e-16	***
treatment:genotype	4	0.0000319	0.0000080	39.51	< 2e-16	***
treatment:year	1	0.0001519	0.0001519	753.33	< 2e-16	***
genotype:year	4	0.0000139	0.0000035	17.23	4.48e-12	***
treatment:genotype:year	4	0.0000127	0.0000032	15.74	3.85e-11	***
Residuals	190	0.0000383	0.0000002			

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

> print(model.tables(anovaE,"means"),digits=3)

Tables of means

Grand mean

0.002329967

treatment	
treatment	
control	drought
0.00368	0.00098

genotype					
genotype	Barke	HOR10151	S42IL-141	S42IL-143	Scarlett
	0.001974	0.001956	0.003039	0.002510	0.002170

```

year
year
  2018    2019
0.00001 0.00326

```

```

treatment:genotype
  genotype
treatment Barke    HOR10151 S42IL-141 S42IL-143 Scarlett
  control  0.00351 0.00354  0.00470   0.00310   0.00354
  drought  0.00044 0.00037  0.00138   0.00192   0.00080

```

```

treatment:year
  year
treatment 2018    2019
  control  0.00001 0.00515
  drought  0.00000 0.00137

```

```

genotype:year
  year
genotype  2018    2019
  Barke    0.00001 0.00276
  HOR10151 0.00001 0.00274
  S42IL-141 0.00001 0.00425
  S42IL-143 0.00001 0.00351
  Scarlett  0.00001 0.00303

```

```

treatment:genotype:year
, , year = 2018
      genotype
treatment Barke    HOR10151 S42IL-141 S42IL-143 Scarlett
  control  0.00001 0.00001  0.00001   0.00001   0.00001
  drought  0.00000 0.00000  0.00000   0.00001   0.00000

```

```

, , year = 2019
      genotype
treatment Barke    HOR10151 S42IL-141 S42IL-143 Scarlett
  control  0.00491 0.00496  0.00658   0.00434   0.00495
  drought  0.00062 0.00052  0.00193   0.00268   0.00112

```

```

*****
*****
*****

```

11. Net Co2 Assimilation rate (A)
Shapiro-Wilk normality test

```

data: resA
W = 0.97315, p-value = 0.7177

```

```

summary(anovaA)
              Df Sum Sq Mean Sq F value    Pr(>F)
treatment    1  10794   10794  5160.57 < 2e-16 ***

```

```

genotype          4      813      203   97.13 < 2e-16 ***
year              1     2341     2341 1118.99 < 2e-16 ***
treatment:genotype 4      797      199   95.23 < 2e-16 ***
treatment:year     1       39       39   18.62 2.57e-05 ***
genotype:year      4      185       46   22.15 5.05e-15 ***
treatment:genotype:year 4      54       13    6.44 7.01e-05 ***
Residuals         190     397       2

```

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

```
> print(model.tables(anovaA,"means"),digits=3)
```

Tables of means

Grand mean

15.69796

treatment

treatment

control drought

22.87 8.53

genotype

genotype

	Barke	HOR10151	S42IL-141	S42IL-143	Scarlett
	15.33	13.63	16.83	18.88	13.82

year

year

2018 2019

20.98 13.59

treatment:genotype

genotype

treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett

control 24.82 22.34 22.68 23.01 21.49

drought 5.85 4.92 10.97 14.75 6.15

treatment:year

year

treatment 2018 2019

control 28.83 20.48

drought 13.13 6.69

genotype:year

year

genotype 2018 2019

Barke 22.47 12.48

HOR10151 18.69 11.61

S42IL-141 19.70 15.68

S42IL-143 25.40 16.27

Scarlett 18.62 11.89

treatment:genotype:year

, , year = 2018


```

          genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
  control 32.3  27.8      27.6      30.5      26.0
  drought 12.7   9.6      11.8      20.3      11.3

```

, , year = 2019

```

          genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
  control 21.8  20.2      20.7      20.0      19.7
  drought  3.1   3.1      10.6      12.5      4.1

```

```

*****
*****
*****

```

12. Intracellular Co2 (Ci)

Shapiro-Wilk normality test

data: resCi

W = 0.98927, p-value = 0.81943

summary(anovaCi)

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
treatment	1	75826	75826	374.96	< 2e-16 ***
genotype	4	20391	5098	25.21	< 2e-16 ***
year	1	3694	3694	18.27	3.03e-05 ***
treatment:genotype	4	32764	8191	40.50	< 2e-16 ***
treatment:year	1	45051	45051	222.77	< 2e-16 ***
genotype:year	4	24991	6248	30.89	< 2e-16 ***
treatment:genotype:year	4	26930	6733	33.29	< 2e-16 ***
Residuals	190	38423	202		

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

> print(model.tables(anovaCi, "means"), digits=3)

Tables of means

Grand mean

225.3296

```

treatment
treatment
control drought
  244.3  206.3

```

```

genotype
genotype
  Barke  HOR10151  S42IL-141  S42IL-143  Scarlett
  221.1    217.9    238.0    213.6    236.0

```

year

year

2018 2019
218.7 228.0

```
treatment:genotype
  genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
  control 242.0 244.6 275.2 217.3 242.7
  drought 200.2 191.2 200.9 210.0 229.4
```

```
treatment:year
  year
treatment 2018 2019
  control 260.9 237.7
  drought 176.5 218.2
```

```
genotype:year
  year
genotype 2018 2019
  Barke 214.9 223.6
  HOR10151 232.0 212.2
  S42IL-141 229.8 241.3
  S42IL-143 217.9 211.9
  Scarlett 198.8 250.9
```

```
treatment:genotype:year
, , year = 2018
```

```
  genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
  control 253.2 278.6 266.1 246.5 259.9
  drought 176.6 185.5 193.6 189.3 137.7
```

```
, , year = 2019
```

```
  genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
  control 237.5 231.0 278.8 205.6 235.8
  drought 209.7 193.5 203.8 218.2 266.0
```

```
*****
*****
*****
```

13.Stomatal Conductance (gsw)
Shapiro-Wilk normality test

data: resgsw
W = 0.98666, p-value = 0.06565

```
summary(anovagsw)
              Df Sum Sq Mean Sq F value Pr(>F)
treatment    1  2.6433   2.6433 2602.609 < 2e-16 ***
genotype      4  0.1293   0.0323   31.821 < 2e-16 ***
year          1  0.5011   0.5011  493.387 < 2e-16 ***
treatment:genotype 4  0.2125   0.0531   52.310 < 2e-16 ***
```

```

treatment:year          1 0.1705  0.1705  167.865 < 2e-16 ***
genotype:year           4 0.0666  0.0166   16.387 1.5e-11 ***
treatment:genotype:year 4 0.0243  0.0061    5.982 0.000148 ***
Residuals               190 0.1930  0.0010
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
' ' 1
> print(model.tables(anovagsw,"means"),digits=3)
Tables of means
Grand mean

0.1922355

treatment
treatment
control drought
 0.3044  0.0800

genotype
genotype
  Barke  HOR10151  S42IL-141  S42IL-143  Scarlett
 0.1867   0.1701   0.2373   0.1972   0.1699

year
year
 2018  2019
0.2695 0.1613

treatment:genotype
genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
control 0.323 0.300 0.376 0.251 0.272
drought 0.050 0.040 0.099 0.143 0.068

treatment:year
year
treatment 2018 2019
control 0.427 0.256
drought 0.112 0.067

genotype:year
year
genotype 2018 2019
Barke 0.2781 0.1501
HOR10151 0.2798 0.1262
S42IL-141 0.2643 0.2265
S42IL-143 0.2856 0.1619
Scarlett 0.2395 0.1421

treatment:genotype:year
, , year = 2018

genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett

```

```

control 0.451 0.482    0.426    0.395    0.380
drought 0.105 0.078    0.103    0.177    0.099

```

```
, , year = 2019
```

```

          genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
  control 0.271 0.227    0.356    0.194    0.229
  drought 0.029 0.025    0.097    0.130    0.055

```

```

*****
*****
*****

```

14. Vapour pressure deficit of the leaf (VPDleaf)
Shapiro-Wilk normality test

```

data: resVPDleaf
W = 0.97926, p-value = 0.5789

```

```
summary(anovaVPDleaf)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
treatment	1	2.361	2.361	296.297	< 2e-16	***
genotype	4	0.331	0.083	10.399	1.23e-07	***
year	1	20.048	20.048	2516.302	< 2e-16	***
treatment:genotype	4	1.380	0.345	43.293	< 2e-16	***
treatment:year	1	8.627	8.627	1082.828	< 2e-16	***
genotype:year	4	2.450	0.613	76.890	< 2e-16	***
treatment:genotype:year	4	0.277	0.069	8.684	1.85e-06	***
Residuals	190	1.514	0.008			

```
---
```

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

```
> print(model.tables(anovaVPDleaf, "means"), digits=3)
```

```
Tables of means
Grand mean
```

```
2.273983
```

```

treatment
treatment
control drought
  2.168    2.380

```

```

genotype
genotype
  Barke  HOR10151 S42IL-141 S42IL-143  Scarlett
  2.279    2.226    2.231    2.315    2.319

```

```

year
year
2018 2019
2.763 2.079

```

```
treatment:genotype
```

```

      genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
  control 2.051 2.223      2.063      2.252      2.251
  drought 2.508 2.228      2.399      2.378      2.386

```

```

treatment:year
  year
treatment 2018 2019
  control 2.34 2.10
  drought 3.19 2.06

```

```

genotype:year
  year
genotype 2018 2019
  Barke    2.967 2.004
  HOR10151 2.487 2.121
  S42IL-141 2.883 1.970
  S42IL-143 2.639 2.185
  Scarlett 2.836 2.112

```

```

treatment:genotype:year
, , year = 2018

```

```

      genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
  control 2.48 2.23      2.37      2.21      2.38
  drought 3.45 2.74      3.40      3.06      3.29

```

```

, , year = 2019

```

```

      genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
  control 1.88 2.22      1.94      2.27      2.20
  drought 2.13 2.02      2.00      2.10      2.02

```

```

*****
*****
*****

```

15. Electron transport rate (ETR)

Shapiro-Wilk normality test

```

data: resETR
W = 0.99375, p-value = 0.6416

```

```

summary(anovaETR)

```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
treatment	1	15474	15474	79.17	4.48e-16	***
genotype	4	72095	18024	92.21	< 2e-16	***
year	1	17597	17597	90.03	< 2e-16	***
treatment:genotype	4	10735	2684	13.73	7.45e-10	***
treatment:year	1	45914	45914	234.91	< 2e-16	***
genotype:year	4	14212	3553	18.18	1.17e-12	***
treatment:genotype:year	4	16105	4026	20.60	4.08e-14	***

```

Residuals          190  37137    195
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
' ' 1
> print(model.tables(anovaETR,"means"),digits=3)
Tables of means
Grand mean

116.2573

treatment
treatment
control drought
  124.8  107.7

genotype
genotype
  Barke  HOR10151  S42IL-141  S42IL-143  Scarlett
    99.4    100.5    114.4    150.6    116.4

year
year
2018  2019
130.7 110.5

treatment:genotype
  genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
control 107.8 121.2 119.8 149.4 126.0
drought 90.9 79.7 109.0 151.8 106.9

treatment:year
  year
treatment 2018 2019
control 162.7 109.7
drought 98.8 111.2

genotype:year
  year
genotype 2018 2019
Barke 138.8 83.6
HOR10151 114.8 94.8
S42IL-141 118.7 112.7
S42IL-143 160.2 146.7
Scarlett 121.2 114.6

treatment:genotype:year
, , year = 2018

  genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
control 190.3 154.5 147.6 189.3 131.7
drought 87.3 75.0 89.9 131.1 110.7

```

```
, , year = 2019
```

```

      genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
  control  74.8 107.9    108.7    133.4    123.7
  drought  92.4  81.6    116.7    160.1    105.4
*****
*****
*****

```

16. Intrinsic water use efficiency (iWUE)

Shapiro-Wilk normality test

```

data: resiWUE
W = 0.98835, p-value = 0.06955

```

```
summary(anovaiWUE)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
treatment	1	41755	41755	404.786	< 2e-16 ***
genotype	4	10817	2704	26.215	< 2e-16 ***
year	1	34	34	0.333	0.564
treatment:genotype	4	17540	4385	42.508	< 2e-16 ***
treatment:year	1	10108	10108	97.987	< 2e-16 ***
genotype:year	4	3953	988	9.581	4.45e-07 ***
treatment:genotype:year	4	4714	1179	11.425	2.49e-08 ***
Residuals	190	19599	103		

```

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

```

```
> print(model.tables(anovaiWUE,"means"),digits=3)
```

```

Tables of means
Grand mean

```

94.01245

```

  treatment
treatment
control drought
  79.9    108.1

```

```

  genotype
genotype
  Barke  HOR10151  S42IL-141  S42IL-143  Scarlett
  97.0    101.0    86.5    101.1    84.4

```

```

  year
year
2018 2019
93.4 94.3

```

```

  treatment:genotype
  genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett

```

control	80.2	80.0	60.8	97.2	81.4
drought	113.9	122.0	112.3	105.1	87.3

```
treatment:year
  year
treatment 2018 2019
  control  68.3 84.6
  drought 118.4 104.0
```

```
genotype:year
  year
genotype 2018 2019
  Barke   96.4 97.3
  HOR10151 90.5 105.2
  S42IL-141 89.8 85.2
  S42IL-143 96.3 103.1
  Scarlett 93.9 80.5
```

```
treatment:genotype:year
, , year = 2018
```

```
  genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
  control  71.4  57.8     65.2     77.5     69.6
  drought 121.4 123.1    114.3    115.1    118.3
```

```
, , year = 2019
```

```
  genotype
treatment Barke HOR10151 S42IL-141 S42IL-143 Scarlett
  control  83.7  88.9     59.0     105.0    86.1
  drought 110.9 121.5    111.5    101.1    74.9
```