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Anova Table (Type III tests)

Response: CCRT

	Sum Sq	Df	F value	Pr(>F)
(Intercept)	632510037	1	2451.1167	< 2.2e-16 ***
Genotype	2655087	1	10.2891	0.001596 **
Treatment	95128239	3	122.8810	< 2.2e-16 ***
Sex	2036796	1	7.8930	0.005537 **
Genotype:Treatment	681154	3	0.8799	0.452748
Treatment:Sex	1774903	3	2.2927	0.079824 .
Genotype:Sex	85239	1	0.3303	0.566223
Genotype:Treatment:Sex	934548	3	1.2072	0.308729
Residuals	44384557	172		

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Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
> summary(model)

Call:

```
lm(formula = CCRT ~ Genotype + Treatment + Sex + Treatment *  
    Genotype + Treatment * Sex + Genotype * Sex + Genotype *  
    Sex * Treatment, data = my_MFdata)
```

Residuals:

Min	1Q	Median	3Q	Max
-1231.50	-283.81	-89.67	197.59	2497.50

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	1835.54	37.07	49.509	< 2e-16 ***
Genotype1	-118.92	37.07	-3.208	0.00160 **
Treatment1	-877.71	64.22	-13.668	< 2e-16 ***
Treatment2	-434.31	63.74	-6.814	1.53e-10 ***
Treatment3	335.51	64.69	5.186	5.97e-07 ***
Sex1	-104.16	37.07	-2.809	0.00554 **
Genotype1:Treatment1	14.55	64.22	0.227	0.82106
Genotype1:Treatment2	-69.14	63.74	-1.085	0.27956
Genotype1:Treatment3	90.96	64.69	1.406	0.16151
Treatment1:Sex1	86.29	64.22	1.344	0.18081
Treatment2:Sex1	107.43	63.74	1.686	0.09370 .
Treatment3:Sex1	-100.79	64.69	-1.558	0.12104
Genotype1:Sex1	-21.31	37.07	-0.575	0.56622
Genotype1:Treatment1:Sex1	80.73	64.22	1.257	0.21042
Genotype1:Treatment2:Sex1	18.54	63.74	0.291	0.77153
Genotype1:Treatment3:Sex1	14.09	64.69	0.218	0.82781

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

Residual standard error: 508 on 172 degrees of freedom

Multiple R-squared: 0.6995, Adjusted R-squared: 0.6733

F-statistic: 26.7 on 15 and 172 DF, p-value: < 2.2e-16

## ANOVA on Ranked Chill Coma Recovery Time data

Anova Table (Type III tests)

Response: CCRT\_rk

	Sum Sq	Df	F value	Pr(>F)
(Intercept)	1680767	1	2319.8063	< 2.2e-16 ***
Genotype	14832	1	20.4711	1.125e-05 ***
Treatment	398980	3	183.5581	< 2.2e-16 ***
Sex	5589	1	7.7138	0.006088 **
Genotype:Treatment	4208	3	1.9360	0.125590
Treatment:Sex	3212	3	1.4778	0.222319
Genotype:Sex	3	1	0.0043	0.947711
Genotype:Treatment:Sex	2355	3	1.0834	0.357621
Residuals	124619	172		

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Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
> summary(model)

Call:

```
lm(formula = CCRT_rk ~ Genotype + Treatment + Sex + Treatment *  
    Genotype + Treatment * Sex + Genotype * Sex + Genotype *  
    Sex * Treatment, data = my_MFdata)
```

Residuals:

Min	1Q	Median	3Q	Max
-54.333	-15.917	-3.583	15.330	102.458

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	94.6200	1.9645	48.164	< 2e-16 ***
Genotype1	-8.8885	1.9645	-4.525	1.13e-05 ***
Treatment1	-61.8530	3.4027	-18.178	< 2e-16 ***
Treatment2	-23.6721	3.3774	-7.009	5.23e-11 ***
Treatment3	27.5694	3.4278	8.043	1.36e-13 ***
Sex1	-5.4562	1.9645	-2.777	0.00609 **
Genotype1:Treatment1	-0.6361	3.4027	-0.187	0.85192
Genotype1:Treatment2	-6.4553	3.3774	-1.911	0.05762 .
Genotype1:Treatment3	6.9036	3.4278	2.014	0.04556 *
Treatment1:Sex1	3.0433	3.4027	0.894	0.37236
Treatment2:Sex1	4.9458	3.3774	1.464	0.14491
Treatment3:Sex1	-5.1877	3.4278	-1.513	0.13200
Genotype1:Sex1	0.1290	1.9645	0.066	0.94771
Genotype1:Treatment1:Sex1	5.2081	3.4027	1.531	0.12771
Genotype1:Treatment2:Sex1	-0.6811	3.3774	-0.202	0.84041
Genotype1:Treatment3:Sex1	0.2195	3.4278	0.064	0.94903

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

Residual standard error: 26.92 on 172 degrees of freedom

Multiple R-squared: 0.7749, Adjusted R-squared: 0.7553

F-statistic: 39.48 on 15 and 172 DF, p-value: < 2.2e-16

## ANOVA on Ranked UV Sensitivity data

Anova Table (Type III tests)

Response: `UVSI_rk`

	Sum Sq	Df	F value	Pr(>F)
(Intercept)	3853058	1	1525.2621	< 2.2e-16 ***
Genotype	19963	1	7.9025	0.005357 **
Treatment	519953	3	68.6092	< 2.2e-16 ***
Genotype:Treatment	7592	3	1.0018	0.392778
Residuals	588596	233		

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Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
> summary(model)

Call:

```
lm(formula = UVSI_rk ~ Genotype + Treatment + Genotype * Treatment,  
    data = my_UVdata)
```

Residuals:

Min	1Q	Median	3Q	Max
-101.72	-37.58	-2.70	31.26	148.41

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	134.625	3.447	39.055	< 2e-16 ***
Genotype1	-9.690	3.447	-2.811	0.00536 **
Treatment1	74.479	6.375	11.682	< 2e-16 ***
Treatment2	5.396	6.492	0.831	0.40675
Treatment3	-25.894	5.891	-4.396	1.68e-05 ***
Genotype1:Treatment1	8.218	6.375	1.289	0.19870
Genotype1:Treatment2	2.947	6.492	0.454	0.65034
Genotype1:Treatment3	-5.299	5.891	-0.900	0.36930

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

Residual standard error: 50.26 on 233 degrees of freedom

Multiple R-squared: 0.495, Adjusted R-squared: 0.4798

F-statistic: 32.62 on 7 and 233 DF, p-value: < 2.2e-16

## ANOVA on UV sensitivity data

Anova Table (Type III tests)

Response: **UVSI**

	Sum Sq	Df	F value	Pr(>F)
(Intercept)	70.998	1	4637.6131	< 2.2e-16 ***
Genotype	0.154	1	10.0680	0.001712 **
Treatment	3.792	3	82.5557	< 2.2e-16 ***
Genotype:Treatment	0.026	3	0.5627	0.640120
Residuals	3.567	233		

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Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
> summary(model)

Call:

```
lm(formula = UVSI ~ Genotype + Treatment + Genotype * Treatment,  
    data = my_UVdata)
```

Residuals:

Min	1Q	Median	3Q	Max
-0.24332	-0.09597	-0.01693	0.09076	0.47355

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-0.577891	0.008486	-68.100	< 2e-16 ***
Genotype1	-0.026926	0.008486	-3.173	0.00171 **
Treatment1	0.216133	0.015695	13.771	< 2e-16 ***
Treatment2	-0.009324	0.015983	-0.583	0.56022
Treatment3	-0.074197	0.014501	-5.117	6.5e-07 ***
Genotype1:Treatment1	0.006457	0.015695	0.411	0.68117
Genotype1:Treatment2	0.014258	0.015983	0.892	0.37327
Genotype1:Treatment3	-0.008768	0.014501	-0.605	0.54601

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

Residual standard error: 0.1237 on 233 degrees of freedom

Multiple R-squared: 0.5429, Adjusted R-squared: 0.5292

F-statistic: 39.54 on 7 and 233 DF, p-value: < 2.2e-16