Supplement S4_SPSS_Statistical Output

The full output of the statistical analysis performed in SPSS follows, with title sheets indicating the specific behavioral measure output on subsequent pages.

Weights (Body and Brain)

```
UNIANOVA BODYWEIGHTg BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(0.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 19:43:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June_Aug 2022 stat sex and effect size/SPSS files/SPSS Data Files/Aug 2022 BrainBodyWT.sav
	Active Dataset	DataSet2
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	34
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA
BODYWEIGHTg BY
GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /CRITERIA=ALPHA
(0.05)
  /DESIGN=GENOTYPE
SEX GENOTYPE*SEX.
```

Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	15
	WT	15
SEX	F	14
	M	16

Tests of Between-Subjects Effects

Dependent Variable: BODY WEIGHT (g)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	186.783[a]	3	62.261	36.222	<.001
Intercept	14010.728	1	14010.728	8151.175	<.001
GENOTYPE	3.069	1	3.069	1.785	.193
SEX	181.634	1	181.634	105.671	<.001
GENOTYPE * SEX	1.749	1	1.749	1.017	.322
Error	44.690	26	1.719		
Total	14519.210	30			
Corrected Total	231.474	29			

a. R Squared = .807 (Adjusted R Squared = .785)

```
UNIANOVA BRAINWEIGHTmg BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(0.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 19:43:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June_Aug 2022 stat sex and effect size/SPSS files/SPSS Data Files/Aug 2022 BrainBodyWT.sav
	Active Dataset	DataSet2
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	34
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA
BRAINWEIGHTmg BY
GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /CRITERIA=ALPHA
(0.05)
  /DESIGN=GENOTYPE
SEX GENOTYPE*SEX.
```

Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	17
	WT	17
SEX	F	14
	M	20

Tests of Between-Subjects Effects

Dependent Variable: BRAIN WEIGHT (mg)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	10302.897 [a]	3	3434.299	9.561	<.001
Intercept	6328113.52	1	6328113.52	17617.164	<.001
GENOTYPE	8076.507	1	8076.507	22.485	<.001
SEX	2220.950	1	2220.950	6.183	.019
GENOTYPE * SEX	183.969	1	183.969	.512	.480
Error	10776.048	30	359.202		
Total	6509480.94	34			
Corrected Total	21078.945	33			

a. R Squared = .489 (Adjusted R Squared = .438)

```
UNIANOVA BODYWEIGHTg BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/CRITERIA=ALPHA(0.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 19:44:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June _Aug 2022 stat sex and effect size/SPSS files/SPSS Data Files/Aug 2022 BrainBodyWT.sav
	Active Dataset	DataSet2
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	34
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA BODYWEIGHTg BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES (GENOTYPE) /EMMEANS=TABLES (SEX) /CRITERIA=ALPHA (0.05) /DESIGN=GENOTYPE SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	15
	WT	15
SEX	F	14
	M	16

Tests of Between-Subjects Effects

Dependent Variable: BODY WEIGHT (g)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	185.035 [a]	2	92.517	53.790	<.001
Intercept	14010.728	1	14010.728	8145.956	<.001
GENOTYPE	3.400	1	3.400	1.977	.171
SEX	181.634	1	181.634	105.604	<.001
Error	46.439	27	1.720		
Total	14519.210	30			
Corrected Total	231.474	29			

a. R Squared = .799 (Adjusted R Squared = .785)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: BODY WEIGHT (g)

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	21.996	.339	21.300	22.691
WT	21.322	.339	20.627	22.018

2. SEX

Dependent Variable: BODY WEIGHT (g)

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	19.193	.351	18.474	19.912
M	24.125	.328	23.452	24.798

```
UNIANOVA BRAINWEIGHTmg BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/CRITERIA=ALPHA(0.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 19:49:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June _Aug 2022 stat sex and effect size/SPSS files/SPSS Data Files/Aug 2022 BrainBodyWT.sav
	Active Dataset	DataSet2
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	34
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA BRAINWEIGHTmg BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES (GENOTYPE) /EMMEANS=TABLES (SEX) /CRITERIA=ALPHA (0.05) /DESIGN=GENOTYPE SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	17
	WT	17
SEX	F	14
	M	20

Tests of Between-Subjects Effects

Dependent Variable: BRAIN WEIGHT (mg)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	10118.928 [a]	2	5059.464	14.311	<.001
Intercept	6328113.52	1	6328113.52	17898.833	<.001
GENOTYPE	7897.978	1	7897.978	22.339	<.001
SEX	2220.950	1	2220.950	6.282	.018
Error	10960.017	31	353.549		
Total	6509480.94	34			
Corrected Total	21078.945	33			

a. R Squared = .480 (Adjusted R Squared = .447)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: BRAIN WEIGHT (mg)

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	423.055	4.597	413.680	432.430
WT	453.537	4.597	444.162	462.913

2. SEX

Dependent Variable: BRAIN WEIGHT (mg)

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	446.507	5.025	436.258	456.756
M	430.085	4.204	421.510	438.660

Rotarod

```
UNIANOVA Day1Average BY SEX GENOTYPE
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=SEX GENOTYPE GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		19-AUG-2022 11:51:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 RR sex EF data.sav
	Active Dataset	DataSet1
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	30
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA Day1Average BY SEX GENOTYPE /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=SEX GENOTYPE GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

```
[DataSet1] /Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 st
at sex and effect size/SPSS files/SPSS Data Files/June 2022 RR sex EF data.sav
```

Between-Subjects Factors

		N
SEX	F	14
	M	16
GENOTYPE	KI	15
	WT	15

Tests of Between-Subjects Effects

Dependent Variable: Day 1 Average

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	8916.031 [a]	3	2972.010	.611	.614
Intercept	1055841.44	1	1055841.44	217.186	<.001
SEX	8908.680	1	8908.680	1.833	.187
GENOTYPE	.343	1	.343	.000	.993
SEX * GENOTYPE	6.772	1	6.772	.001	.971
Error	126398.107	26	4861.466		
Total	1208898.03	30			
Corrected Total	135314.138	29			

a. R Squared = .066 (Adjusted R Squared = -.042)

```
UNIANOVA Day2Average BY SEX GENOTYPE
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=SEX GENOTYPE GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		19-AUG-2022 11:52:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 RR sex EF data.sav
	Active Dataset	DataSet1
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	30
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA Day2Average
BY SEX GENOTYPE
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /CRITERIA=ALPHA(.05)
  /DESIGN=SEX
GENOTYPE
GENOTYPE*SEX.
```

Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
SEX	F	14
	M	16
GENOTYPE	KI	15
	WT	15

Tests of Between-Subjects Effects

Dependent Variable: Day 2 Average

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	4820.426[a]	3	1606.809	.534	.663
Intercept	1458875.03	1	1458875.03	485.153	<.001
SEX	2894.938	1	2894.938	.963	.336
GENOTYPE	16.140	1	16.140	.005	.942
SEX * GENOTYPE	1924.288	1	1924.288	.640	.431
Error	78183.115	26	3007.043		
Total	1539700.67	30			
Corrected Total	83003.541	29			

a. R Squared = .058 (Adjusted R Squared = -.051)

```
UNIANOVA Day3Average BY SEX GENOTYPE
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=SEX GENOTYPE GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		19-AUG-2022 11:52:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 RR sex EF data.sav
	Active Dataset	DataSet1
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	30
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA Day3Average BY SEX GENOTYPE /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=SEX GENOTYPE GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
SEX	F	14
	M	16
GENOTYPE	KI	15
	WT	15

Tests of Between-Subjects Effects

Dependent Variable: Day 3 Average

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	25689.412 [a]	3	8563.137	3.549	.028
Intercept	1685785.74	1	1685785.74	698.720	<.001
SEX	22613.564	1	22613.564	9.373	.005
GENOTYPE	627.815	1	627.815	.260	.614
SEX * GENOTYPE	2275.015	1	2275.015	.943	.340
Error	62729.629	26	2412.678		
Total	1755682.33	30			
Corrected Total	88419.041	29			

a. R Squared = .291 (Adjusted R Squared = .209)

```
UNIANOVA Day1Average BY SEX GENOTYPE
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(SEX)
/EMMEANS=TABLES(GENOTYPE)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=SEX GENOTYPE.
```

Univariate Analysis of Variance

Notes

Output Created		19-AUG-2022 11:55:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 RR sex EF data.sav
	Active Dataset	DataSet1
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	30
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA Day1Average BY SEX GENOTYPE /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES (SEX) /EMMEANS=TABLES (GENOTYPE) /PRINT ETASQ /CRITERIA=ALPHA(.05) /DESIGN=SEX GENOTYPE.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
SEX	F	14
	M	16
GENOTYPE	KI	15
	WT	15

Tests of Between-Subjects Effects

Dependent Variable: Day 1 Average

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	8909.258[a]	2	4454.629	.952	.399	.066
Intercept	1055841.44	1	1055841.44	225.527	<.001	.893
SEX	8908.680	1	8908.680	1.903	.179	.066
GENOTYPE	.579	1	.579	.000	.991	.000
Error	126404.880	27	4681.662			
Total	1208898.03	30				
Corrected Total	135314.138	29				

a. R Squared = .066 (Adjusted R Squared = -.003)

Estimated Marginal Means

1. SEX

Dependent Variable: Day 1 Average

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	170.750	18.287	133.229	208.271
M	205.292	17.106	170.194	240.390

2. GENOTYPE

Dependent Variable: Day 1 Average

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	188.160	17.686	151.870	224.449
WT	187.882	17.686	151.593	224.171

```
UNIANOVA Day2Average BY SEX GENOTYPE
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(SEX)
/EMMEANS=TABLES(GENOTYPE)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=SEX GENOTYPE.
```

Univariate Analysis of Variance

Notes

Output Created		19-AUG-2022 11:55:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 RR sex EF data.sav
	Active Dataset	DataSet1
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	30
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA Day2Average BY SEX GENOTYPE
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES(SEX)
  /EMMEANS=TABLES(GENOTYPE)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=SEX GENOTYPE.
```

Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
SEX	F	14
	M	16
GENOTYPE	KI	15
	WT	15

Tests of Between-Subjects Effects

Dependent Variable: Day 2 Average

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	2896.138[a]	2	1448.069	.488	.619	.035
Intercept	1458875.03	1	1458875.03	491.710	<.001	.948
SEX	2894.938	1	2894.938	.976	.332	.035
GENOTYPE	1.200	1	1.200	.000	.984	.000
Error	80107.403	27	2966.941			
Total	1539700.67	30				
Corrected Total	83003.541	29				

a. R Squared = .035 (Adjusted R Squared = -.037)

Estimated Marginal Means

1. SEX

Dependent Variable: Day 2 Average

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	230.857	14.558	200.987	260.727
M	211.167	13.617	183.226	239.107

2. GENOTYPE

Dependent Variable: Day 2 Average

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	221.212	14.080	192.323	250.101
WT	220.812	14.080	191.923	249.701

```
UNIANOVA Day3Average BY SEX GENOTYPE
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(SEX)
/EMMEANS=TABLES(GENOTYPE)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=SEX GENOTYPE.
```

Univariate Analysis of Variance

Notes

Output Created		19-AUG-2022 11:56:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 RR sex EF data.sav
	Active Dataset	DataSet1
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	30
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA Day3Average
BY SEX GENOTYPE
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES
(SEX)
  /EMMEANS=TABLES
(GENOTYPE)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=SEX
GENOTYPE.
```

Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
SEX	F	14
	M	16
GENOTYPE	KI	15
	WT	15

Tests of Between-Subjects Effects

Dependent Variable: Day 3 Average

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	23414.397 [a]	2	11707.198	4.863	.016	.265
Intercept	1685785.74	1	1685785.74	700.199	<.001	.963
SEX	22613.564	1	22613.564	9.393	.005	.258
GENOTYPE	800.833	1	800.833	.333	.569	.012
Error	65004.644	27	2407.579			
Total	1755682.33	30				
Corrected Total	88419.041	29				

a. R Squared = .265 (Adjusted R Squared = .210)

Estimated Marginal Means

1. SEX

Dependent Variable: Day 3 Average

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	265.095	13.114	238.188	292.002
M	210.063	12.267	184.893	235.232

2. GENOTYPE

Dependent Variable: Day 3 Average

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	232.412	12.683	206.388	258.436
WT	242.746	12.683	216.722	268.769

Open Field Analysis

Univariate Analysis of Variance

Notes

Output Created		19-AUG-2022 12:07:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 OFA sex EF data.sav
	Active Dataset	DataSet2
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	57
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		

```
UNIANOVA
TotalAmbulatoryDistanc
e BY GENDER
GENOTYPE
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENDER
GENOTYPE
GENDER*GENOTYPE.
```

Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENDER	F	28
	M	29
GENOTYPE	KI	31
	WT	26

Tests of Between-Subjects Effects

Dependent Variable: Total Ambulatory Distance

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	14973286 [a]	3	4991095.18	3.451	.023
Intercept	998010650	1	998010650	690.018	<.001
GENDER	2997675.76	1	2997675.76	2.073	.156
GENOTYPE	11388810.0	1	11388810.0	7.874	.007
GENDER * GENOTYPE	1210068.15	1	1210068.15	.837	.365
Error	76656825.9	53	1446355.21		
Total	1.094E+9	57			
Corrected Total	91630111.4	56			

a. R Squared = .163 (Adjusted R Squared = .116)

```
UNIANOVA DistanceCenter BY GENDER GENOTYPE
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENDER GENOTYPE GENDER*GENOTYPE.
```

Univariate Analysis of Variance

Notes

Output Created		19-AUG-2022 12:07:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 OFA sex EF data.sav
	Active Dataset	DataSet2
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	57
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA
DistanceCenter BY
GENDER GENOTYPE
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENDER
GENOTYPE
GENDER*GENOTYPE.
```

Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENDER	F	28
	M	29
GENOTYPE	KI	31
	WT	26

Tests of Between-Subjects Effects

Dependent Variable: % Distance Center

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	4028.722[a]	3	1342.907	18.382	<.001
Intercept	166310.545	1	166310.545	2276.514	<.001
GENDER	5.660	1	5.660	.077	.782
GENOTYPE	3881.746	1	3881.746	53.135	<.001
GENDER * GENOTYPE	71.398	1	71.398	.977	.327
Error	3871.911	53	73.055		
Total	171631.297	57			
Corrected Total	7900.633	56			

a. R Squared = .510 (Adjusted R Squared = .482)

```
UNIANOVA TimeCenter BY GENDER GENOTYPE
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENDER GENOTYPE GENDER*GENOTYPE.
```

Univariate Analysis of Variance

Notes

Output Created		19-AUG-2022 12:08:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 OFA sex EF data.sav
	Active Dataset	DataSet2
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	57
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA TimeCenter BY GENDER GENOTYPE /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENDER GENOTYPE GENDER*GENOTYPE.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENDER	F	28
	M	29
GENOTYPE	KI	31
	WT	26

Tests of Between-Subjects Effects

Dependent Variable: % Time Center

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	697.821[a]	3	232.607	2.388	.079
Intercept	133499.524	1	133499.524	1370.325	<.001
GENDER	.849	1	.849	.009	.926
GENOTYPE	669.918	1	669.918	6.876	.011
GENDER * GENOTYPE	15.062	1	15.062	.155	.696
Error	5163.357	53	97.422		
Total	139469.391	57			
Corrected Total	5861.178	56			

a. R Squared = .119 (Adjusted R Squared = .069)

```
UNIANOVA TotalVerticleCountsBY GENDER GENOTYPE
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENDER GENOTYPE GENDER*GENOTYPE.
```

Univariate Analysis of Variance

Notes

Output Created		19-AUG-2022 12:09:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 OFA sex EF data.sav
	Active Dataset	DataSet2
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	57
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA TotalVerticleCounts BY GENDER GENOTYPE /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENDER GENOTYPE GENDER*GENOTYPE.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENDER	F	28
	M	29
GENOTYPE	KI	31
	WT	26

Tests of Between-Subjects Effects

Dependent Variable: Total Verticle Counts

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	154657.52[a]	3	51552.505	5.383	.003
Intercept	4763390.28	1	4763390.28	497.418	<.001
GENDER	62762.270	1	62762.270	6.554	.013
GENOTYPE	65730.435	1	65730.435	6.864	.011
GENDER * GENOTYPE	29136.155	1	29136.155	3.043	.087
Error	507540.625	53	9576.238		
Total	5484942.00	57			
Corrected Total	662198.140	56			

a. R Squared = .234 (Adjusted R Squared = .190)

```
UNIANOVA TotalAmbulatoryDistance BY GENOTYPE GENDER
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(GENDER)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE GENDER.
```

Univariate Analysis of Variance

Notes

Output Created		19-AUG-2022 12:12:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 OFA sex EF data.sav
	Active Dataset	DataSet2
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	57
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA TotalAmbulatoryDistance BY GENOTYPE GENDER
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES(GENOTYPE)
  /EMMEANS=TABLES(GENDER)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE GENDER.
```

Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	31
	WT	26
GENDER	F	28
	M	29

Tests of Between-Subjects Effects

Dependent Variable: Total Ambulatory Distance

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	13763217 [a]	2	6881608.70	4.772	.012	.150
Intercept	1.011E+9	1	1.011E+9	701.450	<.001	.929
GENOTYPE	11370643.6	1	11370643.6	7.885	.007	.127
GENDER	3359032.52	1	3359032.52	2.329	.133	.041
Error	77866894.0	54	1441979.52			
Total	1.094E+9	57				
Corrected Total	91630111.4	56				

a. R Squared = .150 (Adjusted R Squared = .119)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: Total Ambulatory Distance

GENOTYPE	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
KI	3778.961	216.227	3345.451	4212.471
WT	4679.069	235.821	4206.276	5151.861

2. GENDER

Dependent Variable: Total Ambulatory Distance

GENDER	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
F	3985.308	226.935	3530.331	4440.284
M	4472.722	224.693	4022.239	4923.205

```
UNIANOVA DistanceCenter BY GENOTYPE GENDER
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(GENDER)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE GENDER.
```

Univariate Analysis of Variance

Notes

Output Created		19-AUG-2022 12:12:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 OFA sex EF data.sav
	Active Dataset	DataSet2
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	57
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA DistanceCenter BY GENOTYPE GENDER /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES (GENOTYPE) /EMMEANS=TABLES (GENDER) /PRINT ETASQ /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE GENDER.
Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	31
	WT	26
GENDER	F	28
	M	29

Tests of Between-Subjects Effects

Dependent Variable: % Distance Center

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	3957.325[a]	2	1978.662	27.096	<.001	.501
Intercept	166953.057	1	166953.057	2286.269	<.001	.977
GENOTYPE	3884.357	1	3884.357	53.193	<.001	.496
GENDER	9.718	1	9.718	.133	.717	.002
Error	3943.309	54	73.024			
Total	171631.297	57				
Corrected Total	7900.633	56				

a. R Squared = .501 (Adjusted R Squared = .482)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: % Distance Center

GENOTYPE	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
KI	46.014	1.539	42.929	49.099
WT	62.651	1.678	59.286	66.015

2. GENDER

Dependent Variable: % Distance Center

GENDER	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
F	54.747	1.615	51.509	57.985
M	53.918	1.599	50.712	57.124

```
UNIANOVA TimeCenter BY GENOTYPE GENDER
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(GENDER)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE GENDER.
```

Univariate Analysis of Variance

Notes

Output Created		19-AUG-2022 12:13:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 OFA sex EF data.sav
	Active Dataset	DataSet2
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	57
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA TimeCenter BY GENOTYPE GENDER /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES (GENOTYPE) /EMMEANS=TABLES (GENDER) /PRINT ETASQ /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE GENDER.
Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	31
	WT	26
GENDER	F	28
	M	29

Tests of Between-Subjects Effects

Dependent Variable: % Time Center

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	682.759 [a]	2	341.380	3.560	.035	.116
Intercept	134248.538	1	134248.538	1399.929	<.001	.963
GENOTYPE	670.416	1	670.416	6.991	.011	.115
GENDER	1.587	1	1.587	.017	.898	.000
Error	5178.419	54	95.897			
Total	139469.391	57				
Corrected Total	5861.178	56				

a. R Squared = .116 (Adjusted R Squared = .084)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: % Time Center

GENOTYPE	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
KI	45.265	1.763	41.730	48.800
WT	52.177	1.923	48.321	56.032

2. GENDER

Dependent Variable: % Time Center

GENDER	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
F	48.888	1.851	45.178	52.599
M	48.553	1.832	44.880	52.227

```
UNIANOVA TotalVerticleCountsBY GENOTYPE GENDER
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(GENDER)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE GENDER.
```

Univariate Analysis of Variance

Notes

Output Created		19-AUG-2022 12:13:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 OFA sex EF data.sav
	Active Dataset	DataSet2
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	57
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA
TotalVerticleCounts BY
GENOTYPE GENDER
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES
(GENOTYPE)
  /EMMEANS=TABLES
(GENDER)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE
GENDER.
```

Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	31
	WT	26
GENDER	F	28
	M	29

Tests of Between-Subjects Effects

Dependent Variable: Total Verticle Counts

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	125521.36 [a]	2	62760.680	6.315	.003	.190
Intercept	4863646.57	1	4863646.57	489.376	<.001	.901
GENOTYPE	65515.959	1	65515.959	6.592	.013	.109
GENDER	70856.500	1	70856.500	7.130	.010	.117
Error	536676.780	54	9938.459			
Total	5484942.00	57				
Corrected Total	662198.140	56				

a. R Squared = .190 (Adjusted R Squared = .160)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: Total Verticle Counts

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	259.091	17.951	223.101	295.080
WT	327.415	19.578	288.164	366.666

2. GENDER

Dependent Variable: Total Verticle Counts

GENDER	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	257.857	18.840	220.085	295.629
M	328.649	18.654	291.250	366.047

Elevated Zero Maze

```
UNIANOVA DistanceTotal BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(0.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:39:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 EZM sex EF data.sav
	Active Dataset	DataSet3
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	25
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA DistanceTotal BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(0.05) /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

```
[DataSet3] /Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 st
at sex and effect size/SPSS files/SPSS Data Files/June 2022 EZM sex EF data.sa
v
```

Between-Subjects Factors

		N
GENOTYPE	KI	14
	WT	11
SEX	F	16
	M	9

Tests of Between-Subjects Effects

Dependent Variable: Distance (Total)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	22.276[a]	3	7.425	.252	.859
Intercept	8155.817	1	8155.817	277.014	<.001
GENOTYPE	2.968	1	2.968	.101	.754
SEX	.353	1	.353	.012	.914
GENOTYPE * SEX	12.086	1	12.086	.410	.529
Error	618.279	21	29.442		
Total	10188.816	25			
Corrected Total	640.556	24			

a. R Squared = .035 (Adjusted R Squared = -.103)

```
UNIANOVA TimeOpen BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(0.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:40:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 EZM sex EF data.sav
	Active Dataset	DataSet3
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	25
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA TimeOpen BY GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /CRITERIA=ALPHA(0.05)
  /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	14
	WT	11
SEX	F	16
	M	9

Tests of Between-Subjects Effects

Dependent Variable: % Time Open

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	173.520[a]	3	57.840	.380	.769
Intercept	48738.508	1	48738.508	320.040	<.001
GENOTYPE	101.012	1	101.012	.663	.425
SEX	.477	1	.477	.003	.956
GENOTYPE * SEX	20.439	1	20.439	.134	.718
Error	3198.067	21	152.289		
Total	60730.510	25			
Corrected Total	3371.588	24			

a. R Squared = .051 (Adjusted R Squared = -.084)

```
UNIANOVA DistanceOpen BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(0.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:40:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 EZM sex EF data.sav
	Active Dataset	DataSet3
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	25
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA
DistanceOpen BY
GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /CRITERIA=ALPHA
(0.05)
  /DESIGN=GENOTYPE
SEX GENOTYPE*SEX.
```

Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	14
	WT	11
SEX	F	16
	M	9

Tests of Between-Subjects Effects

Dependent Variable: % Distance Open

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	503.264[a]	3	167.755	3.849	.024
Intercept	41539.772	1	41539.772	953.202	<.001
GENOTYPE	294.039	1	294.039	6.747	.017
SEX	3.118	1	3.118	.072	.792
GENOTYPE * SEX	56.483	1	56.483	1.296	.268
Error	915.163	21	43.579		
Total	50414.320	25			
Corrected Total	1418.427	24			

a. R Squared = .355 (Adjusted R Squared = .263)

```
UNIANOVA DistanceTotal BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:42:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 EZM sex EF data.sav
	Active Dataset	DataSet3
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	25
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA DistanceTotal BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES (GENOTYPE) /PRINT ETASQ /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	14
	WT	11
SEX	F	16
	M	9

Tests of Between-Subjects Effects

Dependent Variable: Distance (Total)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	10.190[a]	2	5.095	.178	.838	.016
Intercept	8433.338	1	8433.338	294.327	<.001	.930
GENOTYPE	9.342	1	9.342	.326	.574	.015
SEX	1.964	1	1.964	.069	.796	.003
Error	630.365	22	28.653			
Total	10188.816	25				
Corrected Total	640.556	24				

a. R Squared = .016 (Adjusted R Squared = -.074)

Estimated Marginal Means

GENOTYPE

Dependent Variable: Distance (Total)

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	20.009	1.440	17.024	22.995
WT	18.761	1.694	15.249	22.274

```
UNIANOVA TimeOpen BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:42:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 EZM sex EF data.sav
	Active Dataset	DataSet3
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	25
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA TimeOpen BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES (GENOTYPE) /PRINT ETASQ /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX.
Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	14
	WT	11
SEX	F	16
	M	9

Tests of Between-Subjects Effects

Dependent Variable: % Time Open

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	153.081[a]	2	76.540	.523	.600	.045
Intercept	50804.801	1	50804.801	347.275	<.001	.940
GENOTYPE	150.272	1	150.272	1.027	.322	.045
SEX	.104	1	.104	.001	.979	.000
Error	3218.507	22	146.296			
Total	60730.510	25				
Corrected Total	3371.588	24				

a. R Squared = .045 (Adjusted R Squared = -.041)

Estimated Marginal Means

GENOTYPE

Dependent Variable: % Time Open

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	50.082	3.253	43.336	56.829
WT	45.078	3.827	37.141	53.015

```
UNIANOVA DistanceOpen BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:43:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 EZM sex EF data.sav
	Active Dataset	DataSet3
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	25
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA
DistanceOpen BY
GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES
(GENOTYPE)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE
SEX.
```

Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	14
	WT	11
SEX	F	16
	M	9

Tests of Between-Subjects Effects

Dependent Variable: % Distance Open

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	446.782[a]	2	223.391	5.058	.016	.315
Intercept	42984.470	1	42984.470	973.254	<.001	.978
GENOTYPE	434.508	1	434.508	9.838	.005	.309
SEX	.010	1	.010	.000	.988	.000
Error	971.646	22	44.166			
Total	50414.320	25				
Corrected Total	1418.427	24				

a. R Squared = .315 (Adjusted R Squared = .253)

Estimated Marginal Means

GENOTYPE

Dependent Variable: % Distance Open

GENOTYPE	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
KI	48.020	1.787	44.313	51.727
WT	39.510	2.103	35.149	43.871

Gait

```
UNIANOVA ForepawStridems BY GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:52:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA ForepawStridems BY GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: ForepawStride (ms)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	3561.621[a]	3	1187.207	1.379	.259
Intercept	4144921.88	1	4144921.88	4815.880	<.001
GENOTYPE	2376.838	1	2376.838	2.762	.103
SEX	1084.747	1	1084.747	1.260	.267
GENOTYPE * SEX	431.261	1	431.261	.501	.482
Error	44755.258	52	860.678		
Total	4244051.19	56			
Corrected Total	48316.879	55			

a. R Squared = .074 (Adjusted R Squared = .020)

```
UNIANOVA ForepawPercofSwingBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:53:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA ForepawPercofSwing BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: ForepawPercofSwing

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	.008[a]	3	.003	2.463	.073
Intercept	14.066	1	14.066	12499.957	<.001
GENOTYPE	.008	1	.008	7.036	.011
SEX	.001	1	.001	.735	.395
GENOTYPE * SEX	6.835E-6	1	6.835E-6	.006	.938
Error	.059	52	.001		
Total	14.412	56			
Corrected Total	.067	55			

a. R Squared = .124 (Adjusted R Squared = .074)

```
UNIANOVA ForepawStrideLenmmBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:53:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA ForepawStrideLenmm BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:01.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: ForepawStrideLen (mm)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	68.917[a]	3	22.972	1.776	.163
Intercept	195002.616	1	195002.616	15072.242	<.001
GENOTYPE	24.871	1	24.871	1.922	.172
SEX	27.970	1	27.970	2.162	.147
GENOTYPE * SEX	13.376	1	13.376	1.034	.314
Error	672.769	52	12.938		
Total	199154.050	56			
Corrected Total	741.686	55			

a. R Squared = .093 (Adjusted R Squared = .041)

```
UNIANOVA ForepawAvPrintAreaBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:53:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA ForepawAvPrintArea BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: ForepawAvPrintArea

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	8712.657[a]	3	2904.219	3.665	.018
Intercept	1131707.78	1	1131707.78	1428.281	<.001
GENOTYPE	5160.165	1	5160.165	6.512	.014
SEX	4448.738	1	4448.738	5.615	.022
GENOTYPE * SEX	3.242	1	3.242	.004	.949
Error	41202.552	52	792.357		
Total	1194257.43	56			
Corrected Total	49915.208	55			

a. R Squared = .175 (Adjusted R Squared = .127)

```
UNIANOVA HindpawStridems BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:54:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA HindpawStridems BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: HindpawStride (ms)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	942.235[a]	3	314.078	.354	.787
Intercept	4435616.86	1	4435616.86	4997.572	<.001
GENOTYPE	21.808	1	21.808	.025	.876
SEX	198.873	1	198.873	.224	.638
GENOTYPE * SEX	644.920	1	644.920	.727	.398
Error	46152.831	52	887.554		
Total	4541914.50	56			
Corrected Total	47095.066	55			

a. R Squared = .020 (Adjusted R Squared = -.037)

```
UNIANOVA HindpawPercofSwingBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:54:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA
HindpawPercofSwing BY
GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE
SEX GENOTYPE*SEX.
```

Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: HindpawPercofSwing

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	.026[a]	3	.009	4.644	.006
Intercept	16.573	1	16.573	8775.500	<.001
GENOTYPE	.022	1	.022	11.629	.001
SEX	.004	1	.004	2.130	.150
GENOTYPE * SEX	.002	1	.002	1.064	.307
Error	.098	52	.002		
Total	17.084	56			
Corrected Total	.125	55			

a. R Squared = .211 (Adjusted R Squared = .166)

```
UNIANOVA HindpawStrideLenmmBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:55:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA
HindpawStrideLenmm
BY GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE
SEX GENOTYPE*SEX.
```

Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: HindpawStrideLen (mm)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	181.084[a]	3	60.361	2.207	.098
Intercept	211971.182	1	211971.182	7749.294	<.001
GENOTYPE	152.475	1	152.475	5.574	.022
SEX	8.348	1	8.348	.305	.583
GENOTYPE * SEX	27.423	1	27.423	1.003	.321
Error	1422.388	52	27.354		
Total	217335.402	56			
Corrected Total	1603.472	55			

a. R Squared = .113 (Adjusted R Squared = .062)

```
UNIANOVA HindpawAvPrintAreaBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:55:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA HindpawAvPrintArea BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: HindpawAvPrintArea

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	11364.791 [a]	3	3788.264	1.402	.253
Intercept	2894901.83	1	2894901.83	1071.487	<.001
GENOTYPE	11332.251	1	11332.251	4.194	.046
SEX	31.538	1	31.538	.012	.914
GENOTYPE * SEX	19.792	1	19.792	.007	.932
Error	140491.555	52	2701.761		
Total	3071417.03	56			
Corrected Total	151856.346	55			

a. R Squared = .075 (Adjusted R Squared = .021)

```
UNIANOVA FrTkWdmm BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:55:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA FrTkWdmm BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: FrTkWd (mm)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	1.272[a]	3	.424	.457	.713
Intercept	7796.063	1	7796.063	8407.829	<.001
GENOTYPE	.041	1	.041	.044	.835
SEX	1.053	1	1.053	1.135	.292
GENOTYPE * SEX	.154	1	.154	.166	.685
Error	48.216	52	.927		
Total	7987.913	56			
Corrected Total	49.488	55			

a. R Squared = .026 (Adjusted R Squared = -.031)

```
UNIANOVA RrTkWdmm BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:56:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA RrTkWdmm BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: RrTkWd (mm)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	14.817[a]	3	4.939	2.935	.042
Intercept	23374.497	1	23374.497	13889.489	<.001
GENOTYPE	7.276	1	7.276	4.323	.043
SEX	7.606	1	7.606	4.519	.038
GENOTYPE * SEX	1.592	1	1.592	.946	.335
Error	87.510	52	1.683		
Total	23797.790	56			
Corrected Total	102.327	55			

a. R Squared = .145 (Adjusted R Squared = .095)

```
UNIANOVA OverallAvgRunSpeedmmsBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:56:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA OverallAvgRunSpeedmms BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: Overall Avg Run Speed (mm/s):

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	581.380[a]	3	193.793	.530	.663
Intercept	1813166.52	1	1813166.52	4962.516	<.001
GENOTYPE	432.628	1	432.628	1.184	.282
SEX	128.013	1	128.013	.350	.556
GENOTYPE * SEX	66.461	1	66.461	.182	.672
Error	18999.367	52	365.372		
Total	1868529.23	56			
Corrected Total	19580.747	55			

a. R Squared = .030 (Adjusted R Squared = -.026)

```
UNIANOVA ForepawHomolatCplBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:56:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA ForepawHomolatCpl BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: ForepawHomolatCpl

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	.006[a]	3	.002	1.612	.198
Intercept	15.735	1	15.735	13353.892	<.001
GENOTYPE	.004	1	.004	3.518	.066
SEX	.002	1	.002	1.502	.226
GENOTYPE * SEX	.000	1	.000	.272	.604
Error	.061	52	.001		
Total	16.106	56			
Corrected Total	.067	55			

a. R Squared = .085 (Adjusted R Squared = .032)

```
UNIANOVA ForepawHomologCplBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:57:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA ForepawHomologCpl BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: ForepawHomologCpl

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	.000[a]	3	8.407E-5	1.088	.362
Intercept	13.500	1	13.500	174730.403	<.001
GENOTYPE	3.616E-5	1	3.616E-5	.468	.497
SEX	.000	1	.000	2.292	.136
GENOTYPE * SEX	1.137E-5	1	1.137E-5	.147	.703
Error	.004	52	7.726E-5		
Total	13.721	56			
Corrected Total	.004	55			

a. R Squared = .059 (Adjusted R Squared = .005)

```
UNIANOVA ForepawDiagonalCplBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:57:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA ForepawDiagonalCpl BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: ForepawDiagonalCpl

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	.002[a]	3	.001	.671	.574
Intercept	.234	1	.234	222.835	<.001
GENOTYPE	.002	1	.002	1.561	.217
SEX	.001	1	.001	.597	.443
GENOTYPE * SEX	4.217E-5	1	4.217E-5	.040	.842
Error	.055	52	.001		
Total	.297	56			
Corrected Total	.057	55			

a. R Squared = .037 (Adjusted R Squared = -.018)

```
UNIANOVA HindpawHomolatCplBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:57:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA HindpawHomolatCpl BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: HindpawHomolatCpl

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	.009[a]	3	.003	2.295	.089
Intercept	10.962	1	10.962	7959.130	<.001
GENOTYPE	.009	1	.009	6.803	.012
SEX	.000	1	.000	.216	.644
GENOTYPE * SEX	3.743E-5	1	3.743E-5	.027	.870
Error	.072	52	.001		
Total	11.181	56			
Corrected Total	.081	55			

a. R Squared = .117 (Adjusted R Squared = .066)

```
UNIANOVA HindpawHomologCplBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:58:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA HindpawHomologCpl BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: HindpawHomologCpl

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	.002[a]	3	.001	1.912	.139
Intercept	13.026	1	13.026	49222.401	<.001
GENOTYPE	.001	1	.001	5.380	.024
SEX	5.734E-5	1	5.734E-5	.217	.644
GENOTYPE * SEX	8.998E-5	1	8.998E-5	.340	.562
Error	.014	52	.000		
Total	13.250	56			
Corrected Total	.015	55			

a. R Squared = .099 (Adjusted R Squared = .047)

```
UNIANOVA HindpawDiagonalCplBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:58:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Syntax:

```
UNIANOVA HindpawDiagonalCpl BY GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: HindpawDiagonalCpl

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	.003[a]	3	.001	.608	.613
Intercept	.031	1	.031	22.781	<.001
GENOTYPE	.001	1	.001	.515	.476
SEX	7.100E-5	1	7.100E-5	.052	.821
GENOTYPE * SEX	.002	1	.002	1.132	.292
Error	.072	52	.001		
Total	.108	56			
Corrected Total	.074	55			

a. R Squared = .034 (Adjusted R Squared = -.022)

```
UNIANOVA ForepawGaitAngle BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:58:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA ForepawGaitAngle BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: ForepawGaitAngle

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	97.727[a]	3	32.576	.986	.407
Intercept	150746.109	1	150746.109	4561.306	<.001
GENOTYPE	5.887	1	5.887	.178	.675
SEX	19.297	1	19.297	.584	.448
GENOTYPE * SEX	78.158	1	78.158	2.365	.130
Error	1718.543	52	33.049		
Total	155853.653	56			
Corrected Total	1816.269	55			

a. R Squared = .054 (Adjusted R Squared = -.001)

```
UNIANOVA HindpawGaitAngle BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:58:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA HindpawGaitAngle BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: HindpawGaitAngle

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	37.753[a]	3	12.584	.296	.828
Intercept	226237.050	1	226237.050	5318.746	<.001
GENOTYPE	15.749	1	15.749	.370	.546
SEX	12.023	1	12.023	.283	.597
GENOTYPE * SEX	13.387	1	13.387	.315	.577
Error	2211.861	52	42.536		
Total	231749.603	56			
Corrected Total	2249.615	55			

a. R Squared = .017 (Adjusted R Squared = -.040)

```
UNIANOVA BdyRotdeg BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:59:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA BdyRotdeg BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: BdyRot(deg)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	70.842[a]	3	23.614	3.726	.017
Intercept	151.435	1	151.435	23.892	<.001
GENOTYPE	67.057	1	67.057	10.580	.002
SEX	.207	1	.207	.033	.857
GENOTYPE * SEX	4.418	1	4.418	.697	.408
Error	329.596	52	6.338		
Total	563.129	56			
Corrected Total	400.438	55			

a. R Squared = .177 (Adjusted R Squared = .129)

```
UNIANOVA LongitdPosmm BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:59:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA LongitdPosmm BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: Longitd Pos(mm)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	491.782[a]	3	163.927	.587	.626
Intercept	438615.947	1	438615.947	1570.882	<.001
GENOTYPE	124.790	1	124.790	.447	.507
SEX	171.791	1	171.791	.615	.436
GENOTYPE * SEX	192.843	1	192.843	.691	.410
Error	14519.253	52	279.216		
Total	460688.138	56			
Corrected Total	15011.036	55			

a. R Squared = .033 (Adjusted R Squared = -.023)

```
UNIANOVA LateralPosmm BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 14:59:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA
LateralPosmm BY
GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE
SEX GENOTYPE*SEX.
```

Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: Lateral Pos(mm)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	1.339[a]	3	.446	.094	.963
Intercept	375670.385	1	375670.385	78882.673	<.001
GENOTYPE	.581	1	.581	.122	.728
SEX	.702	1	.702	.147	.703
GENOTYPE * SEX	.206	1	.206	.043	.836
Error	247.644	52	4.762		
Total	382131.935	56			
Corrected Total	248.983	55			

a. R Squared = .005 (Adjusted R Squared = -.052)

```
UNIANOVA ForepawStridems BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:00:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA ForepawStridems BY GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES(GENOTYPE)
  /EMMEANS=TABLES(SEX)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE SEX.
```

Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: ForepawStride (ms)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	3130.361[a]	2	1565.180	1.836	.169	.065
Intercept	4180790.32	1	4180790.32	4903.717	<.001	.989
GENOTYPE	2421.313	1	2421.313	2.840	.098	.051
SEX	1001.347	1	1001.347	1.174	.283	.022
Error	45186.519	53	852.576			
Total	4244051.19	56				
Corrected Total	48316.879	55				

a. R Squared = .065 (Adjusted R Squared = .029)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: ForepawStride (ms)

			95% Confidence Interval	
GENOTYPE	Mean	Std. Error	Lower Bound	Upper Bound
KI	267.415	5.357	256.671	278.159
WT	280.673	5.734	269.171	292.174

2. SEX

Dependent Variable: ForepawStride (ms)

			95% Confidence Interval	
SEX	Mean	Std. Error	Lower Bound	Upper Bound
F	269.789	5.621	258.514	281.064
M	278.299	5.464	267.338	289.259

```
UNIANOVA ForepawPercofSwingBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:00:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA ForepawPercofSwing BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES (GENOTYPE) /EMMEANS=TABLES (SEX) /PRINT ETASQ /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX.
Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: ForepawPercofSwing

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	.008[a]	2	.004	3.762	.030
Intercept	14.220	1	14.220	12878.060	<.001
GENOTYPE	.008	1	.008	7.183	.010
SEX	.001	1	.001	.743	.393
Error	.059	53	.001		
Total	14.412	56			
Corrected Total	.067	55			

Tests of Between-Subjects Effects

Dependent Variable: ForepawPercofSwing

Source	Partial Eta Squared
Corrected Model	.124
Intercept	.996
GENOTYPE	.119
SEX	.014
Error	
Total	
Corrected Total	

a. R Squared = .124 (Adjusted R Squared = .091)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: ForepawPercofSwing

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	.517	.006	.505	.530
WT	.493	.007	.480	.506

2. SEX

Dependent Variable: ForepawPercofSwing

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	.509	.006	.496	.522
M	.502	.006	.489	.514

```
UNIANOVA ForepawStrideLenmmBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:01:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Notes

Syntax

```
UNIANOVA
ForepawStrideLenmm BY
GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES
(GENOTYPE)
  /EMMEANS=TABLES
(SEX)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE
SEX.
```

Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: ForepawStrideLen (mm)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	55.541[a]	2	27.771	2.145	.127
Intercept	196768.115	1	196768.115	15199.000	<.001
GENOTYPE	24.110	1	24.110	1.862	.178
SEX	25.605	1	25.605	1.978	.165
Error	686.145	53	12.946		
Total	199154.050	56			
Corrected Total	741.686	55			

Tests of Between-Subjects Effects

Dependent Variable: ForepawStrideLen (mm)

Source	Partial Eta Squared
Corrected Model	.075
Intercept	.997
GENOTYPE	.034
SEX	.036
Error	
Total	
Corrected Total	

a. R Squared = .075 (Adjusted R Squared = .040)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: ForepawStrideLen (mm)

GENOTYPE	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
KI	60.114	.660	58.790	61.438
WT	58.791	.707	57.373	60.208

2. SEX

Dependent Variable: ForepawStrideLen (mm)

SEX	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
F	58.772	.693	57.382	60.161
M	60.133	.673	58.782	61.483

```
UNIANOVA ForepawAvPrintAreaBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:01:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		

```
UNIANOVA
ForepawAvPrintArea BY
GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES
(GENOTYPE)
  /EMMEANS=TABLES
(SEX)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE
SEX.
```

Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: ForepawAvPrintArea

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	8709.415 [a]	2	4354.707	5.601	.006	.174
Intercept	1143510.18	1	1143510.18	1470.814	<.001	.965
GENOTYPE	5168.032	1	5168.032	6.647	.013	.111
SEX	4452.105	1	4452.105	5.726	.020	.098
Error	41205.794	53	777.468			
Total	1194257.43	56				
Corrected Total	49915.208	55				

a. R Squared = .174 (Adjusted R Squared = .143)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: ForepawAvPrintArea

GENOTYPE	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
KI	133.637	5.115	123.377	143.896
WT	153.006	5.476	142.023	163.989

2. SEX

Dependent Variable: ForepawAvPrintArea

SEX	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
F	134.350	5.368	123.583	145.116
M	152.293	5.218	141.827	162.759

```
UNIANOVA HindpawStridems BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:01:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA HindpawStridems BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES (GENOTYPE) /EMMEANS=TABLES (SEX) /PRINT ETASQ /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: HindpawStride (ms)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	297.315[a]	2	148.658	.168	.845	.006
Intercept	4472282.35	1	4472282.35	5065.008	<.001	.990
GENOTYPE	27.172	1	27.172	.031	.861	.001
SEX	249.589	1	249.589	.283	.597	.005
Error	46797.750	53	882.976			
Total	4541914.50	56				
Corrected Total	47095.066	55				

a. R Squared = .006 (Adjusted R Squared = -.031)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: HindpawStride (ms)

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	282.734	5.451	271.800	293.668
WT	284.138	5.836	272.434	295.843

2. SEX

Dependent Variable: HindpawStride (ms)

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	285.560	5.721	274.086	297.034
M	281.312	5.561	270.158	292.466

```
UNIANOVA HindpawPercofSwingBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:01:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA HindpawPercofSwing BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES (GENOTYPE) /EMMEANS=TABLES (SEX) /PRINT ETASQ /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX.
Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: HindpawPercofSwing

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	.024[a]	2	.012	6.426	.003	.195
Intercept	16.789	1	16.789	8879.548	<.001	.994
GENOTYPE	.022	1	.022	11.770	.001	.182
SEX	.004	1	.004	1.943	.169	.035
Error	.100	53	.002			
Total	17.084	56				
Corrected Total	.125	55				

a. R Squared = .195 (Adjusted R Squared = .165)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: HindpawPercofSwing

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	.569	.008	.553	.585
WT	.529	.009	.512	.546

2. SEX

Dependent Variable: HindpawPercofSwing

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	.557	.008	.541	.574
M	.541	.008	.525	.557

```
UNIANOVA HindpawStrideLenmmBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:02:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA HindpawStrideLenmm BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES (GENOTYPE) /EMMEANS=TABLES (SEX) /PRINT ETASQ /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX.
Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: HindpawStrideLen (mm)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	153.661[a]	2	76.831	2.809	.069	.096
Intercept	213753.601	1	213753.601	7814.084	<.001	.993
GENOTYPE	149.798	1	149.798	5.476	.023	.094
SEX	10.491	1	10.491	.384	.538	.007
Error	1449.810	53	27.355			
Total	217335.402	56				
Corrected Total	1603.472	55				

a. R Squared = .096 (Adjusted R Squared = .062)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: HindpawStrideLen (mm)

GENOTYPE	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
KI	63.614	.959	61.689	65.538
WT	60.316	1.027	58.256	62.377

2. SEX

Dependent Variable: HindpawStrideLen (mm)

SEX	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
F	62.401	1.007	60.381	64.420
M	61.530	.979	59.566	63.493

```
UNIANOVA HindpawAvPrintAreaBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:02:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA
HindpawAvPrintArea BY
GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES
(GENOTYPE)
  /EMMEANS=TABLES
(SEX)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE
SEX.
```

Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: HindpawAvPrintArea

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	11344.999[a]	2	5672.499	2.140	.128	.075
Intercept	2927695.87	1	2927695.87	1104.309	<.001	.954
GENOTYPE	11317.208	1	11317.208	4.269	.044	.075
SEX	35.044	1	35.044	.013	.909	.000
Error	140511.347	53	2651.157			
Total	3071417.03	56				
Corrected Total	151856.346	55				

a. R Squared = .075 (Adjusted R Squared = .040)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: HindpawAvPrintArea

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	214.995	9.446	196.049	233.941
WT	243.658	10.112	223.376	263.940

2. SEX

Dependent Variable: HindpawAvPrintArea

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	228.530	9.912	208.648	248.412
M	230.122	9.636	210.795	249.449

```
UNIANOVA FrTkWdmm BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:02:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA FrTkWdmm BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES (GENOTYPE) /EMMEANS=TABLES (SEX) /PRINT ETASQ /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX.
Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: FrTkWd (mm)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	1.118[a]	2	.559	.612	.546	.023
Intercept	7887.363	1	7887.363	8642.236	<.001	.994
GENOTYPE	.038	1	.038	.041	.840	.001
SEX	1.111	1	1.111	1.217	.275	.022
Error	48.371	53	.913			
Total	7987.913	56				
Corrected Total	49.488	55				

a. R Squared = .023 (Adjusted R Squared = -.014)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: FrTkWd (mm)

GENOTYPE	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
KI	11.877	.175	11.525	12.228
WT	11.929	.188	11.553	12.305

2. SEX

Dependent Variable: FrTkWd (mm)

SEX	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
F	11.761	.184	11.392	12.130
M	12.045	.179	11.686	12.403

```
UNIANOVA RrTkWdmm BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:02:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA RrTkWdmm BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES (GENOTYPE) /EMMEANS=TABLES (SEX) /PRINT ETASQ /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: RrTkWd (mm)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	13.225[a]	2	6.613	3.933	.026
Intercept	23586.268	1	23586.268	14029.658	<.001
GENOTYPE	7.425	1	7.425	4.417	.040
SEX	7.188	1	7.188	4.275	.044
Error	89.102	53	1.681		
Total	23797.790	56			
Corrected Total	102.327	55			

Tests of Between-Subjects Effects

Dependent Variable: RrTkWd (mm)

Source	Partial Eta Squared
Corrected Model	.129
Intercept	.996
GENOTYPE	.077
SEX	.075
Error	
Total	
Corrected Total	

a. R Squared = .129 (Adjusted R Squared = .096)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: RrTkWd (mm)

GENOTYPE	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
KI	20.216	.238	19.739	20.694
WT	20.951	.255	20.440	21.461

2. SEX

Dependent Variable: RrTkWd (mm)

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	20.223	.250	19.722	20.724
M	20.944	.243	20.457	21.431

```
UNIANOVA OverallAvgRunSpeedmmsBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:02:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Notes

Syntax

```
UNIANOVA
OverallAvgRunSpeedmm
s BY GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES
(GENOTYPE)
  /EMMEANS=TABLES
(SEX)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE
SEX.
```

Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: Overall Avg Run Speed (mm/s):

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	514.919[a]	2	257.460	.716	.494	.026
Intercept	1835009.15	1	1835009.15	5101.037	<.001	.990
GENOTYPE	440.090	1	440.090	1.223	.274	.023
SEX	116.723	1	116.723	.324	.571	.006
Error	19065.828	53	359.733			
Total	1868529.23	56				
Corrected Total	19580.747	55				

a. R Squared = .026 (Adjusted R Squared = -.010)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: Overall Avg Run Speed (mm/s):

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	184.382	3.479	177.403	191.361
WT	178.730	3.725	171.258	186.201

2. SEX

Dependent Variable: Overall Avg Run Speed (mm/s):

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	183.008	3.651	175.685	190.332
M	180.103	3.549	172.984	187.222

```
UNIANOVA ForepawHomolatCplBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:03:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA ForepawHomolatCpl BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES (GENOTYPE) /EMMEANS=TABLES (SEX) /PRINT ETASQ /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: ForepawHomolatCpl

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	.005[a]	2	.003	2.314	.109
Intercept	15.919	1	15.919	13698.520	<.001
GENOTYPE	.004	1	.004	3.611	.063
SEX	.002	1	.002	1.446	.235
Error	.062	53	.001		
Total	16.106	56			
Corrected Total	.067	55			

Tests of Between-Subjects Effects

Dependent Variable: ForepawHomolatCpl

Source	Partial Eta Squared
Corrected Model	.080
Intercept	.996
GENOTYPE	.064
SEX	.027
Error	
Total	
Corrected Total	

a. R Squared = .080 (Adjusted R Squared = .046)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: ForepawHomolatCpl

GENOTYPE	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
KI	.543	.006	.531	.556
WT	.526	.007	.513	.539

2. SEX

Dependent Variable: ForepawHomolatCpl

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	.540	.007	.527	.553
M	.529	.006	.516	.542

```
UNIANOVA ForepawHomologCplBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:03:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Notes

Syntax

```
UNIANOVA
ForepawHomologCpl BY
GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES
(GENOTYPE)
  /EMMEANS=TABLES
(SEX)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE
SEX.
```

Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: ForepawHomologCpl

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	.000[a]	2	.000	1.584	.215
Intercept	13.643	1	13.643	179468.999	<.001
GENOTYPE	3.705E-5	1	3.705E-5	.487	.488
SEX	.000	1	.000	2.418	.126
Error	.004	53	7.602E-5		
Total	13.721	56			
Corrected Total	.004	55			

Tests of Between-Subjects Effects

Dependent Variable: ForepawHomologCpl

Source	Partial Eta Squared
Corrected Model	.056
Intercept	1.000
GENOTYPE	.009
SEX	.044
Error	
Total	
Corrected Total	

a. R Squared = .056 (Adjusted R Squared = .021)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: ForepawHomologCpl

GENOTYPE	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
KI	.494	.002	.491	.497
WT	.496	.002	.492	.499

2. SEX

Dependent Variable: ForepawHomologCpl

SEX	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
F	.497	.002	.493	.500
M	.493	.002	.490	.496

```
UNIANOVA ForepawDiagonalCplBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:03:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA ForepawDiagonalCpl BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES (GENOTYPE) /EMMEANS=TABLES (SEX) /PRINT ETASQ /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX.
Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: ForepawDiagonalCpl

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	.002[a]	2	.001	1.005	.373	.037
Intercept	.237	1	.237	230.029	<.001	.813
GENOTYPE	.002	1	.002	1.601	.211	.029
SEX	.001	1	.001	.590	.446	.011
Error	.055	53	.001			
Total	.297	56				
Corrected Total	.057	55				

a. R Squared = .037 (Adjusted R Squared = .000)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: ForepawDiagonalCpl

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	.071	.006	.059	.083
WT	.060	.006	.047	.072

2. SEX

Dependent Variable: ForepawDiagonalCpl

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	.069	.006	.056	.081
M	.062	.006	.050	.074

```
UNIANOVA HindpawHomolatCplBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:03:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		

```
UNIANOVA
HindpawHomolatCpl BY
GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES
(GENOTYPE)
  /EMMEANS=TABLES
(SEX)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE
SEX.
```

Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: HindpawHomolatCpl

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	.009[a]	2	.005	3.493	.038	.116
Intercept	11.076	1	11.076	8192.246	<.001	.994
GENOTYPE	.009	1	.009	6.952	.011	.116
SEX	.000	1	.000	.211	.648	.004
Error	.072	53	.001			
Total	11.181	56				
Corrected Total	.081	55				

a. R Squared = .116 (Adjusted R Squared = .083)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: HindpawHomolatCpl

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	.433	.007	.419	.447
WT	.459	.007	.445	.474

2. SEX

Dependent Variable: HindpawHomolatCpl

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	.444	.007	.430	.458
M	.448	.007	.435	.462

```
UNIANOVA HindpawHomologCplBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:04:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA HindpawHomologCpl BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES (GENOTYPE) /EMMEANS=TABLES (SEX) /PRINT ETASQ /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX.
Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: HindpawHomologCpl

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	.001[a]	2	.001	2.732	.074
Intercept	13.174	1	13.174	50407.863	<.001
GENOTYPE	.001	1	.001	5.392	.024
SEX	6.741E-5	1	6.741E-5	.258	.614
Error	.014	53	.000		
Total	13.250	56			
Corrected Total	.015	55			

Tests of Between-Subjects Effects

Dependent Variable: HindpawHomologCpl

Source	Partial Eta Squared
Corrected Model	.093
Intercept	.999
GENOTYPE	.092
SEX	.005
Error	
Total	
Corrected Total	

a. R Squared = .093 (Adjusted R Squared = .059)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: HindpawHomologCpl

GENOTYPE	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
KI	.481	.003	.475	.487
WT	.492	.003	.485	.498

2. SEX

Dependent Variable: HindpawHomologCpl

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	.485	.003	.479	.492
M	.488	.003	.481	.494

```
UNIANOVA HindpawDiagonalCplBY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:04:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Notes

Syntax

```
UNIANOVA HindpawDiagonalCpl BY GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES(GENOTYPE)
  /EMMEANS=TABLES(SEX)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE SEX.
```

Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: HindpawDiagonalCpl

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	.001[a]	2	.000	.345	.710	.013
Intercept	.033	1	.033	24.039	<.001	.312
GENOTYPE	.001	1	.001	.547	.463	.010
SEX	.000	1	.000	.088	.768	.002
Error	.073	53	.001			
Total	.108	56				
Corrected Total	.074	55				

a. R Squared = .013 (Adjusted R Squared = -.024)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: HindpawDiagonalCpl

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	-.028	.007	-.042	-.014
WT	-.021	.007	-.035	-.006

2. SEX

Dependent Variable: HindpawDiagonalCpl

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	-.023	.007	-.037	-.009
M	-.026	.007	-.040	-.012

```
UNIANOVA ForepawGaitAngle BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:04:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA ForepawGaitAngle BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES (GENOTYPE) /EMMEANS=TABLES (SEX) /PRINT ETASQ /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX.
Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: ForepawGaitAngle

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	19.569[a]	2	9.784	.289	.750	.011
Intercept	153088.999	1	153088.999	4515.899	<.001	.988
GENOTYPE	6.841	1	6.841	.202	.655	.004
SEX	14.611	1	14.611	.431	.514	.008
Error	1796.700	53	33.900			
Total	155853.653	56				
Corrected Total	1816.269	55				

a. R Squared = .011 (Adjusted R Squared = -.027)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: ForepawGaitAngle

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	52.792	1.068	50.650	54.935
WT	52.088	1.143	49.794	54.381

2. SEX

Dependent Variable: ForepawGaitAngle

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	52.954	1.121	50.706	55.202
M	51.926	1.090	49.741	54.112

```
UNIANOVA HindpawGaitAngle BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:04:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA
HindpawGaitAngle BY
GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES
(GENOTYPE)
  /EMMEANS=TABLES
(SEX)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE
SEX.
```

Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: HindpawGaitAngle

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	24.366[a]	2	12.183	.290	.749	.011
Intercept	228313.165	1	228313.165	5437.864	<.001	.990
GENOTYPE	16.382	1	16.382	.390	.535	.007
SEX	10.464	1	10.464	.249	.620	.005
Error	2225.248	53	41.986			
Total	231749.603	56				
Corrected Total	2249.615	55				

a. R Squared = .011 (Adjusted R Squared = -.026)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: HindpawGaitAngle

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	63.495	1.189	61.111	65.880
WT	64.586	1.273	62.034	67.138

2. SEX

Dependent Variable: HindpawGaitAngle

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	63.606	1.247	61.104	66.108
M	64.476	1.213	62.043	66.908

```
UNIANOVA BdyRotdeg BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:04:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA BdyRotdeg
BY GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES
(GENOTYPE)
  /EMMEANS=TABLES
(SEX)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE
SEX.
```

Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: BdyRot(deg)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	66.424[a]	2	33.212	5.270	.008	.166
Intercept	147.715	1	147.715	23.439	<.001	.307
GENOTYPE	66.355	1	66.355	10.529	.002	.166
SEX	.353	1	.353	.056	.814	.001
Error	334.014	53	6.302			
Total	563.129	56				
Corrected Total	400.438	55				

a. R Squared = .166 (Adjusted R Squared = .134)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: BdyRot(deg)

GENOTYPE	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
KI	-2.726	.461	-3.650	-1.803
WT	-.532	.493	-1.520	.457

2. SEX

Dependent Variable: BdyRot(deg)

SEX	Mean	Std. Error	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
F	-1.709	.483	-2.678	-.739
M	-1.549	.470	-2.491	-.607

```
UNIANOVA LongitdPosmm BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:04:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA LongitdPosmm BY GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES(GENOTYPE)
  /EMMEANS=TABLES(SEX)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE SEX.
```

Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: Longitd Pos(mm)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	298.939[a]	2	149.470	.538	.587	.020
Intercept	441427.023	1	441427.023	1590.231	<.001	.968
GENOTYPE	118.315	1	118.315	.426	.517	.008
SEX	149.430	1	149.430	.538	.466	.010
Error	14712.096	53	277.587			
Total	460688.138	56				
Corrected Total	15011.036	55				

a. R Squared = .020 (Adjusted R Squared = -.017)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: Longitd Pos(mm)

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	90.513	3.056	84.382	96.643
WT	87.582	3.272	81.019	94.145

2. SEX

Dependent Variable: Longitd Pos(mm)

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	87.404	3.207	80.970	93.837
M	90.691	3.118	84.437	96.945

```
UNIANOVA LateralPosmm BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 15:05:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Gait sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	56
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA LateralPosmm BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES (GENOTYPE) /EMMEANS=TABLES (SEX) /PRINT ETASQ /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX.
Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	30
	WT	26
SEX	F	27
	M	29

Tests of Between-Subjects Effects

Dependent Variable: Lateral Pos(mm)

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	1.133[a]	2	.567	.121	.886
Intercept	379662.921	1	379662.921	81186.734	<.001
GENOTYPE	.596	1	.596	.127	.722
SEX	.656	1	.656	.140	.710
Error	247.850	53	4.676		
Total	382131.935	56			
Corrected Total	248.983	55			

Tests of Between-Subjects Effects

Dependent Variable: Lateral Pos(mm)

Source	Partial Eta Squared
Corrected Model	.005
Intercept	.999
GENOTYPE	.002
SEX	.003
Error	
Total	
Corrected Total	

a. R Squared = .005 (Adjusted R Squared = -.033)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: Lateral Pos(mm)

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	82.479	.397	81.683	83.275
WT	82.687	.425	81.835	83.539

2. SEX

Dependent Variable: Lateral Pos(mm)

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	82.474	.416	81.639	83.309
M	82.692	.405	81.880	83.503

Fear Conditioning

```
UNIANOVA Prestim BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 16:01:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 CF sex EF data.sav
	Active Dataset	DataSet5
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	30
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA Prestim BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	15
	WT	15
SEX	F	14
	M	16

Tests of Between-Subjects Effects

Dependent Variable: Pre-stim

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	.093[a]	3	.031	4.811	.009
Intercept	2.695	1	2.695	417.729	<.001
GENOTYPE	.083	1	.083	12.801	.001
SEX	.010	1	.010	1.561	.223
GENOTYPE * SEX	4.409E-6	1	4.409E-6	.001	.979
Error	.168	26	.006		
Total	2.990	30			
Corrected Total	.261	29			

a. R Squared = .357 (Adjusted R Squared = .283)

```
UNIANOVA ContextPrestim BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 16:01:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 CF sex EF data.sav
	Active Dataset	DataSet5
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	30
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA ContextPrestim BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	15
	WT	15
SEX	F	14
	M	16

Tests of Between-Subjects Effects

Dependent Variable: Context-Prestim

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	.383[a]	3	.128	8.295	<.001
Intercept	4.547	1	4.547	295.587	<.001
GENOTYPE	.376	1	.376	24.417	<.001
SEX	.003	1	.003	.195	.663
GENOTYPE * SEX	.001	1	.001	.037	.848
Error	.400	26	.015		
Total	5.335	30			
Corrected Total	.783	29			

a. R Squared = .489 (Adjusted R Squared = .430)

```
UNIANOVA CuePrestim BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 16:01:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 CF sex EF data.sav
	Active Dataset	DataSet5
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	30
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA CuePrestim BY GENOTYPE SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(.05) /DESIGN=GENOTYPE SEX GENOTYPE*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	15
	WT	15
SEX	F	14
	M	16

Tests of Between-Subjects Effects

Dependent Variable: Cue-Prestim

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	.323[a]	3	.108	9.118	<.001
Intercept	7.643	1	7.643	647.674	<.001
GENOTYPE	.300	1	.300	25.389	<.001
SEX	.016	1	.016	1.316	.262
GENOTYPE * SEX	.003	1	.003	.219	.644
Error	.307	26	.012		
Total	8.261	30			
Corrected Total	.630	29			

a. R Squared = .513 (Adjusted R Squared = .456)

```
UNIANOVA Prestim BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 16:03:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 CF sex EF data.sav
	Active Dataset	DataSet5
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	30
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA Prestim BY
GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES
(GENOTYPE)
  /EMMEANS=TABLES
(SEX)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE
SEX.
```

Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	15
	WT	15
SEX	F	14
	M	16

Tests of Between-Subjects Effects

Dependent Variable: Pre-stim

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	.093[a]	2	.047	7.493	.003	.357
Intercept	2.695	1	2.695	433.784	<.001	.941
GENOTYPE	.083	1	.083	13.365	.001	.331
SEX	.010	1	.010	1.621	.214	.057
Error	.168	27	.006			
Total	2.990	30				
Corrected Total	.261	29				

a. R Squared = .357 (Adjusted R Squared = .309)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: Pre-stim

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	.353	.020	.311	.395
WT	.248	.020	.206	.290

2. SEX

Dependent Variable: Pre-stim

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	.282	.021	.239	.325
M	.319	.020	.278	.359

```
UNIANOVA ContextPrestim BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 16:04:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 CF sex EF data.sav
	Active Dataset	DataSet5
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	30
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA
ContextPrestim BY
GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES
(GENOTYPE)
  /EMMEANS=TABLES
(SEX)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE
SEX.
```

Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	15
	WT	15
SEX	F	14
	M	16

Tests of Between-Subjects Effects

Dependent Variable: Context-Prestim

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	.382[a]	2	.191	12.884	<.001	.488
Intercept	4.547	1	4.547	306.515	<.001	.919
GENOTYPE	.379	1	.379	25.566	<.001	.486
SEX	.003	1	.003	.202	.657	.007
Error	.401	27	.015			
Total	5.335	30				
Corrected Total	.783	29				

a. R Squared = .488 (Adjusted R Squared = .450)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: Context-Prestim

GENOTYPE	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	.278	.031	.213	.342
WT	.503	.031	.438	.567

2. SEX

Dependent Variable: Context-Prestim

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	.400	.033	.333	.467
M	.380	.030	.318	.443

```
UNIANOVA CuePrestim BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 16:04:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 CF sex EF data.sav
	Active Dataset	DataSet5
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	30
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA CuePrestim BY GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES(GENOTYPE)
  /EMMEANS=TABLES(SEX)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE SEX.
```

Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	15
	WT	15
SEX	F	14
	M	16

Tests of Between-Subjects Effects

Dependent Variable: Cue-Prestim

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	.320[a]	2	.160	13.972	<.001	.509
Intercept	7.643	1	7.643	666.962	<.001	.961
GENOTYPE	.305	1	.305	26.588	<.001	.496
SEX	.016	1	.016	1.355	.255	.048
Error	.309	27	.011			
Total	8.261	30				
Corrected Total	.630	29				

a. R Squared = .509 (Adjusted R Squared = .472)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: Cue-Prestim

			95% Confidence Interval	
GENOTYPE	Mean	Std. Error	Lower Bound	Upper Bound
KI	.405	.028	.348	.462
WT	.607	.028	.550	.663

2. SEX

Dependent Variable: Cue-Prestim

			95% Confidence Interval	
SEX	Mean	Std. Error	Lower Bound	Upper Bound
F	.529	.029	.470	.587
M	.483	.027	.428	.538

Marble Burying

```
UNIANOVA BURRIED BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(0.05)
/DESIGN=GENOTYPE SEX GENOTYPE*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 16:28:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 marble sex EF data.sav
	Active Dataset	DataSet6
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	30
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA BURRIED BY
GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /CRITERIA=ALPHA
(0.05)
  /DESIGN=GENOTYPE
SEX GENOTYPE*SEX.
```

Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	15
	WT	15
SEX	F	14
	M	16

Tests of Between-Subjects Effects

Dependent Variable: % BURRIED

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	2612.649[a]	3	870.883	1.723	.187
Intercept	71696.801	1	71696.801	141.849	<.001
GENOTYPE	2275.015	1	2275.015	4.501	.044
SEX	196.801	1	196.801	.389	.538
GENOTYPE * SEX	75.015	1	75.015	.148	.703
Error	13141.518	26	505.443		
Total	88275.000	30			
Corrected Total	15754.167	29			

a. R Squared = .166 (Adjusted R Squared = .070)

```
UNIANOVA BURRIED BY GENOTYPE SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(GENOTYPE)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=GENOTYPE SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 16:28:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 marble sex EF data.sav
	Active Dataset	DataSet6
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	30
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA BURRIED BY
GENOTYPE SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES
(GENOTYPE)
  /EMMEANS=TABLES
(SEX)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=GENOTYPE
SEX.
```

Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
GENOTYPE	KI	15
	WT	15
SEX	F	14
	M	16

Tests of Between-Subjects Effects

Dependent Variable: % BURRIED

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	2537.634[a]	2	1268.817	2.592	.093	.161
Intercept	71696.801	1	71696.801	146.469	<.001	.844
GENOTYPE	2340.833	1	2340.833	4.782	.038	.150
SEX	196.801	1	196.801	.402	.531	.015
Error	13216.533	27	489.501			
Total	88275.000	30				
Corrected Total	15754.167	29				

a. R Squared = .161 (Adjusted R Squared = .099)

Estimated Marginal Means

1. GENOTYPE

Dependent Variable: % BURRIED

			95% Confidence Interval	
GENOTYPE	Mean	Std. Error	Lower Bound	Upper Bound
KI	40.162	5.719	28.428	51.896
WT	57.829	5.719	46.095	69.563

2. SEX

Dependent Variable: % BURRIED

			95% Confidence Interval	
SEX	Mean	Std. Error	Lower Bound	Upper Bound
F	46.429	5.913	34.296	58.561
M	51.563	5.531	40.213	62.912

Tube Test

```
UNIANOVA Average BY Genotype Sex
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(0.05)
/DESIGN=Genotype Sex Genotype*Sex.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 16:41:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Tubesex EF data.sav
	Active Dataset	DataSet7
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	30
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA Average BY Genotype Sex /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(0.05) /DESIGN=Genotype Sex Genotype*Sex.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
Genotype	KI	15
	WT	15
Sex	F	14
	M	16

Tests of Between-Subjects Effects

Dependent Variable: Average

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	1.694[a]	3	.565	3.627	.026
Intercept	6.649	1	6.649	42.712	<.001
Genotype	1.064	1	1.064	6.834	.015
Sex	.337	1	.337	2.162	.153
Genotype * Sex	.337	1	.337	2.162	.153
Error	4.048	26	.156		
Total	12.750	30			
Corrected Total	5.742	29			

a. R Squared = .295 (Adjusted R Squared = .214)

```
UNIANOVA Average BY Genotype Sex
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(Genotype)
/EMMEANS=TABLES(Sex)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=Genotype Sex.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 16:41:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Tubesex EF data.sav
	Active Dataset	DataSet7
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	30
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA Average BY Genotype Sex /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES (Genotype) /EMMEANS=TABLES (Sex) /PRINT ETASQ /CRITERIA=ALPHA(.05) /DESIGN=Genotype Sex.
Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
Genotype	KI	15
	WT	15
Sex	F	14
	M	16

Tests of Between-Subjects Effects

Dependent Variable: Average

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	1.357[a]	2	.679	4.180	.026	.236
Intercept	7.188	1	7.188	44.268	<.001	.621
Genotype	1.154	1	1.154	7.105	.013	.208
Sex	.349	1	.349	2.150	.154	.074
Error	4.384	27	.162			
Total	12.750	30				
Corrected Total	5.742	29				

a. R Squared = .236 (Adjusted R Squared = .180)

Estimated Marginal Means

1. Genotype

Dependent Variable: Average

Genotype	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	.688	.105	.473	.904
WT	.293	.104	.079	.506

2. Sex

Dependent Variable: Average

Sex	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	.600	.108	.378	.822
M	.382	.101	.174	.589

Nest Building

```
UNIANOVA NestScore BY Genotype Sex
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(0.05)
/DESIGN=Genotype Sex Genotype*Sex.
```

Univariate Analysis of Variance

Notes

Output Created		23-AUG-2022 14:24:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June_Aug 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Nest sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	30
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA NestScore BY Genotype Sex /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(0.05) /DESIGN=Genotype Sex Genotype*Sex.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

```
[DataSet4] /Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June_Aug 202
2 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Nest sex EF da
ta.sav
```

Between-Subjects Factors

		N
Genotype	KI	15
	WT	15
Sex	F	14
	M	16

Tests of Between-Subjects Effects

Dependent Variable: Nest Score

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	7.094[a]	3	2.365	2.340	.097
Intercept	535.507	1	535.507	529.957	<.001
Genotype	6.254	1	6.254	6.189	.020
Sex	.007	1	.007	.007	.933
Genotype * Sex	.554	1	.554	.548	.466
Error	26.272	26	1.010		
Total	571.000	30			
Corrected Total	33.367	29			

a. R Squared = .213 (Adjusted R Squared = .122)

```
UNIANOVA shredded BY Genotype Sex
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(0.05)
/DESIGN=Genotype Sex Genotype*Sex.
```

Univariate Analysis of Variance

Notes

Output Created		23-AUG-2022 14:24:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June _Aug 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Nest sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	30
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		

```
UNIANOVA shredded BY
Genotype Sex
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /CRITERIA=ALPHA
(0.05)
  /DESIGN=Genotype
Sex Genotype*Sex.
```

Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
Genotype	KI	15
	WT	15
Sex	F	14
	M	16

Tests of Between-Subjects Effects

Dependent Variable: % shredded

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	3075.830 [a]	3	1025.277	1.871	.159
Intercept	162169.074	1	162169.074	295.895	<.001
Genotype	2062.888	1	2062.888	3.764	.063
Sex	69.192	1	69.192	.126	.725
Genotype * Sex	763.098	1	763.098	1.392	.249
Error	14249.641	26	548.063		
Total	179770.198	30			
Corrected Total	17325.471	29			

a. R Squared = .178 (Adjusted R Squared = .083)

```
UNIANOVA NestScore BY Genotype Sex
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(Genotype)
/EMMEANS=TABLES(Sex)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=Genotype Sex.
```

Univariate Analysis of Variance

Notes

Output Created		23-AUG-2022 14:25:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June_Aug 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Nest sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	30
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA NestScore BY Genotype Sex /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES (Genotype) /EMMEANS=TABLES (Sex) /PRINT ETASQ /CRITERIA=ALPHA(.05) /DESIGN=Genotype Sex.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
Genotype	KI	15
	WT	15
Sex	F	14
	M	16

Tests of Between-Subjects Effects

Dependent Variable: Nest Score

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	6.541[a]	2	3.270	3.292	.053	.196
Intercept	535.507	1	535.507	538.980	<.001	.952
Genotype	6.533	1	6.533	6.576	.016	.196
Sex	.007	1	.007	.007	.932	.000
Error	26.826	27	.994			
Total	571.000	30				
Corrected Total	33.367	29				

a. R Squared = .196 (Adjusted R Squared = .136)

Estimated Marginal Means

1. Genotype

Dependent Variable: Nest Score

			95% Confidence Interval	
Genotype	Mean	Std. Error	Lower Bound	Upper Bound
KI	3.768	.258	3.239	4.296
WT	4.701	.258	4.172	5.230

2. Sex

Dependent Variable: Nest Score

			95% Confidence Interval	
Sex	Mean	Std. Error	Lower Bound	Upper Bound
F	4.250	.266	3.703	4.797
M	4.219	.249	3.707	4.730

```
UNIANOVA shredded BY Genotype Sex
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(Genotype)
/EMMEANS=TABLES(Sex)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=Genotype Sex.
```

Univariate Analysis of Variance

Notes

Output Created		23-AUG-2022 14:25:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June_Aug 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 Nest sex EF data.sav
	Active Dataset	DataSet4
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	30
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA shredded BY Genotype Sex /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES (Genotype) /EMMEANS=TABLES (Sex) /PRINT ETASQ /CRITERIA=ALPHA(.05) /DESIGN=Genotype Sex.
Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
Genotype	KI	15
	WT	15
Sex	F	14
	M	16

Tests of Between-Subjects Effects

Dependent Variable: % shredded

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	2312.731[a]	2	1156.366	2.080	.145	.133
Intercept	162169.074	1	162169.074	291.657	<.001	.915
Genotype	2243.540	1	2243.540	4.035	.055	.130
Sex	69.192	1	69.192	.124	.727	.005
Error	15012.740	27	556.027			
Total	179770.198	30				
Corrected Total	17325.471	29				

a. R Squared = .133 (Adjusted R Squared = .069)

Estimated Marginal Means

1. Genotype

Dependent Variable: % shredded

Genotype	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	65.039	6.095	52.533	77.545
WT	82.335	6.095	69.828	94.841

2. Sex

Dependent Variable: % shredded

Sex	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	75.209	6.302	62.278	88.140
M	72.165	5.895	60.069	84.261

3 Chamber

```
UNIANOVA SocialIndexCup BY Geno SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(0.05)
/DESIGN=Geno SEX Geno*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 16:59:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 3CH Social sex EF data.sav
	Active Dataset	DataSet9
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	27
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA SocialIndexCup BY Geno SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(0.05) /DESIGN=Geno SEX Geno*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
Geno	KI	16
	WT	11
SEX	F	14
	M	13

Tests of Between-Subjects Effects

Dependent Variable: Social Index Cup

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	.205[a]	3	.068	1.395	.269
Intercept	.727	1	.727	14.818	<.001
Geno	.191	1	.191	3.903	.060
SEX	.040	1	.040	.808	.378
Geno * SEX	.001	1	.001	.013	.910
Error	1.128	23	.049		
Total	2.310	27			
Corrected Total	1.334	26			

a. R Squared = .154 (Adjusted R Squared = .044)

```
UNIANOVA SocialIndexChamberBY Geno SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(0.05)
/DESIGN=Geno SEX Geno*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 16:59:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 3CH Social sex EF data.sav
	Active Dataset	DataSet9
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	27
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA SocialIndexChamber BY Geno SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(0.05) /DESIGN=Geno SEX Geno*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
Geno	KI	16
	WT	11
SEX	F	14
	M	13

Tests of Between-Subjects Effects

Dependent Variable: Social Index Chamber

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	.137[a]	3	.046	1.550	.228
Intercept	.474	1	.474	16.022	<.001
Geno	.137	1	.137	4.637	.042
SEX	.007	1	.007	.238	.630
Geno * SEX	.004	1	.004	.135	.716
Error	.680	23	.030		
Total	1.467	27			
Corrected Total	.817	26			

a. R Squared = .168 (Adjusted R Squared = .060)

```
UNIANOVA SocialIndexCup BY Geno SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(Geno)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=Geno SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 16:59:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 3CH Social sex EF data.sav
	Active Dataset	DataSet9
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	27
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA
SocialIndexCup BY Geno
SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES
(Geno)
  /EMMEANS=TABLES
(SEX)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=Geno SEX.
```

Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
Geno	KI	16
	WT	11
SEX	F	14
	M	13

Tests of Between-Subjects Effects

Dependent Variable: Social Index Cup

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	.205[a]	2	.102	2.176	.135	.154
Intercept	.772	1	.772	16.407	<.001	.406
Geno	.191	1	.191	4.071	.055	.145
SEX	.039	1	.039	.836	.370	.034
Error	1.129	24	.047			
Total	2.310	27				
Corrected Total	1.334	26				

a. R Squared = .154 (Adjusted R Squared = .083)

Estimated Marginal Means

1. Geno

Dependent Variable: Social Index Cup

Geno	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	.260	.054	.147	.372
WT	.085	.066	-.052	.222

2. SEX

Dependent Variable: Social Index Cup

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	.211	.058	.092	.331
M	.134	.062	.005	.262

```
UNIANOVA SocialIndexChamberBY Geno SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(Geno)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=Geno SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 17:00:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 3CH Social sex EF data.sav
	Active Dataset	DataSet9
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	27
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA SocialIndexChamber BY Geno SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES(Geno) /EMMEANS=TABLES(SEX) /PRINT ETASQ /CRITERIA=ALPHA(.05) /DESIGN=Geno SEX.
Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
Geno	KI	16
	WT	11
SEX	F	14
	M	13

Tests of Between-Subjects Effects

Dependent Variable: Social Index Chamber

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	.133[a]	2	.067	2.342	.118	.163
Intercept	.516	1	.516	18.119	<.001	.430
Geno	.133	1	.133	4.684	.041	.163
SEX	.005	1	.005	.182	.674	.008
Error	.684	24	.028			
Total	1.467	27				
Corrected Total	.817	26				

a. R Squared = .163 (Adjusted R Squared = .094)

Estimated Marginal Means

1. Geno

Dependent Variable: Social Index Chamber

Geno	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	.214	.042	.127	.302
WT	.068	.052	-.039	.175

2. SEX

Dependent Variable: Social Index Chamber

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	.155	.045	.062	.248
M	.127	.049	.027	.227

```
UNIANOVA NoveltyIndexCup BY Geno SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(0.05)
/DESIGN=Geno SEX Geno*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 17:11:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 3CH Novelty sex EF data.sav
	Active Dataset	DataSet10
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	27
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA NoveltyIndexCup BY Geno SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(0.05) /DESIGN=Geno SEX Geno*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
Geno	KI	16
	WT	11
SEX	F	14
	M	13

Tests of Between-Subjects Effects

Dependent Variable: Novelty Index Cup

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	.394[a]	3	.131	1.485	.245
Intercept	1.275	1	1.275	14.414	<.001
Geno	.318	1	.318	3.597	.071
SEX	.001	1	.001	.013	.910
Geno * SEX	.091	1	.091	1.032	.320
Error	2.035	23	.088		
Total	3.450	27			
Corrected Total	2.429	26			

a. R Squared = .162 (Adjusted R Squared = .053)

```
UNIANOVA NoveltyIndexChamberBY Geno SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/CRITERIA=ALPHA(0.05)
/DESIGN=Geno SEX Geno*SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 17:11:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 3CH Novelty sex EF data.sav
	Active Dataset	DataSet10
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	27
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA NoveltyIndexChamber BY Geno SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /CRITERIA=ALPHA(0.05) /DESIGN=Geno SEX Geno*SEX.
Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
Geno	KI	16
	WT	11
SEX	F	14
	M	13

Tests of Between-Subjects Effects

Dependent Variable: Novelty Index Chamber

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	.332[a]	3	.111	2.590	.077
Intercept	1.428	1	1.428	33.428	<.001
Geno	.224	1	.224	5.234	.032
SEX	.028	1	.028	.654	.427
Geno * SEX	.032	1	.032	.739	.399
Error	.982	23	.043		
Total	2.589	27			
Corrected Total	1.314	26			

a. R Squared = .253 (Adjusted R Squared = .155)

```
UNIANOVA NoveltyIndexCup BY Geno SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(Geno)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=Geno SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 17:12:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 3CH Novelty sex EF data.sav
	Active Dataset	DataSet10
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	27
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.

Syntax

```
UNIANOVA
NoveltyIndexCup BY
Geno SEX
  /METHOD=SSTYPE(3)
  /INTERCEPT=INCLUDE
  /EMMEANS=TABLES
(Geno)
  /EMMEANS=TABLES
(SEX)
  /PRINT ETASQ
  /CRITERIA=ALPHA(.05)
  /DESIGN=Geno SEX.
```

Resources	Processor Time	00:00:00.01
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
Geno	KI	16
	WT	11
SEX	F	14
	M	13

Tests of Between-Subjects Effects

Dependent Variable: Novelty Index Cup

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	.303[a]	2	.151	1.709	.202	.125
Intercept	1.187	1	1.187	13.406	.001	.358
Geno	.284	1	.284	3.201	.086	.118
SEX	.001	1	.001	.011	.916	.000
Error	2.126	24	.089			
Total	3.450	27				
Corrected Total	2.429	26				

a. R Squared = .125 (Adjusted R Squared = .052)

Estimated Marginal Means

1. Geno

Dependent Variable: Novelty Index Cup

Geno	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
KI	.108	.075	-.047	.262
WT	.320	.091	.132	.508

2. SEX

Dependent Variable: Novelty Index Cup

SEX	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
F	.220	.080	.056	.384
M	.208	.086	.031	.385

```
UNIANOVA NoveltyIndexChamberBY Geno SEX
/METHOD=SSTYPE(3)
/INTERCEPT=INCLUDE
/EMMEANS=TABLES(Geno)
/EMMEANS=TABLES(SEX)
/PRINT ETASQ
/CRITERIA=ALPHA(.05)
/DESIGN=Geno SEX.
```

Univariate Analysis of Variance

Notes

Output Created		22-AUG-2022 17:12:...
Comments		
Input	Data	/Users/jeffneul/Jeff's Research/Neul Manuscripts/FoxG1/June 2022 stat sex and effect size/SPSS files/SPSS Data Files/June 2022 3CH Novelty sex EF data.sav
	Active Dataset	DataSet10
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	27
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics are based on all cases with valid data for all variables in the model.
Syntax		UNIANOVA NoveltyIndexChamber BY Geno SEX /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /EMMEANS=TABLES(Geno) /EMMEANS=TABLES(SEX) /PRINT ETASQ /CRITERIA=ALPHA(.05) /DESIGN=Geno SEX.
Resources	Processor Time	00:00:00.02
	Elapsed Time	00:00:00.00

Between-Subjects Factors

		N
Geno	KI	16
	WT	11
SEX	F	14
	M	13

Tests of Between-Subjects Effects

Dependent Variable: Novelty Index Chamber

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	Partial Eta Squared
Corrected Model	.300[a]	2	.150	3.554	.044	.229
Intercept	1.403	1	1.403	33.202	<.001	.580
Geno	.207	1	.207	4.905	.037	.170
SEX	.044	1	.044	1.046	.317	.042
Error	1.014	24	.042			
Total	2.589	27				
Corrected Total	1.314	26				

a. R Squared = .229 (Adjusted R Squared = .164)

Estimated Marginal Means

1. Geno

Dependent Variable: Novelty Index Chamber

			95% Confidence Interval	
Geno	Mean	Std. Error	Lower Bound	Upper Bound
KI	.142	.052	.035	.248
WT	.323	.063	.194	.453

2. SEX

Dependent Variable: Novelty Index Chamber

			95% Confidence Interval	
SEX	Mean	Std. Error	Lower Bound	Upper Bound
F	.274	.055	.160	.387
M	.191	.059	.069	.313