## 1 2way ANOVA of stat Rit Frequency 15 D intergroup

| | | | | | |
|---|---|---|---|---|---|
| **Table Analyzed** | stat Rit Frequency 15 D | | | | |
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 11,25 | 0,0163 | * | Yes | |
| **genotype** | 36,79 | <0,0001 | **** | Yes | |
| **injury** | 3,712 | 0,1533 | ns | No | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 69,03 | 1 | 69,03 | F (1, 28) = 6,527 | P=0,0163 |
| **genotype** | 225,8 | 1 | 225,8 | F (1, 28) = 21,35 | P<0,0001 |
| **injury** | 22,78 | 1 | 22,78 | F (1, 28) = 2,154 | P=0,1533 |
| **Residual** | 296,1 | 28 | 10,58 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Mean of sham** | 6,750 | | | | |
| **Mean of mTBI** | 8,438 | | | | |
| **Difference between means** | -1,688 | | | | |
| **SE of difference** | 1,150 | | | | |
| **95% CI of difference** | -4,043 to 0,6677 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of wt** | 4,938 | | | | |
| **Mean of app** | 10,25 | | | | |
| **Difference between means** | -5,313 | | | | |
| **SE of difference** | 1,150 | | | | |
| **95% CI of difference** | -7,668 to -2,957 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | -4,625 | | | | |
| **Mean diff, A2 - B2** | 1,250 | | | | |
| **(A1 -B1) - (A2 - B2)** | -5,875 | | | | |
| **95% CI of difference** | -10,59 to -1,165 | | | | |
| **(B1 - A1) - (B2 - A2)** | 5,875 | | | | |
| **95% CI of difference** | 1,165 to 10,59 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0,05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 33,12 | <0,0001 | No | **** | |
| **Anderson-Darling (A2*)** | 1,691 | 0,0002 | No | *** | |
| **Shapiro-Wilk (W)** | 0,8018 | <0,0001 | No | **** | |
| **Kolmogorov-Smirnov (distance)** | 0,2166 | 0,0005 | No | *** | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (injury)** | 2 | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of rows (genotype)** | 2 | | | | |
| **Number of values** | 32 | | | | |

|  | WT-sham | WT-mTBI | APP-sham | APP-mTBI |
|---|---|---|---|---|
| Test for normal distribution |  |  |  |  |
| D'Agostino & Pearson test |  |  |  |  |
| K2 | 10,93 | 4,078 | 1,235 | 1,925 |
| P value | 0,0042 | 0,1302 | 0,5393 | 0,3819 |
| Passed n | No | Yes | Yes | Yes |
| P value su | ** | ns | ns | ns |
|  |  |  |  |  |
| Anderson-Darling test |  |  |  |  |
| A2* | 1,175 | 0,4708 | 0,4 | 0,6169 |
| P value | 0,0019 | 0,1744 | 0,2736 | 0,069 |
| Passed n | No | Yes | Yes | Yes |
| P value su | ** | ns | ns | ns |
|  |  |  |  |  |
| Shapiro-Wilk test |  |  |  |  |
| W | 0,6756 | 0,868 | 0,894 | 0,8443 |
| P value | 0,0012 | 0,1439 | 0,2547 | 0,0834 |
| Passed n | No | Yes | Yes | Yes |
| P value su | ** | ns | ns | ns |
|  |  |  |  |  |
| Kolmogorov-Smirnov test |  |  |  |  |
| KS distan | 0,3472 | 0,2602 | 0,2224 | 0,2372 |
| P value | 0,0052 | >0,1000 | >0,1000 | >0,1000 |
| Passed n | No | Yes | Yes | Yes |
| P value su | ** | ns | ns | ns |
|  |  |  |  |  |
| Number of | 8 | 8 | 8 | 8 |

## 2. 2way ANOVA of stat Rit Duration 15 D intergroup

| | | | | | |
|---|---|---|---|---|---|
| **Table Analyzed** | stat Rit Duration 15 D | | | | |
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 21,01 | 0,0066 | ** | Yes | |
| **WT/APP** | 0,9237 | 0,5437 | ns | No | |
| **Model** | 9,630 | 0,0570 | ns | No | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 2493 | 1 | 2493 | F (1, 28) = 8,594 | P=0,0066 |
| **WT/APP** | 109,6 | 1 | 109,6 | F (1, 28) = 0,3779 | P=0,5437 |
| **Model** | 1143 | 1 | 1143 | F (1, 28) = 3,940 | P=0,0570 |
| **Residual** | 8120 | 28 | 290,0 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Mean of sham** | 28,57 | | | | |
| **Mean of mTBI** | 40,53 | | | | |
| **Difference between means** | -11,95 | | | | |
| **SE of difference** | 6,021 | | | | |
| **95% CI of difference** | -24,28 to 0,3821 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of wt** | 32,70 | | | | |
| **Mean of app** | 36,40 | | | | |
| **Difference between means** | -3,701 | | | | |
| **SE of difference** | 6,021 | | | | |
| **95% CI of difference** | -16,03 to 8,632 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | -29,60 | | | | |
| **Mean diff, A2 - B2** | 5,700 | | | | |
| **(A1 -B1) - (A2 - B2)** | -35,30 | | | | |
| **95% CI of difference** | -59,97 to -10,64 | | | | |
| **(B1 - A1) - (B2 - A2)** | 35,30 | | | | |
| **95% CI of difference** | 10,64 to 59,97 | | | | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Model)** | 2 | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of rows (WT/APP)** | 2 | | | | |
| **Number of values** | 32 | | | | |

|  | WT-sham | WT-mTBI | APP-sham | APP-mTBI |
|---|---|---|---|---|
| Test for normal distribution |  |  |  |  |
| D'Agostino & Pearson test |  |  |  |  |
| K2 | 1,906 | 0,6978 | 2,644 | 0,6657 |
| P value | 0,3856 | 0,7055 | 0,2666 | 0,7169 |
| Passed n | Yes | Yes | Yes | Yes |
| P value s | ns | ns | ns | ns |
|  |  |  |  |  |
| Anderson-Darling test |  |  |  |  |
| A2* | 0,3602 | 0,1865 | 0,7888 | 0,2527 |
| P value | 0,3497 | 0,8598 | 0,0229 | 0,6276 |
| Passed n | Yes | Yes | No | Yes |
| P value s | ns | ns | * | ns |
|  |  |  |  |  |
| Shapiro-Wilk test |  |  |  |  |
| W | 0,9112 | 0,9593 | 0,8078 | 0,9436 |
| P value | 0,3628 | 0,8034 | 0,0346 | 0,6463 |
| Passed n | Yes | Yes | No | Yes |
| P value s | ns | ns | * | ns |
|  |  |  |  |  |
| Kolmogorov-Smirnov test |  |  |  |  |
| KS distan | 0,2374 | 0,1518 | 0,3295 | 0,1733 |
| P value | >0,1000 | >0,1000 | 0,0108 | >0,1000 |
| Passed n | Yes | Yes | No | Yes |
| P value s | ns | ns | * | ns |
|  |  |  |  |  |
| Number of | 8 | 8 | 8 | 8 |

# 3. 2way ANOVA of stat Rit Latency 15 D intergroup

| | | | | | |
|---|---|---|---|---|---|
| **Table Analyzed** | stat Rit Latency 15 D | | | | |
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 10,54 | 0,0063 | ** | Yes | |
| **wt or ko** | 26,99 | <0,0001 | **** | Yes | |
| **tipe of injury** | 28,64 | <0,0001 | **** | Yes | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 10706 | 1 | 10706 | F (1, 28) = 8,725 | P=0,0063 |
| **wt or ko** | 27407 | 1 | 27407 | F (1, 28) = 22,34 | P<0,0001 |
| **tipe of injury** | 29083 | 1 | 29083 | F (1, 28) = 23,70 | P<0,0001 |
| **Residual** | 34354 | 28 | 1227 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Mean of sham** | 100,7 | | | | |
| **Mean of mTBI** | 40,40 | | | | |
| **Difference between means** | 60,29 | | | | |
| **SE of difference** | 12,38 | | | | |
| **95% CI of difference** | 34,93 to 85,66 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of wt** | 99,81 | | | | |
| **Mean of app** | 41,28 | | | | |
| **Difference between means** | 58,53 | | | | |
| **SE of difference** | 12,38 | | | | |
| **95% CI of difference** | 33,16 to 83,90 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | 96,88 | | | | |
| **Mean diff, A2 - B2** | 23,71 | | | | |
| **(A1 -B1) - (A2 - B2)** | 73,16 | | | | |
| **95% CI of difference** | 22,43 to 123,9 | | | | |
| **(B1 - A1) - (B2 - A2)** | -73,16 | | | | |
| **95% CI of difference** | -123,9 to -22,43 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0,05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 1,498 | 0,4728 | Yes | ns | |
| **Anderson-Darling (A2*)** | 1,029 | 0,0090 | No | ** | |
| **Shapiro-Wilk (W)** | 0,9385 | 0,0679 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1770 | 0,0122 | No | * | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (tipe of injury)** | 2 | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of rows (wt or ko)** | 2 | | | | |
| **Number of values** | 32 | | | | |

|  | WT-sham | WT-mTBI | APP-sham | APP-mTBI |
|---|---|---|---|---|
| Test for normal distribution |  |  |  |  |
| D'Agostino & Pearson test |  |  |  |  |
| K2 | 0,5863 | 1,455 | 0,7054 | 2,755 |
| P value | 0,7459 | 0,4831 | 0,7028 | 0,2522 |
| Passed n | Yes | Yes | Yes | Yes |
| P value s | ns | ns | ns | ns |
|  |  |  |  |  |
| Anderson-Darling test |  |  |  |  |
| A2* | 0,4308 | 0,3399 | 0,1648 | 0,8397 |
| P value | 0,2254 | 0,3956 | 0,906 | 0,0166 |
| Passed n | Yes | Yes | Yes | No |
| P value s | ns | ns | ns | * |
|  |  |  |  |  |
| Shapiro-Wilk test |  |  |  |  |
| W | 0,9164 | 0,9204 | 0,9663 | 0,7877 |
| P value | 0,4013 | 0,4328 | 0,8677 | 0,0211 |
| Passed n | Yes | Yes | Yes | No |
| P value s | ns | ns | ns | * |
|  |  |  |  |  |
| Kolmogorov-Smirnov test |  |  |  |  |
| KS distan | 0,2712 | 0,2095 | 0,1407 | 0,2852 |
| P value | 0,0853 | >0,1000 | >0,1000 | 0,0543 |
| Passed n | Yes | Yes | Yes | Yes |
| P value s | ns | ns | ns | ns |
|  |  |  |  |  |
| Number of | 8 | 8 | 8 | 8 |

# 4. 2way ANOVA of Y-maze 30 d and 60 d intergroup

| | | | | | |
|---|---|---|---|---|---|
| **Table Analyzed** | Y-maze 30 d and 60 d | | | | |
| | | | | | |
| **Two-way RM ANOVA** | Matching: Stacked | | | | |
| **Assume sphericity?** | Yes | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Time x Column Factor** | 4,856 | 0,4036 | ns | No | |
| **Time** | 0,1928 | 0,7315 | ns | No | |
| **Column Factor** | 1,729 | 0,8007 | ns | No | |
| **Subject** | 48,29 | 0,4251 | ns | No | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Time x Column Factor** | 392,9 | 3 | 131,0 | F (3, 28) = 1,009 | P=0,4036 |
| **Time** | 15,60 | 1 | 15,60 | F (1, 28) = 0,1202 | P=0,7315 |
| **Column Factor** | 139,9 | 3 | 46,63 | F (3, 28) = 0,3342 | P=0,8007 |
| **Subject** | 3908 | 28 | 139,6 | F (28, 28) = 1,075 | P=0,4251 |
| **Residual** | 3636 | 28 | 129,9 | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of 30** | 64,32 | | | | |
| **Mean of 60** | 65,31 | | | | |
| **Difference between means** | -0,9875 | | | | |
| **SE of difference** | 2,849 | | | | |
| **95% CI of difference** | -6,823 to 4,848 | | | | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Column Factor)** | 4 | | | | |
| **Number of rows (Time)** | 2 | | | | |
| **Number of subjects (Subject)** | 32 | | | | |
| **Number of missing values** | 0 | | | | |

| | WT-sham 3 | WT-Sham 6 | WT-mTBI 3 | WT-mTBI 6 | APP-Sham | APP-Sham | APP-mTBI | APP-mTBI 6 |
|---|---|---|---|---|---|---|---|---|
| Test for normal distribution | | | | | | | | |
| D'Agostino & Pearson test | | | | | | | | |
| K2 | 2,679 | 0,6738 | 2,753 | 1,42 | 1,319 | 2,383 | 0,7214 | 1,175 |
| P value | 0,262 | 0,714 | 0,2525 | 0,4917 | 0,5172 | 0,3037 | 0,6972 | 0,5558 |
| Passed n | Yes | Yes | Yes | Yes | Yes | Yes | Yes | Yes |
| P value s | ns | ns | ns | ns | ns | ns | ns | ns |
| | | | | | | | | |
| Anderson-Darling test | | | | | | | | |
| A2* | 0,4159 | 0,2514 | 0,4396 | 0,4711 | 0,2226 | 0,6829 | 0,2055 | 0,412 |
| P value | 0,2476 | 0,6321 | 0,2132 | 0,174 | 0,7403 | 0,0452 | 0,8011 | 0,2539 |
| Passed n | Yes | Yes | Yes | Yes | Yes | No | Yes | Yes |
| P value s | ns | ns | ns | ns | ns | * | ns | ns |
| | | | | | | | | |
| Shapiro-Wilk test | | | | | | | | |
| W | 0,8865 | 0,9564 | 0,905 | 0,8644 | 0,9669 | 0,8191 | 0,955 | 0,8988 |
| P value | 0,2169 | 0,7755 | 0,3203 | 0,1328 | 0,873 | 0,0457 | 0,7615 | 0,2817 |
| Passed n | Yes | Yes | Yes | Yes | Yes | No | Yes | Yes |
| P value s | ns | ns | ns | ns | ns | * | ns | ns |
| | | | | | | | | |
| Kolmogorov-Smirnov test | | | | | | | | |
| KS distan | 0,2234 | 0,1972 | 0,2372 | 0,205 | 0,189 | 0,2824 | 0,1502 | 0,2376 |
| P value | >0,1000 | >0,1000 | >0,1000 | >0,1000 | >0,1000 | 0,0597 | >0,1000 | >0,1000 |
| Passed n | Yes | Yes | Yes | Yes | Yes | Yes | Yes | Yes |
| P value s | ns | ns | ns | ns | ns | ns | ns | ns |
| | | | | | | | | |
| Number of | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 |

0

5. 2way ANOVA of Y-maze FORCED_latency 30-60D intergroup

| | | | | | |
|---|---|---|---|---|---|
| **Table Analyzed** | Y-maze FORCED_latency 30-60D | | | | |
| | | | | | |
| **Two-way RM ANOVA** | Matching: Stacked | | | | |
| **Assume sphericity?** | Yes | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Time x Column Factor** | 27,93 | <0,0001 | **** | Yes | |
| **Time** | 0,2183 | 0,5902 | ns | No | |
| **Column Factor** | 24,11 | 0,0004 | *** | Yes | |
| **Subject** | 27,15 | 0,2345 | ns | No | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Time x Column Factor** | 4072 | 3 | 1357 | F (3, 28) = 12,66 | P<0,0001 |
| **Time** | 31,82 | 1 | 31,82 | F (1, 28) = 0,2968 | P=0,5902 |
| **Column Factor** | 3514 | 3 | 1171 | F (3, 28) = 8,287 | P=0,0004 |
| **Subject** | 3958 | 28 | 141,4 | F (28, 28) = 1,319 | P=0,2345 |
| **Residual** | 3002 | 28 | 107,2 | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of 30** | 11,88 | | | | |
| **Mean of 60** | 13,29 | | | | |
| **Difference between means** | -1,410 | | | | |
| **SE of difference** | 2,589 | | | | |
| **95% CI of difference** | -6,713 to 3,892 | | | | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Column Factor)** | 4 | | | | |
| **Number of rows (Time)** | 2 | | | | |
| **Number of subjects (Subject)** | 32 | | | | |
| **Number of missing values** | 0 | | | | |

|  | WT-sham 3 | WT-Sham 6 | WT-mTBI 3 | WT-mTBI 6 | APP-Sham | APP-Sham | APP-mTBI | APP-mTBI 6 |
|---|---|---|---|---|---|---|---|---|
| Test for normal distribution |  |  |  |  |  |  |  |  |
| D'Agostino & Pearson test |  |  |  |  |  |  |  |  |
| K2 | 12,12 | 16,87 | 3,586 | 1,328 | 12,34 | 6,566 | 8,02 | 21,51 |
| P value | 0,0023 | 0,0002 | 0,1665 | 0,5149 | 0,0021 | 0,0375 | 0,0181 | <0,0001 |
| Passed n | No | No | Yes | Yes | No | No | No | No |
| P value su | ** | *** | ns | ns | ** | * | * | **** |
|  |  |  |  |  |  |  |  |  |
| Anderson-Darling test |  |  |  |  |  |  |  |  |
| A2* | 0,7332 | 1,231 | 0,6284 | 0,3612 | 0,8482 | 1,483 | 0,6157 | 1,755 |
| P value | 0,0327 | 0,0014 | 0,0641 | 0,3477 | 0,0157 | 0,0003 | 0,0696 | <0,0001 |
| Passed n | No | No | Yes | Yes | No | No | Yes | No |
| P value su | * | ** | ns | ns | * | *** | ns | **** |
|  |  |  |  |  |  |  |  |  |
| Shapiro-Wilk test |  |  |  |  |  |  |  |  |
| W | 0,7884 | 0,6567 | 0,8216 | 0,8952 | 0,7766 | 0,6301 | 0,8317 | 0,5361 |
| P value | 0,0215 | 0,0007 | 0,0485 | 0,2616 | 0,016 | 0,0004 | 0,0619 | <0,0001 |
| Passed n | No | No | No | Yes | No | No | Yes | No |
| P value su | * | *** | * | ns | * | *** | ns | **** |
|  |  |  |  |  |  |  |  |  |
| Kolmogorov-Smirnov test |  |  |  |  |  |  |  |  |
| KS distan | 0,2417 | 0,3039 | 0,255 | 0,2248 | 0,255 | 0,4237 | 0,2929 | 0,4001 |
| P value | >0,1000 | 0,0284 | >0,1000 | >0,1000 | >0,1000 | 0,0001 | 0,0419 | 0,0004 |
| Passed n | Yes | No | Yes | Yes | Yes | No | No | No |
| P value su | ns | * | ns | ns | ns | *** | * | *** |
|  |  |  |  |  |  |  |  |  |
| Number of | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 |

# 6. 2way ANOVA of Y-maze FORCED_Duration 30-60D intergroup

| | | | | | |
|---|---|---|---|---|---|
| **Table Analyzed** | Y-maze FORCED_Duration 30-60D | | | | |
| | | | | | |
| **Two-way RM ANOVA** | Matching: Stacked | | | | |
| **Assume sphericity?** | Yes | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Time x Column Factor** | 8,507 | 0,0067 | ** | Yes | |
| **Time** | 25,63 | <0,0001 | **** | Yes | |
| **Column Factor** | 31,65 | <0,0001 | **** | Yes | |
| **Subject** | 18,30 | 0,3569 | ns | No | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Time x Column Factor** | 2010 | 3 | 670,0 | F (3, 28) = 4,990 | P=0,0067 |
| **Time** | 6057 | 1 | 6057 | F (1, 28) = 45,11 | P<0,0001 |
| **Column Factor** | 7477 | 3 | 2492 | F (3, 28) = 16,14 | P<0,0001 |
| **Subject** | 4324 | 28 | 154,4 | F (28, 28) = 1,150 | P=0,3569 |
| **Residual** | 3759 | 28 | 134,3 | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of 30** | 35,47 | | | | |
| **Mean of 60** | 16,02 | | | | |
| **Difference between means** | 19,46 | | | | |
| **SE of difference** | 2,897 | | | | |
| **95% CI of difference** | 13,52 to 25,39 | | | | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Column Factor)** | 4 | | | | |
| **Number of rows (Time)** | 2 | | | | |
| **Number of subjects (Subject)** | 32 | | | | |
| **Number of missing values** | 0 | | | | |

|  | WT-sham 3 | WT-Sham 6 | WT-mTBI 3( | WT-mTBI 6( | APP-Sham | APP-Sham | APP-mTBI | APP-mTBI 6 |
|---|---|---|---|---|---|---|---|---|
| Test for normal distribution |  |  |  |  |  |  |  |  |
| D'Agostino & Pearson test |  |  |  |  |  |  |  |  |
| K2 | 0,1594 | 0,1181 | 1,561 | 3,937 | 0,9235 | 4,325 | 0,4407 | 21,4 |
| P value | 0,9234 | 0,9427 | 0,4583 | 0,1397 | 0,6302 | 0,115 | 0,8022 | <0,0001 |
| Passed n | Yes | Yes | Yes | Yes | Yes | Yes | Yes | No |
| P value s | ns | ns | ns | ns | ns | ns | ns | **** |
|  |  |  |  |  |  |  |  |  |
| Anderson-Darling test |  |  |  |  |  |  |  |  |
| A2* | 0,1571 | 0,1605 | 0,3721 | 0,7254 | 0,3025 | 1,552 | 0,2461 | 1,848 |
| P value | 0,9208 | 0,9142 | 0,3252 | 0,0344 | 0,4943 | 0,0002 | 0,6518 | <0,0001 |
| Passed n | Yes | Yes | Yes | No | Yes | No | Yes | No |
| P value s | ns | ns | ns | * | ns | *** | ns | **** |
|  |  |  |  |  |  |  |  |  |
| Shapiro-Wilk test |  |  |  |  |  |  |  |  |
| W | 0,979 | 0,9716 | 0,8925 | 0,7985 | 0,9324 | 0,6211 | 0,9428 | 0,5192 |
| P value | 0,9579 | 0,91 | 0,2468 | 0,0276 | 0,5381 | 0,0003 | 0,6387 | <0,0001 |
| Passed n | Yes | Yes | Yes | No | Yes | No | Yes | No |
| P value s | ns | ns | ns | * | ns | *** | ns | **** |
|  |  |  |  |  |  |  |  |  |
| Kolmogorov-Smirnov test |  |  |  |  |  |  |  |  |
| KS distan | 0,1314 | 0,131 | 0,1885 | 0,2546 | 0,2132 | 0,44 | 0,154 | 0,3787 |
| P value | >0,1000 | >0,1000 | >0,1000 | >0,1000 | >0,1000 | <0,0001 | >0,1000 | 0,0012 |
| Passed n | Yes | Yes | Yes | Yes | Yes | No | Yes | No |
| P value s | ns | ns | ns | ns | ns | **** | ns | ** |
|  |  |  |  |  |  |  |  |  |
| Number of | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 |

# 7. 2way ANOVA of OF Travelling (primi 5 min) 30-60D intergroup

| | | | | | |
|---|---|---|---|---|---|
| **Table Analyzed** | OF Travelling (primi 5 min)  30-60D | | | | |
| | | | | | |
| **Two-way RM ANOVA** | Matching: Stacked | | | | |
| **Assume sphericity?** | Yes | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Time x Column Factor** | 3,126 | 0,1523 | ns | No | |
| **Time** | 3,600 | 0,0160 | * | Yes | |
| **Column Factor** | 44,22 | <0,0001 | **** | Yes | |
| **Subject** | 33,71 | 0,0208 | * | Yes | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Time x Column Factor** | 1732997 | 3 | 577666 | F (3, 28) = 1,901 | P=0,1523 |
| **Time** | 1995788 | 1 | 1995788 | F (1, 28) = 6,569 | P=0,0160 |
| **Column Factor** | 24517259 | 3 | 8172420 | F (3, 28) = 12,24 | P<0,0001 |
| **Subject** | 18687491 | 28 | 667410 | F (28, 28) = 2,197 | P=0,0208 |
| **Residual** | 8506473 | 28 | 303803 | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of 30** | 1926 | | | | |
| **Mean of 60** | 2279 | | | | |
| **Difference between means** | -353,2 | | | | |
| **SE of difference** | 137,8 | | | | |
| **95% CI of difference** | -635,4 to -70,92 | | | | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Column Factor)** | 4 | | | | |
| **Number of rows (Time)** | 2 | | | | |
| **Number of subjects (Subject)** | 32 | | | | |
| **Number of missing values** | 0 | | | | |

|  | WT-sham 3 | WT-Sham 6 | WT-mTBI 3 | WT-mTBI 6 | APP-Sham | APP-Sham | APP-mTBI 3 | APP-mTBI 6 |
|---|---|---|---|---|---|---|---|---|
| Test for normal distribution |  |  |  |  |  |  |  |  |
| D'Agostino & Pearson test |  |  |  |  |  |  |  |  |
| K2 | 2,934 | 0,1069 | 0,4349 | 0,7351 | 0,4067 | 1,783 | 13,35 | 3,372 |
| P value | 0,2306 | 0,948 | 0,8046 | 0,6924 | 0,816 | 0,41 | 0,0013 | 0,1853 |
| Passed n | Yes | Yes | Yes | Yes | Yes | Yes | No | Yes |
| P value s | ns | ns | ns | ns | ns | ns | ** | ns |
|  |  |  |  |  |  |  |  |  |
| Anderson-Darling test |  |  |  |  |  |  |  |  |
| A2* | 0,3399 | 0,2826 | 0,2311 | 0,2482 | 0,2303 | 0,2363 | 0,8635 | 0,5294 |
| P value | 0,3955 | 0,5347 | 0,7086 | 0,6438 | 0,7115 | 0,6887 | 0,0142 | 0,1186 |
| Passed n | Yes | Yes | Yes | Yes | Yes | Yes | No | Yes |
| P value s | ns | ns | ns | ns | ns | ns | * | ns |
|  |  |  |  |  |  |  |  |  |
| Shapiro-Wilk test |  |  |  |  |  |  |  |  |
| W | 0,9006 | 0,9359 | 0,9478 | 0,9528 | 0,9449 | 0,9406 | 0,7514 | 0,8816 |
| P value | 0,2923 | 0,5716 | 0,6895 | 0,7393 | 0,6599 | 0,6169 | 0,0085 | 0,1951 |
| Passed n | Yes | Yes | Yes | Yes | Yes | Yes | No | Yes |
| P value s | ns | ns | ns | ns | ns | ns | ** | ns |
|  |  |  |  |  |  |  |  |  |
| Kolmogorov-Smirnov test |  |  |  |  |  |  |  |  |
| KS distan | 0,1636 | 0,1689 | 0,1579 | 0,1616 | 0,1452 | 0,1365 | 0,2641 | 0,2617 |
| P value | >0,1000 | >0,1000 | >0,1000 | >0,1000 | >0,1000 | >0,1000 | >0,1000 | >0,1000 |
| Passed n | Yes | Yes | Yes | Yes | Yes | Yes | Yes | Yes |
| P value s | ns | ns | ns | ns | ns | ns | ns | ns |
|  |  |  |  |  |  |  |  |  |
| Number of | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 |

## 8. 2way ANOVA of OFT time in center % primi 10 min 30-60D intergroup

| | | | | | |
|---|---|---|---|---|---|
| **Table Analyzed** | OFT time in center % primi 10 min 30-60D | | | | |
| | | | | | |
| **Two-way RM ANOVA** | Matching: Stacked | | | | |
| **Assume sphericity?** | Yes | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Time x Column Factor** | 0,4184 | 0,9250 | ns | No | |
| **Time** | 0,002467 | 0,9585 | ns | No | |
| **Column Factor** | 40,98 | <0,0001 | **** | Yes | |
| **Subject** | 33,55 | 0,2220 | ns | No | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Time x Column Factor** | 2,867 | 3 | 0,9555 | F (3, 28) = 0,1559 | P=0,9250 |
| **Time** | 0,01690 | 1 | 0,01690 | F (1, 28) = 0,002758 | P=0,9585 |
| **Column Factor** | 280,7 | 3 | 93,58 | F (3, 28) = 11,40 | P<0,0001 |
| **Subject** | 229,9 | 28 | 8,210 | F (28, 28) = 1,340 | P=0,2220 |
| **Residual** | 171,6 | 28 | 6,128 | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of 30** | 7,958 | | | | |
| **Mean of 60** | 7,990 | | | | |
| **Difference between means** | -0,03250 | | | | |
| **SE of difference** | 0,6189 | | | | |
| **95% CI of difference** | -1,300 to 1,235 | | | | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Column Factor)** | 4 | | | | |
| **Number of rows (Time)** | 2 | | | | |
| **Number of subjects (Subject)** | 32 | | | | |
| **Number of missing values** | 0 | | | | |

|  | WT-sham 3 | WT-Sham 6 | WT-mTBI 3 | WT-mTBI 6 | APP-Sham | APP-Sham | APP-mTBI | APP-mTBI 6 |
|---|---|---|---|---|---|---|---|---|
| Test for normal distribution |  |  |  |  |  |  |  |  |
| D'Agostino & Pearson test |  |  |  |  |  |  |  |  |
| K2 | 1,697 | 0,5699 | 2,365 | 1,388 | 1,065 | 2,163 | 1,119 | 7,277 |
| P value | 0,428 | 0,7521 | 0,3065 | 0,4995 | 0,587 | 0,339 | 0,5715 | 0,0263 |
| Passed n | Yes | Yes | Yes | Yes | Yes | Yes | Yes | No |
| P value s | ns | ns | ns | ns | ns | ns | ns | * |
|  |  |  |  |  |  |  |  |  |
| Anderson-Darling test |  |  |  |  |  |  |  |  |
| A2* | 0,3792 | 0,229 | 0,3674 | 0,2693 | 0,2245 | 0,389 | 0,3084 | 0,9561 |
| P value | 0,3113 | 0,7163 | 0,3347 | 0,5714 | 0,7333 | 0,2931 | 0,4775 | 0,0079 |
| Passed n | Yes | Yes | Yes | Yes | Yes | Yes | Yes | No |
| P value s | ns | ns | ns | ns | ns | ns | ns | ** |
|  |  |  |  |  |  |  |  |  |
| Shapiro-Wilk test |  |  |  |  |  |  |  |  |
| W | 0,8997 | 0,9469 | 0,9074 | 0,9279 | 0,943 | 0,9238 | 0,9545 | 0,7445 |
| P value | 0,2873 | 0,6804 | 0,3363 | 0,4971 | 0,6412 | 0,4618 | 0,7563 | 0,0071 |
| Passed n | Yes | Yes | Yes | Yes | Yes | Yes | Yes | No |
| P value s | ns | ns | ns | ns | ns | ns | ns | ** |
|  |  |  |  |  |  |  |  |  |
| Kolmogorov-Smirnov test |  |  |  |  |  |  |  |  |
| KS distan | 0,1956 | 0,1341 | 0,224 | 0,173 | 0,1687 | 0,2182 | 0,1955 | 0,3499 |
| P value | >0,1000 | >0,1000 | >0,1000 | >0,1000 | >0,1000 | >0,1000 | >0,1000 | 0,0046 |
| Passed n | Yes | Yes | Yes | Yes | Yes | Yes | Yes | No |
| P value s | ns | ns | ns | ns | ns | ns | ns | ** |
|  |  |  |  |  |  |  |  |  |
| Number of | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 |

# 9 2way ANOVA of NOR 30-60D 1

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **Within each row, compare columns (simple effects within rows)** | | | | | | | | |
| | | | | | | | | |
| **Number of families** | 2 | | | | | | | |
| **Number of comparisons per family** | 3 | | | | | | | |
| **Alpha** | 0,05 | | | | | | | |
| | | | | | | | | |
| **Dunnett's multiple comparisons test** | Mean Diff, | 95,00% CI of diff, | Below threshold? | Summary | | | | |
| | | | | | | | | |
| **30** | | | | | | | | |
| **WT-sham vs. WT-mTBI** | 0,2100 | -0,01609 to 0,4361 | No | ns | | | | |
| **WT-sham vs. APP-sham** | 0,1082 | -0,1179 to 0,3343 | No | ns | | | | |
| **WT-sham vs. APP-mTBI** | 0,1132 | -0,1129 to 0,3393 | No | ns | | | | |
| | | | | | | | | |
| **60** | | | | | | | | |
| **WT-sham vs. WT-mTBI** | 0,5710 | 0,3448 to 0,7971 | Yes | **** | | | | |
| **WT-sham vs. APP-sham** | 0,1875 | -0,03861 to 0,4136 | No | ns | | | | |
| **WT-sham vs. APP-mTBI** | 0,2401 | 0,01400 to 0,4662 | Yes | * | | | | |
| | | | | | | | | |
| | | | | | | | | |
| **Test details** | Mean 1 | Mean 2 | Mean Diff, | SE of diff, | N1 | N2 | q | DF |
| | | | | | | | | |
| **30** | | | | | | | | |
| **WT-sham vs. WT-mTBI** | 0,3794 | 0,1694 | 0,2100 | 0,09365 | 8 | 8 | 2,243 | 56,00 |
| **WT-sham vs. APP-sham** | 0,3794 | 0,2713 | 0,1082 | 0,09365 | 8 | 8 | 1,155 | 56,00 |
| **WT-sham vs. APP-mTBI** | 0,3794 | 0,2663 | 0,1132 | 0,09365 | 8 | 8 | 1,209 | 56,00 |
| | | | | | | | | |
| **60** | | | | | | | | |
| **WT-sham vs. WT-mTBI** | 0,3963 | -0,1747 | 0,5710 | 0,09365 | 8 | 8 | 6,097 | 56,00 |
| **WT-sham vs. APP-sham** | 0,3963 | 0,2088 | 0,1875 | 0,09365 | 8 | 8 | 2,002 | 56,00 |
| **WT-sham vs. APP-mTBI** | 0,3963 | 0,1561 | 0,2401 | 0,09365 | 8 | 8 | 2,564 | 56,00 |

|  | WT-sham 3 | WT-Sham 6 | WT-mTBI 3 | WT-mTBI 6 | APP-Sham | APP-Sham | APP-mTBI | APP-mTBI 6 |
|---|---|---|---|---|---|---|---|---|
| Test for normal distribution |  |  |  |  |  |  |  |  |
| D'Agostino & Pearson test |  |  |  |  |  |  |  |  |
| K2 | 3,883 | 4,519 | 2,675 | 0,6672 | 7,396 | 3,235 | 0,05592 | 3,365 |
| P value | 0,1435 | 0,1044 | 0,2625 | 0,7163 | 0,0248 | 0,1984 | 0,9724 | 0,1859 |
| Passed n | Yes | Yes | Yes | Yes | No | Yes | Yes | Yes |
| P value s | ns | ns | ns | ns | * | ns | ns | ns |
|  |  |  |  |  |  |  |  |  |
| Anderson-Darling test |  |  |  |  |  |  |  |  |
| A2* | 0,449 | 0,709 | 0,4098 | 0,2534 | 0,5313 | 0,3173 | 0,2808 | 0,3409 |
| P value | 0,2007 | 0,0382 | 0,2573 | 0,6248 | 0,117 | 0,4529 | 0,5391 | 0,3932 |
| Passed n | Yes | No | Yes | Yes | Yes | Yes | Yes | Yes |
| P value s | ns | * | ns | ns | ns | ns | ns | ns |
|  |  |  |  |  |  |  |  |  |
| Shapiro-Wilk test |  |  |  |  |  |  |  |  |
| W | 0,8856 | 0,8181 | 0,8966 | 0,9516 | 0,8657 | 0,9199 | 0,9471 | 0,9151 |
| P value | 0,2127 | 0,0446 | 0,2694 | 0,727 | 0,1367 | 0,429 | 0,6817 | 0,3914 |
| Passed n | Yes | No | Yes | Yes | Yes | Yes | Yes | Yes |
| P value s | ns | * | ns | ns | ns | ns | ns | ns |
|  |  |  |  |  |  |  |  |  |
| Kolmogorov-Smirnov test |  |  |  |  |  |  |  |  |
| KS distan | 0,2393 | 0,2722 | 0,2079 | 0,2159 | 0,24 | 0,1618 | 0,1704 | 0,2065 |
| P value | >0,1000 | 0,0828 | >0,1000 | >0,1000 | >0,1000 | >0,1000 | >0,1000 | >0,1000 |
| Passed n | Yes | Yes | Yes | Yes | Yes | Yes | Yes | Yes |
| P value s | ns | ns | ns | ns | ns | ns | ns | ns |
|  |  |  |  |  |  |  |  |  |
| Number of | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 |

0

## 10 2way ANOVA of NOR 30-60D 24h intergroup

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **Within each row, compare columns (simple effects within rows)** | | | | | | | | |
| | | | | | | | | |
| **Number of families** | 2 | | | | | | | |
| **Number of comparisons per family** | 3 | | | | | | | |
| **Alpha** | 0,05 | | | | | | | |
| | | | | | | | | |
| **Dunnett's multiple comparisons test** | Mean Diff, | 95,00% CI of diff, | Below threshold? | Summary | | | | |
| | | | | | | | | |
| **30** | | | | | | | | |
| **WT-sham vs. WT-mTBI** | 0,1011 | -0,1928 to 0,3950 | No | ns | | | | |
| **WT-sham vs. APP-sham** | -0,02431 | -0,3182 to 0,2696 | No | ns | | | | |
| **WT-sham vs. APP-mTBI** | 0,2557 | -0,03822 to 0,5496 | No | ns | | | | |
| | | | | | | | | |
| **60** | | | | | | | | |
| **WT-sham vs. WT-mTBI** | 0,3446 | 0,05066 to 0,6385 | Yes | * | | | | |
| **WT-sham vs. APP-sham** | 0,08928 | -0,2046 to 0,3832 | No | ns | | | | |
| **WT-sham vs. APP-mTBI** | 0,09365 | -0,2003 to 0,3876 | No | ns | | | | |
| | | | | | | | | |
| | | | | | | | | |
| **Test details** | Mean 1 | Mean 2 | Mean Diff, | SE of diff, | N1 | N2 | q | DF |
| | | | | | | | | |
| **30** | | | | | | | | |
| **WT-sham vs. WT-mTBI** | 0,1594 | 0,05838 | 0,1011 | 0,1217 | 8 | 8 | 0,8303 | 56,00 |
| **WT-sham vs. APP-sham** | 0,1594 | 0,1838 | -0,02431 | 0,1217 | 8 | 8 | 0,1997 | 56,00 |
| **WT-sham vs. APP-mTBI** | 0,1594 | -0,09625 | 0,2557 | 0,1217 | 8 | 8 | 2,101 | 56,00 |
| | | | | | | | | |
| **60** | | | | | | | | |
| **WT-sham vs. WT-mTBI** | 0,2149 | -0,1297 | 0,3446 | 0,1217 | 8 | 8 | 2,831 | 56,00 |
| **WT-sham vs. APP-sham** | 0,2149 | 0,1256 | 0,08928 | 0,1217 | 8 | 8 | 0,7335 | 56,00 |
| **WT-sham vs. APP-mTBI** | 0,2149 | 0,1213 | 0,09365 | 0,1217 | 8 | 8 | 0,7694 | 56,00 |

| | WT-sham 3 | WT-Sham 6 | WT-mTBI 3( | WT-mTBI 6( | APP-Sham | APP-Sham | APP-mTBI 3 | APP-mTBI 6 |
|---|---|---|---|---|---|---|---|---|
| Test for normal distribution | | | | | | | | |
| D'Agostino & Pearson test | | | | | | | | |
| K2 | 1,05 | 1,466 | 0,403 | 0,8877 | 0,4505 | 3,345 | 3,763 | 0,2435 |
| P value | 0,5915 | 0,4805 | 0,8175 | 0,6416 | 0,7983 | 0,1878 | 0,1523 | 0,8854 |
| Passed n | Yes | Yes | Yes | Yes | Yes | Yes | Yes | Yes |
| P value s | ns | ns | ns | ns | ns | ns | ns | ns |
| | | | | | | | | |
| Anderson-Darling test | | | | | | | | |
| A2* | 0,2164 | 0,2732 | 0,236 | 0,3762 | 0,1464 | 0,562 | 0,537 | 0,1336 |
| P value | 0,7631 | 0,5598 | 0,6897 | 0,317 | 0,941 | 0,0982 | 0,1153 | 0,962 |
| Passed n | Yes | Yes | Yes | Yes | Yes | Yes | Yes | Yes |
| P value s | ns | ns | ns | ns | ns | ns | ns | ns |
| | | | | | | | | |
| Shapiro-Wilk test | | | | | | | | |
| W | 0,9471 | 0,9245 | 0,965 | 0,8935 | 0,9753 | 0,873 | 0,878 | 0,9813 |
| P value | 0,6819 | 0,4673 | 0,8561 | 0,2524 | 0,9358 | 0,1611 | 0,1804 | 0,969 |
| Passed n | Yes | Yes | Yes | Yes | Yes | Yes | Yes | Yes |
| P value s | ns | ns | ns | ns | ns | ns | ns | ns |
| | | | | | | | | |
| Kolmogorov-Smirnov test | | | | | | | | |
| KS distan | 0,1428 | 0,1542 | 0,1764 | 0,2053 | 0,1216 | 0,2496 | 0,2726 | 0,1151 |
| P value | >0,1000 | >0,1000 | >0,1000 | >0,1000 | >0,1000 | >0,1000 | 0,0818 | >0,1000 |
| Passed n | Yes | Yes | Yes | Yes | Yes | Yes | Yes | Yes |
| P value s | ns | ns | ns | ns | ns | ns | ns | ns |
| | | | | | | | | |
| Number of | 8 | 8 | 8 | 8 | 8 | 8 | 8 | 8 |

## 2way ANOVA of Ab1-42 cortex

| Table Analyzed | Ab1-42 cortex | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 47,55 | 0,0015 | ** | Yes | |
| Injury | 2,382 | 0,3213 | ns | No | |
| Genotype | 33,02 | 0,0043 | ** | Yes | |
| | | | | | |
| ANOVA table | SS | DF | MS | F (DFn, DFd) | P value |
| Interaction | 0,1323 | 1 | 0,1323 | F (1, 8) = 22.31 | P=0.0015 |
| Injury | 0,006627 | 1 | 0,006627 | F (1, 8) = 1.118 | P=0.3213 |
| Genotype | 0,09188 | 1 | 0,09188 | F (1, 8) = 15.49 | P=0.0043 |
| Residual | 0,04744 | 8 | 0,005930 | | |
| | | | | | |
| Difference between column means | | | | | |
| Mean of WT | 0,4658 | | | | |
| Mean of APP-SWE | 0,6408 | | | | |
| Difference between means | -0,1750 | | | | |
| SE of difference | 0,04446 | | | | |
| 95% CI of difference | -0.2775 to -0.07247 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Mean of Sham | 0,5298 | | | | |
| Mean of mTBI | 0,5768 | | | | |
| Difference between means | -0,04700 | | | | |
| SE of difference | 0,04446 | | | | |
| 95% CI of difference | -0.1495 to 0.05553 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | 0,03500 | | | | |
| Mean diff, A2 - B2 | -0,3850 | | | | |
| (A1 -B1) - (A2 - B2) | 0,4200 | | | | |
| 95% CI of difference | 0.2149 to 0.6251 | | | | |
| (B1 - A1) - (B2 - A2) | -0,4200 | | | | |
| 95% CI of difference | -0.6251 to -0.2149 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 3,171 | 0,2049 | Yes | ns | |
| Anderson-Darling (A2*) | 0,5666 | 0,1123 | Yes | ns | |
| Shapiro-Wilk (W) | 0,9184 | 0,2730 | Yes | ns | |
| Kolmogorov-Smirnov (distance) | 0,1975 | 0,1000 | Yes | ns | |
| | | | | | |
| Data summary | | | | | |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| **Number of columns (Genotype)** | 2 |  |  |  |  |
| **Number of rows (Injury)** | 2 |  |  |  |  |
| **Number of values** | 12 |  |  |  |  |

# 2way ANOVA of Ab1-42 hipp

| Table Analyzed | Ab1-42 hipp | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 18,52 | 0,0587 | ns | No | |
| Injury | 3,936 | 0,3395 | ns | No | |
| Genotype | 47,02 | 0,0080 | ** | Yes | |
| | | | | | |
| ANOVA table | SS | DF | MS | F (DFn, DFd) | P value |
| Interaction | 0,01031 | 1 | 0,01031 | F (1, 8) = 4.853 | P=0.0587 |
| Injury | 0,002192 | 1 | 0,002192 | F (1, 8) = 1.032 | P=0.3395 |
| Genotype | 0,02619 | 1 | 0,02619 | F (1, 8) = 12.32 | P=0.0080 |
| Residual | 0,01700 | 8 | 0,002125 | | |
| | | | | | |
| Difference between column means | | | | | |
| Mean of WT | 0,1922 | | | | |
| Mean of APP-SWE | 0,09873 | | | | |
| Difference between means | 0,09343 | | | | |
| SE of difference | 0,02662 | | | | |
| 95% CI of difference | 0.03205 to 0.1548 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Mean of Sham | 0,1319 | | | | |
| Mean of mTBI | 0,1590 | | | | |
| Difference between means | -0,02703 | | | | |
| SE of difference | 0,02662 | | | | |
| 95% CI of difference | -0.08841 to 0.03435 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | 0,03480 | | | | |
| Mean diff, A2 - B2 | 0,1521 | | | | |
| (A1 -B1) - (A2 - B2) | -0,1173 | | | | |
| 95% CI of difference | -0.2400 to 0.005492 | | | | |
| (B1 - A1) - (B2 - A2) | 0,1173 | | | | |
| 95% CI of difference | -0.005492 to 0.2400 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 0,3082 | 0,8572 | Yes | ns | |
| Anderson-Darling (A2*) | 0,2616 | 0,6380 | Yes | ns | |
| Shapiro-Wilk (W) | 0,9561 | 0,7265 | Yes | ns | |
| Kolmogorov-Smirnov (distance) | 0,1464 | 0,1000 | Yes | ns | |
| | | | | | |
| Data summary | | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |
| **Number of values** | 12 | | | | |

# 2way ANOVA of Ab1-40 cortex

| Table Analyzed | Ab1-40 cortex | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 24,85 | 0,0661 | ns | No | |
| Injury | 16,97 | 0,1168 | ns | No | |
| Genotype | 14,25 | 0,1458 | ns | No | |
| | | | | | |
| ANOVA table | SS | DF | MS | F (DFn, DFd) | P value |
| Interaction | 0,02162 | 1 | 0,02162 | F (1, 8) = 4.526 | P=0.0661 |
| Injury | 0,01477 | 1 | 0,01477 | F (1, 8) = 3.091 | P=0.1168 |
| Genotype | 0,01240 | 1 | 0,01240 | F (1, 8) = 2.596 | P=0.1458 |
| Residual | 0,03822 | 8 | 0,004778 | | |
| | | | | | |
| Difference between column means | | | | | |
| Mean of WT | 0,1435 | | | | |
| Mean of APP-SWE | 0,07917 | | | | |
| Difference between means | 0,06430 | | | | |
| SE of difference | 0,03991 | | | | |
| 95% CI of difference | -0.02773 to 0.1563 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Mean of Sham | 0,1464 | | | | |
| Mean of mTBI | 0,07623 | | | | |
| Difference between means | 0,07017 | | | | |
| SE of difference | 0,03991 | | | | |
| 95% CI of difference | -0.02186 to 0.1622 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | 0,1492 | | | | |
| Mean diff, A2 - B2 | -0,02060 | | | | |
| (A1 -B1) - (A2 - B2) | 0,1698 | | | | |
| 95% CI of difference | -0.01426 to 0.3539 | | | | |
| (B1 - A1) - (B2 - A2) | -0,1698 | | | | |
| 95% CI of difference | -0.3539 to 0.01426 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 7,321 | 0,0257 | No | * | |
| Anderson-Darling (A2*) | 0,9416 | 0,0113 | No | * | |
| Shapiro-Wilk (W) | 0,8396 | 0,0274 | No | * | |
| Kolmogorov-Smirnov (distance) | 0,2873 | 0,0071 | No | ** | |
| | | | | | |
| Data summary | | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |
| **Number of values** | 12 | | | | |

# 2way ANOVA of Ab1-40 hipp

| Table Analyzed | Ab1-40 hipp | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 2,414 | 0,6086 | ns | No | |
| **Injury** | 13,08 | 0,2499 | ns | No | |
| **Genotype** | 16,50 | 0,2011 | ns | No | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 0,0005575 | 1 | 0,0005575 | F (1, 8) = 0.2840 | P=0.6086 |
| **Injury** | 0,003021 | 1 | 0,003021 | F (1, 8) = 1.539 | P=0.2499 |
| **Genotype** | 0,003809 | 1 | 0,003809 | F (1, 8) = 1.940 | P=0.2011 |
| **Residual** | 0,01571 | 8 | 0,001963 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Mean of WT** | 0,06405 | | | | |
| **Mean of APP-SWE** | 0,02842 | | | | |
| **Difference between means** | 0,03563 | | | | |
| **SE of difference** | 0,02558 | | | | |
| **95% CI of difference** | -0.02336 to 0.09462 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of Sham** | 0,06210 | | | | |
| **Mean of mTBI** | 0,03037 | | | | |
| **Difference between means** | 0,03173 | | | | |
| **SE of difference** | 0,02558 | | | | |
| **95% CI of difference** | -0.02726 to 0.09072 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | 0,04927 | | | | |
| **Mean diff, A2 - B2** | 0,02200 | | | | |
| **(A1 -B1) - (A2 - B2)** | 0,02726 | | | | |
| **95% CI of difference** | -0.09072 to 0.1452 | | | | |
| **(B1 - A1) - (B2 - A2)** | -0,02726 | | | | |
| **95% CI of difference** | -0.1452 to 0.09072 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 5,442 | 0,0658 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,3788 | 0,3464 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,9146 | 0,2446 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1564 | 0,1000 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| **Number of columns (Genotype)** | 2 |  |  |  |  |
| **Number of rows (Injury)** | 2 |  |  |  |  |
| **Number of values** | 12 |  |  |  |  |

## 2way ANOVA of BACE1 cortex

| Table Analyzed | BACE1 cortex | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 16,15 | 0,0462 | * | Yes | |
| Injury | 10,44 | 0,1005 | ns | No | |
| Genotype | 13,06 | 0,0694 | ns | No | |
| | | | | | |
| ANOVA table | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| Interaction | 1,513 | 1 | 1,513 | F (1, 14) = 4.783 | P=0.0462 |
| Injury | 0,9778 | 1 | 0,9778 | F (1, 14) = 3.092 | P=0.1005 |
| Genotype | 1,222 | 1 | 1,222 | F (1, 14) = 3.866 | P=0.0694 |
| Residual | 4,427 | 14 | 0,3162 | | |
| | | | | | |
| Difference between column means | | | | | |
| Predicted (LS) mean of WT | 0,9398 | | | | |
| Predicted (LS) mean of APP-SWE | 1,493 | | | | |
| Difference between predicted means | -0,5528 | | | | |
| SE of difference | 0,2812 | | | | |
| 95% CI of difference | -1.156 to 0.05022 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Predicted (LS) mean of Sham | 0,9689 | | | | |
| Predicted (LS) mean of mTBI | 1,463 | | | | |
| Difference between predicted means | -0,4944 | | | | |
| SE of difference | 0,2812 | | | | |
| 95% CI of difference | -1.097 to 0.1086 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | 0,06211 | | | | |
| Mean diff, A2 - B2 | -1,168 | | | | |
| (A1 -B1) - (A2 - B2) | 1,230 | | | | |
| 95% CI of difference | 0.02378 to 2.436 | | | | |
| (B1 - A1) - (B2 - A2) | -1,230 | | | | |
| 95% CI of difference | -2.436 to -0.02378 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 3,940 | 0,1394 | Yes | ns | |
| Anderson-Darling (A2*) | 1,272 | 0,0019 | No | ** | |
| Shapiro-Wilk (W) | 0,8560 | 0,0106 | No | * | |
| Kolmogorov-Smirnov (distance) | 0,2341 | 0,0102 | No | * | |
| | | | | | |
| Data summary | | | | | |
| Number of columns (Genotype) | 2 | | | | |
| Number of rows (Injury) | 2 | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of values** | 18 | | | | |

## 2way ANOVA of BACE1 hipp

| Table Analyzed | BACE1 hipp | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 2,128 | 0,4547 | ns | No | |
| **Injury** | 9,010 | 0,1310 | ns | No | |
| **Genotype** | 2,749 | 0,3963 | ns | No | |
| | | | | | |
| **ANOVA table** | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 0,08917 | 1 | 0,08917 | F (1, 24) = 0.5775 | P=0.4547 |
| **Injury** | 0,3775 | 1 | 0,3775 | F (1, 24) = 2.445 | P=0.1310 |
| **Genotype** | 0,1152 | 1 | 0,1152 | F (1, 24) = 0.7459 | P=0.3963 |
| **Residual** | 3,706 | 24 | 0,1544 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Predicted (LS) mean of WT** | 0,8088 | | | | |
| **Predicted (LS) mean of APP-SWE** | 0,6666 | | | | |
| **Difference between predicted means** | 0,1422 | | | | |
| **SE of difference** | 0,1646 | | | | |
| **95% CI of difference** | -0.1976 to 0.4819 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Predicted (LS) mean of Sham** | 0,8664 | | | | |
| **Predicted (LS) mean of mTBI** | 0,6090 | | | | |
| **Difference between predicted means** | 0,2574 | | | | |
| **SE of difference** | 0,1646 | | | | |
| **95% CI of difference** | -0.08235 to 0.5971 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | 0,2673 | | | | |
| **Mean diff, A2 - B2** | 0,01707 | | | | |
| **(A1 -B1) - (A2 - B2)** | 0,2502 | | | | |
| **95% CI of difference** | -0.4293 to 0.9297 | | | | |
| **(B1 - A1) - (B2 - A2)** | -0,2502 | | | | |
| **95% CI of difference** | -0.9297 to 0.4293 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 3,096 | 0,2126 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,5180 | 0,1726 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,9512 | 0,2120 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1411 | 0,1000 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| **Number of values** | 28 |  |  |  |  |

# 2way ANOVA of BACE2 cortex

| **Table Analyzed** | **BACE2 cortex** | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 2,699 | 0,4603 | ns | No | |
| **Injury** | 11,88 | 0,1319 | ns | No | |
| **Genotype** | 1,808 | 0,5445 | ns | No | |
| | | | | | |
| **ANOVA table** | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 0,2239 | 1 | 0,2239 | F (1, 16) = 0.5725 | P=0.4603 |
| **Injury** | 0,9856 | 1 | 0,9856 | F (1, 16) = 2.521 | P=0.1319 |
| **Genotype** | 0,1500 | 1 | 0,1500 | F (1, 16) = 0.3835 | P=0.5445 |
| **Residual** | 6,257 | 16 | 0,3910 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Predicted (LS) mean of WT** | 1,127 | | | | |
| **Predicted (LS) mean of APP-SWE** | 1,316 | | | | |
| **Difference between predicted means** | -0,1890 | | | | |
| **SE of difference** | 0,3051 | | | | |
| **95% CI of difference** | -0.8358 to 0.4579 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Predicted (LS) mean of Sham** | 0,9790 | | | | |
| **Predicted (LS) mean of mTBI** | 1,463 | | | | |
| **Difference between predicted means** | -0,4844 | | | | |
| **SE of difference** | 0,3051 | | | | |
| **95% CI of difference** | -1.131 to 0.1624 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | 0,04193 | | | | |
| **Mean diff, A2 - B2** | -0,4198 | | | | |
| **(A1 -B1) - (A2 - B2)** | 0,4618 | | | | |
| **95% CI of difference** | -0.8319 to 1.755 | | | | |
| **(B1 - A1) - (B2 - A2)** | -0,4618 | | | | |
| **95% CI of difference** | -1.755 to 0.8319 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 0,7414 | 0,6903 | Yes | ns | |
| **Anderson-Darling (A2*)** | 1,333 | 0,0014 | No | ** | |
| **Shapiro-Wilk (W)** | 0,8651 | 0,0096 | No | ** | |
| **Kolmogorov-Smirnov (distance)** | 0,2243 | 0,0096 | No | ** | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| **Number of values** | 20 |  |  |  |  |

2way ANOVA of BACE2 hipp

| Table Analyzed | BACE2 hipp | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 0,2423 | 0,7556 | ns | No | |
| Injury | 7,805 | 0,0859 | ns | No | |
| Genotype | 27,70 | 0,0024 | ** | Yes | |
| | | | | | |
| ANOVA table | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| Interaction | 0,01819 | 1 | 0,01819 | F (1, 26) = 0.09898 | P=0.7556 |
| Injury | 0,5859 | 1 | 0,5859 | F (1, 26) = 3.188 | P=0.0859 |
| Genotype | 2,079 | 1 | 2,079 | F (1, 26) = 11.31 | P=0.0024 |
| Residual | 4,778 | 26 | 0,1838 | | |
| | | | | | |
| Difference between column means | | | | | |
| Predicted (LS) mean of WT | 0,8142 | | | | |
| Predicted (LS) mean of APP-SWE | 1,409 | | | | |
| Difference between predicted means | -0,5953 | | | | |
| SE of difference | 0,1770 | | | | |
| 95% CI of difference | -0.9591 to -0.2315 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Predicted (LS) mean of Sham | 1,270 | | | | |
| Predicted (LS) mean of mTBI | 0,9538 | | | | |
| Difference between predicted means | 0,3160 | | | | |
| SE of difference | 0,1770 | | | | |
| 95% CI of difference | -0.04780 to 0.6798 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | -0,5397 | | | | |
| Mean diff, A2 - B2 | -0,6510 | | | | |
| (A1 -B1) - (A2 - B2) | 0,1114 | | | | |
| 95% CI of difference | -0.6162 to 0.8390 | | | | |
| (B1 - A1) - (B2 - A2) | -0,1114 | | | | |
| 95% CI of difference | -0.8390 to 0.6162 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 7,696 | 0,0213 | No | * | |
| Anderson-Darling (A2*) | 0,7163 | 0,0551 | Yes | ns | |
| Shapiro-Wilk (W) | 0,9356 | 0,0691 | Yes | ns | |
| Kolmogorov-Smirnov (distance) | 0,1419 | 0,1000 | Yes | ns | |
| | | | | | |
| Data summary | | | | | |
| Number of columns (Genotype) | 2 | | | | |
| Number of rows (Injury) | 2 | | | | |
| Number of values | 30 | | | | |

# 2way ANOVA of IFN-g plasma

| **Table Analyzed** | **IFN-g plasma** | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 0,6451 | 0,4686 | ns | No | |
| **Injury** | 10,40 | 0,0118 | * | Yes | |
| **Genotype** | 74,26 | <0.0001 | **** | Yes | |
| | | | | | |
| **ANOVA table** | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 1,842E-05 | 1 | 1,842E-05 | F (1, 11) = 0.5635 | P=0.4686 |
| **Injury** | 0,0002968 | 1 | 0,0002968 | F (1, 11) = 9.081 | P=0.0118 |
| **Genotype** | 0,002120 | 1 | 0,002120 | F (1, 11) = 64.86 | P<0.0001 |
| **Residual** | 0,0003595 | 11 | 3,268E-05 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Predicted (LS) mean of WT** | 0,02422 | | | | |
| **Predicted (LS) mean of APP-SWE** | 0,04854 | | | | |
| **Difference between predicted means** | -0,02433 | | | | |
| **SE of difference** | 0,003021 | | | | |
| **95% CI of difference** | -0.03098 to -0.01768 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Predicted (LS) mean of Sham** | 0,03183 | | | | |
| **Predicted (LS) mean of mTBI** | 0,04093 | | | | |
| **Difference between predicted means** | -0,009103 | | | | |
| **SE of difference** | 0,003021 | | | | |
| **95% CI of difference** | -0.01575 to -0.002454 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | -0,02660 | | | | |
| **Mean diff, A2 - B2** | -0,02206 | | | | |
| **(A1 -B1) - (A2 - B2)** | -0,004535 | | | | |
| **95% CI of difference** | -0.01783 to 0.008762 | | | | |
| **(B1 - A1) - (B2 - A2)** | 0,004535 | | | | |
| **95% CI of difference** | -0.008762 to 0.01783 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 0,1052 | 0,9488 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,1947 | 0,8697 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,9694 | 0,8491 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1098 | 0,1000 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |
| **Number of values** | 15 | | | | |

# 2way ANOVA of IL-17A plasma

| **Table Analyzed** | **IL-17A plasma** | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 17,26 | 0,0050 | ** | Yes | |
| **Injury** | 50,06 | 0,0001 | *** | Yes | |
| **Genotype** | 24,08 | 0,0018 | ** | Yes | |
| | | | | | |
| **ANOVA table** | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 0,09225 | 1 | 0,09225 | F (1, 9) = 13.59 | P=0.0050 |
| **Injury** | 0,2675 | 1 | 0,2675 | F (1, 9) = 39.42 | P=0.0001 |
| **Genotype** | 0,1287 | 1 | 0,1287 | F (1, 9) = 18.96 | P=0.0018 |
| **Residual** | 0,06107 | 9 | 0,006786 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Predicted (LS) mean of WT** | 0,7767 | | | | |
| **Predicted (LS) mean of APP-SWE** | 0,9772 | | | | |
| **Difference between predicted means** | -0,2005 | | | | |
| **SE of difference** | 0,04605 | | | | |
| **95% CI of difference** | -0.3047 to -0.09637 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Predicted (LS) mean of Sham** | 0,7324 | | | | |
| **Predicted (LS) mean of mTBI** | 1,022 | | | | |
| **Difference between predicted means** | -0,2891 | | | | |
| **SE of difference** | 0,04605 | | | | |
| **95% CI of difference** | -0.3933 to -0.1850 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | -0,03075 | | | | |
| **Mean diff, A2 - B2** | -0,3703 | | | | |
| **(A1 -B1) - (A2 - B2)** | 0,3396 | | | | |
| **95% CI of difference** | 0.1312 to 0.5479 | | | | |
| **(B1 - A1) - (B2 - A2)** | -0,3396 | | | | |
| **95% CI of difference** | -0.5479 to -0.1312 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 0,7892 | 0,6740 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,2879 | 0,5598 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,9582 | 0,7253 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1595 | 0,1000 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| **Number of values** | 13 |  |  |  |  |

# 2way ANOVA of IL-1beta plasma

| **Table Analyzed** | **IL-1beta plasma** | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 0,7104 | 0,3525 | ns | No | |
| **Injury** | 46,99 | <0.0001 | **** | Yes | |
| **Genotype** | 48,81 | <0.0001 | **** | Yes | |
| | | | | | |
| **ANOVA table** | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 0,0003415 | 1 | 0,0003415 | F (1, 11) = 0.9424 | P=0.3525 |
| **Injury** | 0,02258 | 1 | 0,02258 | F (1, 11) = 62.33 | P<0.0001 |
| **Genotype** | 0,02346 | 1 | 0,02346 | F (1, 11) = 64.75 | P<0.0001 |
| **Residual** | 0,003986 | 11 | 0,0003623 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Predicted (LS) mean of WT** | 0,06075 | | | | |
| **Predicted (LS) mean of APP-SWE** | 0,1417 | | | | |
| **Difference between predicted means** | -0,08093 | | | | |
| **SE of difference** | 0,01006 | | | | |
| **95% CI of difference** | -0.1031 to -0.05879 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Predicted (LS) mean of Sham** | 0,06151 | | | | |
| **Predicted (LS) mean of mTBI** | 0,1409 | | | | |
| **Difference between predicted means** | -0,07940 | | | | |
| **SE of difference** | 0,01006 | | | | |
| **95% CI of difference** | -0.1015 to -0.05727 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | -0,09069 | | | | |
| **Mean diff, A2 - B2** | -0,07117 | | | | |
| **(A1 -B1) - (A2 - B2)** | -0,01953 | | | | |
| **95% CI of difference** | -0.06380 to 0.02475 | | | | |
| **(B1 - A1) - (B2 - A2)** | 0,01953 | | | | |
| **95% CI of difference** | -0.02475 to 0.06380 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 1,374 | 0,5030 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,2769 | 0,6015 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,9733 | 0,9039 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1324 | 0,1000 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |
| **Number of values** | 15 | | | | |

2way ANOVA of TNF-a plasma

| Table Analyzed | TNF-a plasma | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 8,830 | 0,1336 | ns | No | |
| Injury | 50,42 | 0,0023 | ** | Yes | |
| Genotype | 6,555 | 0,1909 | ns | No | |
| | | | | | |
| ANOVA table | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| Interaction | 0,008536 | 1 | 0,008536 | F (1, 12) = 2.589 | P=0.1336 |
| Injury | 0,04874 | 1 | 0,04874 | F (1, 12) = 14.78 | P=0.0023 |
| Genotype | 0,006336 | 1 | 0,006336 | F (1, 12) = 1.922 | P=0.1909 |
| Residual | 0,03956 | 12 | 0,003297 | | |
| | | | | | |
| Difference between column means | | | | | |
| Predicted (LS) mean of WT | 0,5189 | | | | |
| Predicted (LS) mean of APP-SWE | 0,5594 | | | | |
| Difference between predicted means | -0,04046 | | | | |
| SE of difference | 0,02918 | | | | |
| 95% CI of difference | -0.1040 to 0.02313 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Predicted (LS) mean of Sham | 0,4830 | | | | |
| Predicted (LS) mean of mTBI | 0,5953 | | | | |
| Difference between predicted means | -0,1122 | | | | |
| SE of difference | 0,02918 | | | | |
| 95% CI of difference | -0.1758 to -0.04862 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | -0,08742 | | | | |
| Mean diff, A2 - B2 | 0,006500 | | | | |
| (A1 -B1) - (A2 - B2) | -0,09392 | | | | |
| 95% CI of difference | -0.2211 to 0.03326 | | | | |
| (B1 - A1) - (B2 - A2) | 0,09392 | | | | |
| 95% CI of difference | -0.03326 to 0.2211 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 4,182 | 0,1236 | Yes | ns | |
| Anderson-Darling (A2*) | 0,6144 | 0,0906 | Yes | ns | |
| Shapiro-Wilk (W) | 0,9284 | 0,2298 | Yes | ns | |
| Kolmogorov-Smirnov (distance) | 0,2001 | 0,0864 | Yes | ns | |
| | | | | | |
| Data summary | | | | | |
| Number of columns (Genotype) | 2 | | | | |
| Number of rows (Injury) | 2 | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of values** | 16 | | | | |

## 2way ANOVA of IL22 plasma

| **Table Analyzed** | **IL22 plasma** | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 26,37 | 0,0717 | ns | No | |
| **Injury** | 0,8996 | 0,7199 | ns | No | |
| **Genotype** | 0,9514 | 0,7123 | ns | No | |
| | | | | | |
| **ANOVA table** | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 0,05500 | 1 | 0,05500 | F (1, 11) = 3.970 | P=0.0717 |
| **Injury** | 0,001876 | 1 | 0,001876 | F (1, 11) = 0.1354 | P=0.7199 |
| **Genotype** | 0,001984 | 1 | 0,001984 | F (1, 11) = 0.1432 | P=0.7123 |
| **Residual** | 0,1524 | 11 | 0,01385 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Predicted (LS) mean of WT** | 0,1776 | | | | |
| **Predicted (LS) mean of APP-SWE** | 0,2011 | | | | |
| **Difference between predicted means** | -0,02354 | | | | |
| **SE of difference** | 0,06219 | | | | |
| **95% CI of difference** | -0.1604 to 0.1133 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Predicted (LS) mean of Sham** | 0,1779 | | | | |
| **Predicted (LS) mean of mTBI** | 0,2008 | | | | |
| **Difference between predicted means** | -0,02289 | | | | |
| **SE of difference** | 0,06219 | | | | |
| **95% CI of difference** | -0.1598 to 0.1140 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | -0,1475 | | | | |
| **Mean diff, A2 - B2** | 0,1004 | | | | |
| **(A1 -B1) - (A2 - B2)** | -0,2478 | | | | |
| **95% CI of difference** | -0.5216 to 0.02592 | | | | |
| **(B1 - A1) - (B2 - A2)** | 0,2478 | | | | |
| **95% CI of difference** | -0.02592 to 0.5216 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 1,408 | 0,4945 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,2220 | 0,7911 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,9642 | 0,7643 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1292 | 0,1000 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| **Number of values** | 15 |  |  |  |  |

## 2way ANOVA of IL6 plasma

| Table Analyzed | IL6 plasma | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 37,35 | 0,0449 | * | Yes | |
| **Injury** | 0,2756 | 0,8460 | ns | No | |
| **Genotype** | 1,308 | 0,6735 | ns | No | |
| | | | | | |
| **ANOVA table** | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 0,0003779 | 1 | 0,0003779 | F (1, 9) = 5.416 | P=0.0449 |
| **Injury** | 2,788E-06 | 1 | 2,788E-06 | F (1, 9) = 0.03996 | P=0.8460 |
| **Genotype** | 1,323E-05 | 1 | 1,323E-05 | F (1, 9) = 0.1896 | P=0.6735 |
| **Residual** | 0,0006279 | 9 | 6,977E-05 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Predicted (LS) mean of WT** | 0,01843 | | | | |
| **Predicted (LS) mean of APP-SWE** | 0,02047 | | | | |
| **Difference between predicted means** | -0,002033 | | | | |
| **SE of difference** | 0,004669 | | | | |
| **95% CI of difference** | -0.01260 to 0.008529 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Predicted (LS) mean of Sham** | 0,01898 | | | | |
| **Predicted (LS) mean of mTBI** | 0,01992 | | | | |
| **Difference between predicted means** | -0,0009333 | | | | |
| **SE of difference** | 0,004669 | | | | |
| **95% CI of difference** | -0.01150 to 0.009629 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | -0,01290 | | | | |
| **Mean diff, A2 - B2** | 0,008833 | | | | |
| **(A1 -B1) - (A2 - B2)** | -0,02173 | | | | |
| **95% CI of difference** | -0.04286 to -0.0006081 | | | | |
| **(B1 - A1) - (B2 - A2)** | 0,02173 | | | | |
| **95% CI of difference** | 0.0006081 to 0.04286 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 0,3931 | 0,8216 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,3098 | 0,5117 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,9539 | 0,6578 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1620 | 0,1000 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |
| **Number of values** | 13 | | | | |

## 2way ANOVA of AEA pmol:g cortex

| Table Analyzed | AEA pmol/g cortex | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 2,322 | 0,3989 | ns | No | |
| Injury | 20,71 | 0,0198 | * | Yes | |
| Genotype | 27,53 | 0,0088 | ** | Yes | |
| | | | | | |
| ANOVA table | SS | DF | MS | F (DFn, DFd) | P value |
| Interaction | 489,0 | 1 | 489,0 | F (1, 16) = 0.7514 | P=0.3989 |
| Injury | 4360 | 1 | 4360 | F (1, 16) = 6.701 | P=0.0198 |
| Genotype | 5798 | 1 | 5798 | F (1, 16) = 8.910 | P=0.0088 |
| Residual | 10412 | 16 | 650,7 | | |
| | | | | | |
| Difference between column means | | | | | |
| Mean of WT | 43,40 | | | | |
| Mean of APP-SWE | 77,45 | | | | |
| Difference between means | -34,05 | | | | |
| SE of difference | 11,41 | | | | |
| 95% CI of difference | -58.24 to -9.869 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Mean of Sham | 75,19 | | | | |
| Mean of mTBI | 45,66 | | | | |
| Difference between means | 29,53 | | | | |
| SE of difference | 11,41 | | | | |
| 95% CI of difference | 5.347 to 53.72 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | -43,94 | | | | |
| Mean diff, A2 - B2 | -24,16 | | | | |
| (A1 -B1) - (A2 - B2) | -19,78 | | | | |
| 95% CI of difference | -68.15 to 28.59 | | | | |
| (B1 - A1) - (B2 - A2) | 19,78 | | | | |
| 95% CI of difference | -28.59 to 68.15 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 12,86 | 0,0016 | No | ** | |
| Anderson-Darling (A2*) | 1,326 | 0,0014 | No | ** | |
| Shapiro-Wilk (W) | 0,8237 | 0,0020 | No | ** | |
| Kolmogorov-Smirnov (distance) | 0,2228 | 0,0104 | No | * | |
| | | | | | |
| Data summary | | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |
| **Number of values** | 20 | | | | |

## 2way ANOVA of 2-AG pmol:mg cortex

| Table Analyzed | 2-AG pmol/mg cortex | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 0,2764 | 0,7197 | ns | No | |
| Injury | 1,754 | 0,3711 | ns | No | |
| Genotype | 64,83 | <0.0001 | **** | Yes | |
| | | | | | |
| ANOVA table | SS | DF | MS | F (DFn, DFd) | P value |
| Interaction | 0,1248 | 1 | 0,1248 | F (1, 16) = 0.1334 | P=0.7197 |
| Injury | 0,7920 | 1 | 0,7920 | F (1, 16) = 0.8468 | P=0.3711 |
| Genotype | 29,28 | 1 | 29,28 | F (1, 16) = 31.31 | P<0.0001 |
| Residual | 14,97 | 16 | 0,9353 | | |
| | | | | | |
| Difference between column means | | | | | |
| Mean of WT | 0,6600 | | | | |
| Mean of APP-SWE | 3,080 | | | | |
| Difference between means | -2,420 | | | | |
| SE of difference | 0,4325 | | | | |
| 95% CI of difference | -3.337 to -1.503 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Mean of Sham | 2,069 | | | | |
| Mean of mTBI | 1,671 | | | | |
| Difference between means | 0,3980 | | | | |
| SE of difference | 0,4325 | | | | |
| 95% CI of difference | -0.5189 to 1.315 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | -2,262 | | | | |
| Mean diff, A2 - B2 | -2,578 | | | | |
| (A1 -B1) - (A2 - B2) | 0,3160 | | | | |
| 95% CI of difference | -1.518 to 2.150 | | | | |
| (B1 - A1) - (B2 - A2) | -0,3160 | | | | |
| 95% CI of difference | -2.150 to 1.518 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 7,349 | 0,0254 | No | * | |
| Anderson-Darling (A2*) | 0,7249 | 0,0492 | No | * | |
| Shapiro-Wilk (W) | 0,9030 | 0,0470 | No | * | |
| Kolmogorov-Smirnov (distance) | 0,1813 | 0,0837 | Yes | ns | |
| | | | | | |
| Data summary | | | | | |
| Number of columns (Genotype) | 2 | | | | |
| Number of rows (Injury) | 2 | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of values** | 20 | | | | |

## 2way ANOVA of PEA pmol:mg cortex

| Table Analyzed | PEA pmol/mg cortex | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 1,460 | 0,5533 | ns | No | |
| Injury | 12,58 | 0,0945 | ns | No | |
| Genotype | 22,24 | 0,0311 | * | Yes | |
| | | | | | |
| ANOVA table | SS | DF | MS | F (DFn, DFd) | P value |
| Interaction | 0,004805 | 1 | 0,004805 | F (1, 16) = 0.3667 | P=0.5533 |
| Injury | 0,04141 | 1 | 0,04141 | F (1, 16) = 3.159 | P=0.0945 |
| Genotype | 0,07321 | 1 | 0,07321 | F (1, 16) = 5.586 | P=0.0311 |
| Residual | 0,2097 | 16 | 0,01311 | | |
| | | | | | |
| Difference between column means | | | | | |
| Mean of WT | 0,3710 | | | | |
| Mean of APP-SWE | 0,2500 | | | | |
| Difference between means | 0,1210 | | | | |
| SE of difference | 0,05120 | | | | |
| 95% CI of difference | 0.01247 to 0.2295 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Mean of Sham | 0,3560 | | | | |
| Mean of mTBI | 0,2650 | | | | |
| Difference between means | 0,09100 | | | | |
| SE of difference | 0,05120 | | | | |
| 95% CI of difference | -0.01753 to 0.1995 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | 0,1520 | | | | |
| Mean diff, A2 - B2 | 0,09000 | | | | |
| (A1 -B1) - (A2 - B2) | 0,06200 | | | | |
| 95% CI of difference | -0.1551 to 0.2791 | | | | |
| (B1 - A1) - (B2 - A2) | -0,06200 | | | | |
| 95% CI of difference | -0.2791 to 0.1551 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 13,13 | 0,0014 | No | ** | |
| Anderson-Darling (A2*) | 0,9306 | 0,0145 | No | * | |
| Shapiro-Wilk (W) | 0,8671 | 0,0105 | No | * | |
| Kolmogorov-Smirnov (distance) | 0,2121 | 0,0188 | No | * | |
| | | | | | |
| Data summary | | | | | |
| Number of columns (Genotype) | 2 | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of rows (Injury)** | 2 | | | | |
| **Number of values** | 20 | | | | |

## 2way ANOVA of OEA pmol:mg cortex

| Table Analyzed | OEA pmol/mg cortex | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 5,327 | 0,1518 | ns | No | |
| Injury | 9,109 | 0,0666 | ns | No | |
| Genotype | 47,94 | 0,0004 | *** | Yes | |
| | | | | | |
| ANOVA table | SS | DF | MS | F (DFn, DFd) | P value |
| Interaction | 0,02113 | 1 | 0,02113 | F (1, 16) = 2.265 | P=0.1518 |
| Injury | 0,03613 | 1 | 0,03613 | F (1, 16) = 3.874 | P=0.0666 |
| Genotype | 0,1901 | 1 | 0,1901 | F (1, 16) = 20.39 | P=0.0004 |
| Residual | 0,1492 | 16 | 0,009325 | | |
| | | | | | |
| Difference between column means | | | | | |
| Mean of WT | 0,2350 | | | | |
| Mean of APP-SWE | 0,4300 | | | | |
| Difference between means | -0,1950 | | | | |
| SE of difference | 0,04319 | | | | |
| 95% CI of difference | -0.2865 to -0.1035 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Mean of Sham | 0,3750 | | | | |
| Mean of mTBI | 0,2900 | | | | |
| Difference between means | 0,08500 | | | | |
| SE of difference | 0,04319 | | | | |
| 95% CI of difference | -0.006549 to 0.1765 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | -0,1300 | | | | |
| Mean diff, A2 - B2 | -0,2600 | | | | |
| (A1 -B1) - (A2 - B2) | 0,1300 | | | | |
| 95% CI of difference | -0.05310 to 0.3131 | | | | |
| (B1 - A1) - (B2 - A2) | -0,1300 | | | | |
| 95% CI of difference | -0.3131 to 0.05310 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 11,54 | 0,0031 | No | ** | |
| Anderson-Darling (A2*) | 1,251 | 0,0022 | No | ** | |
| Shapiro-Wilk (W) | 0,8574 | 0,0071 | No | ** | |
| Kolmogorov-Smirnov (distance) | 0,2500 | 0,0020 | No | ** | |
| | | | | | |
| Data summary | | | | | |
| Number of columns (Genotype) | 2 | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of rows (Injury)** | 2 | | | | |
| **Number of values** | 20 | | | | |

## 2way ANOVA of DHEA pmol:mg cortex

| Table Analyzed | DHEA pmol/mg cortex | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 0,01510 | 0,9548 | ns | No | |
| **Injury** | 4,720 | 0,3240 | ns | No | |
| **Genotype** | 22,34 | 0,0417 | * | Yes | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 3,802E-05 | 1 | 3,802E-05 | F (1, 16) = 0.003312 | P=0.9548 |
| **Injury** | 0,01189 | 1 | 0,01189 | F (1, 16) = 1.035 | P=0.3240 |
| **Genotype** | 0,05626 | 1 | 0,05626 | F (1, 16) = 4.901 | P=0.0417 |
| **Residual** | 0,1837 | 16 | 0,01148 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Mean of WT** | 0,2430 | | | | |
| **Mean of APP-SWE** | 0,3491 | | | | |
| **Difference between means** | -0,1061 | | | | |
| **SE of difference** | 0,04792 | | | | |
| **95% CI of difference** | -0.2076 to -0.004496 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of Sham** | 0,3204 | | | | |
| **Mean of mTBI** | 0,2717 | | | | |
| **Difference between means** | 0,04876 | | | | |
| **SE of difference** | 0,04792 | | | | |
| **95% CI of difference** | -0.05282 to 0.1503 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | -0,1088 | | | | |
| **Mean diff, A2 - B2** | -0,1033 | | | | |
| **(A1 -B1) - (A2 - B2)** | -0,005515 | | | | |
| **95% CI of difference** | -0.2087 to 0.1976 | | | | |
| **(B1 - A1) - (B2 - A2)** | 0,005515 | | | | |
| **95% CI of difference** | -0.1976 to 0.2087 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 2,619 | 0,2700 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,4596 | 0,2344 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,9361 | 0,2019 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1404 | 0,1000 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |
| **Number of values** | 20 | | | | |

## 2way ANOVA of EPEA pmol:mg cortex

| Table Analyzed | EPEA pmol/mg cortex | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 13,31 | 0,0273 | * | Yes | |
| **Injury** | 26,31 | 0,0036 | ** | Yes | |
| **Genotype** | 24,26 | 0,0047 | ** | Yes | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 0,0001468 | 1 | 0,0001468 | F (1, 16) = 5.897 | P=0.0273 |
| **Injury** | 0,0002902 | 1 | 0,0002902 | F (1, 16) = 11.66 | P=0.0036 |
| **Genotype** | 0,0002675 | 1 | 0,0002675 | F (1, 16) = 10.75 | P=0.0047 |
| **Residual** | 0,0003983 | 16 | 2,489E-05 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Mean of WT** | 0,006900 | | | | |
| **Mean of APP-SWE** | 0,01421 | | | | |
| **Difference between means** | -0,007315 | | | | |
| **SE of difference** | 0,002231 | | | | |
| **95% CI of difference** | -0.01204 to -0.002585 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of Sham** | 0,01437 | | | | |
| **Mean of mTBI** | 0,006748 | | | | |
| **Difference between means** | 0,007618 | | | | |
| **SE of difference** | 0,002231 | | | | |
| **95% CI of difference** | 0.002888 to 0.01235 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | -0,01273 | | | | |
| **Mean diff, A2 - B2** | -0,001897 | | | | |
| **(A1 -B1) - (A2 - B2)** | -0,01084 | | | | |
| **95% CI of difference** | -0.02030 to -0.001377 | | | | |
| **(B1 - A1) - (B2 - A2)** | 0,01084 | | | | |
| **95% CI of difference** | 0.001377 to 0.02030 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 0,9544 | 0,6205 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,3318 | 0,4827 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,9605 | 0,5542 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1326 | 0,1000 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of values** | 20 | | | | |

## 2way ANOVA of 2-DHG pmol:mg cortex

| **Compare cell means regardless of rows and columns** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | | | | | | | |
| **Number of families** | 1 | | | | | | | |
| **Number of comparisons per family** | 6 | | | | | | | |
| **Alpha** | 0,05 | | | | | | | |
| | | | | | | | | |
| **Tukey's multiple comparisons test** | Mean Diff. | 95.00% CI of diff. | Below threshold? | Summary | Adjusted P Value | | | |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | -5,810 | -19.19 to 7.573 | No | ns | 0,6105 | | | |
| **Sham:WT vs. mTBI:WT** | -5,014 | -18.40 to 8.369 | No | ns | 0,7109 | | | |
| **Sham:WT vs. mTBI:APP-SWE** | 0,6700 | -12.71 to 14.05 | No | ns | 0,9989 | | | |
| **Sham:APP-SWE vs. mTBI:WT** | 0,7960 | -12.59 to 14.18 | No | ns | 0,9982 | | | |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 6,480 | -6.903 to 19.86 | No | ns | 0,5257 | | | |
| **mTBI:WT vs. mTBI:APP-SWE** | 5,684 | -7.699 to 19.07 | No | ns | 0,6266 | | | |
| | | | | | | | | |
| | | | | | | | | |
| **Test details** | Mean 1 | Mean 2 | Mean Diff. | SE of diff. | N1 | N2 | q | DF |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | 11,97 | 17,78 | -5,810 | 4,678 | 5 | 5 | 1,757 | 16,00 |
| **Sham:WT vs. mTBI:WT** | 11,97 | 16,98 | -5,014 | 4,678 | 5 | 5 | 1,516 | 16,00 |
| **Sham:WT vs. mTBI:APP-SWE** | 11,97 | 11,30 | 0,6700 | 4,678 | 5 | 5 | 0,2026 | 16,00 |
| **Sham:APP-SWE vs. mTBI:WT** | 17,78 | 16,98 | 0,7960 | 4,678 | 5 | 5 | 0,2407 | 16,00 |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 17,78 | 11,30 | 6,480 | 4,678 | 5 | 5 | 1,959 | 16,00 |
| **mTBI:WT vs. mTBI:APP-SWE** | 16,98 | 11,30 | 5,684 | 4,678 | 5 | 5 | 1,718 | 16,00 |

2way ANOVA of OlGly pmol:mg cortex

| **Compare cell means regardless of rows and columns** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | | | | | | | |
| **Number of families** | 1 | | | | | | | |
| **Number of comparisons per family** | 6 | | | | | | | |
| **Alpha** | 0,05 | | | | | | | |
| | | | | | | | | |
| **Tukey's multiple comparisons test** | Mean Diff. | 95.00% CI of diff. | Below threshold? | Summary | Adjusted P Value | | | |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | -0,3860 | -1.785 to 1.013 | No | ns | 0,8582 | | | |
| **Sham:WT vs. mTBI:WT** | 0,4740 | -0.9251 to 1.873 | No | ns | 0,7684 | | | |
| **Sham:WT vs. mTBI:APP-SWE** | -0,3060 | -1.705 to 1.093 | No | ns | 0,9223 | | | |
| **Sham:APP-SWE vs. mTBI:WT** | 0,8600 | -0.5391 to 2.259 | No | ns | 0,3279 | | | |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 0,08000 | -1.319 to 1.479 | No | ns | 0,9984 | | | |
| **mTBI:WT vs. mTBI:APP-SWE** | -0,7800 | -2.179 to 0.6191 | No | ns | 0,4088 | | | |
| | | | | | | | | |
| | | | | | | | | |
| **Test details** | Mean 1 | Mean 2 | Mean Diff. | SE of diff. | N1 | N2 | q | DF |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | 1,634 | 2,020 | -0,3860 | 0,4890 | 5 | 5 | 1,116 | 16,00 |
| **Sham:WT vs. mTBI:WT** | 1,634 | 1,160 | 0,4740 | 0,4890 | 5 | 5 | 1,371 | 16,00 |
| **Sham:WT vs. mTBI:APP-SWE** | 1,634 | 1,940 | -0,3060 | 0,4890 | 5 | 5 | 0,8849 | 16,00 |
| **Sham:APP-SWE vs. mTBI:WT** | 2,020 | 1,160 | 0,8600 | 0,4890 | 5 | 5 | 2,487 | 16,00 |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 2,020 | 1,940 | 0,08000 | 0,4890 | 5 | 5 | 0,2313 | 16,00 |
| **mTBI:WT vs. mTBI:APP-SWE** | 1,160 | 1,940 | -0,7800 | 0,4890 | 5 | 5 | 2,256 | 16,00 |

# 2way ANOVA of OA5HT pmol:mg cortex

| Table Analyzed | OA5HT pmol/mg cortex | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 30,68 | 0,0006 | *** | Yes | |
| Injury | 30,92 | 0,0006 | *** | Yes | |
| Genotype | 33,14 | 0,0005 | *** | Yes | |
| | | | | | |
| ANOVA table | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| Interaction | 813,6 | 1 | 813,6 | F (1, 12) = 20.95 | P=0.0006 |
| Injury | 820,0 | 1 | 820,0 | F (1, 12) = 21.12 | P=0.0006 |
| Genotype | 878,8 | 1 | 878,8 | F (1, 12) = 22.64 | P=0.0005 |
| Residual | 465,9 | 12 | 38,83 | | |
| | | | | | |
| Difference between column means | | | | | |
| Predicted (LS) mean of WT | 15,66 | | | | |
| Predicted (LS) mean of APP-SWE | 0,3530 | | | | |
| Difference between predicted means | 15,31 | | | | |
| SE of difference | 3,218 | | | | |
| 95% CI of difference | 8.298 to 22.32 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Predicted (LS) mean of Sham | 0,6137 | | | | |
| Predicted (LS) mean of mTBI | 15,40 | | | | |
| Difference between predicted means | -14,79 | | | | |
| SE of difference | 3,218 | | | | |
| 95% CI of difference | -21.80 to -7.777 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | 0,5793 | | | | |
| Mean diff, A2 - B2 | 30,04 | | | | |
| (A1 -B1) - (A2 - B2) | -29,46 | | | | |
| 95% CI of difference | -43.48 to -15.44 | | | | |
| (B1 - A1) - (B2 - A2) | 29,46 | | | | |
| 95% CI of difference | 15.44 to 43.48 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 19,11 | <0.0001 | No | **** | |
| Anderson-Darling (A2*) | 3,030 | <0.0001 | No | **** | |
| Shapiro-Wilk (W) | 0,6034 | <0.0001 | No | **** | |
| Kolmogorov-Smirnov (distance) | 0,3963 | <0.0001 | No | **** | |
| | | | | | |
| Data summary | | | | | |
| Number of columns (Genotype) | 2 | | | | |
| Number of rows (Injury) | 2 | | | | |
| Number of values | 16 | | | | |

# 2way ANOVA of DHA5HT pmol:mg cortex

| **Table Analyzed** | **DHA5HT pmol/mg cortex** | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 23,55 | 0,0194 | * | Yes | |
| **Injury** | 23,32 | 0,0199 | * | Yes | |
| **Genotype** | 25,97 | 0,0152 | * | Yes | |
| | | | | | |
| **ANOVA table** | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 4146 | 1 | 4146 | F (1, 11) = 7.475 | P=0.0194 |
| **Injury** | 4106 | 1 | 4106 | F (1, 11) = 7.404 | P=0.0199 |
| **Genotype** | 4572 | 1 | 4572 | F (1, 11) = 8.244 | P=0.0152 |
| **Residual** | 6101 | 11 | 554,6 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Predicted (LS) mean of WT** | 36,24 | | | | |
| **Predicted (LS) mean of APP-SWE** | 0,5110 | | | | |
| **Difference between predicted means** | 35,73 | | | | |
| **SE of difference** | 12,44 | | | | |
| **95% CI of difference** | 8.341 to 63.11 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Predicted (LS) mean of Sham** | 1,446 | | | | |
| **Predicted (LS) mean of mTBI** | 35,30 | | | | |
| **Difference between predicted means** | -33,86 | | | | |
| **SE of difference** | 12,44 | | | | |
| **95% CI of difference** | -61.24 to -6.471 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | 1,708 | | | | |
| **Mean diff, A2 - B2** | 69,75 | | | | |
| **(A1 -B1) - (A2 - B2)** | -68,04 | | | | |
| **95% CI of difference** | -122.8 to -13.27 | | | | |
| **(B1 - A1) - (B2 - A2)** | 68,04 | | | | |
| **95% CI of difference** | 13.27 to 122.8 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 13,72 | 0,0010 | No | ** | |
| **Anderson-Darling (A2*)** | 2,880 | <0.0001 | No | **** | |
| **Shapiro-Wilk (W)** | 0,6227 | <0.0001 | No | **** | |
| **Kolmogorov-Smirnov (distance)** | 0,3982 | <0.0001 | No | **** | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |
| **Number of values** | 15 | | | | |

2way ANOVA of EPA5HT pmol:mg cortex

| Table Analyzed | EPA5HT pmol/mg cortex | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 2,347 | 0,4340 | ns | No | |
| Injury | 3,059 | 0,3733 | ns | No | |
| Genotype | 37,86 | 0,0056 | ** | Yes | |
| | | | | | |
| ANOVA table | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| Interaction | 0,7361 | 1 | 0,7361 | F (1, 15) = 0.6462 | P=0.4340 |
| Injury | 0,9593 | 1 | 0,9593 | F (1, 15) = 0.8421 | P=0.3733 |
| Genotype | 11,87 | 1 | 11,87 | F (1, 15) = 10.42 | P=0.0056 |
| Residual | 17,09 | 15 | 1,139 | | |
| | | | | | |
| Difference between column means | | | | | |
| Predicted (LS) mean of WT | 2,869 | | | | |
| Predicted (LS) mean of APP-SWE | 1,280 | | | | |
| Difference between predicted means | 1,589 | | | | |
| SE of difference | 0,4920 | | | | |
| 95% CI of difference | 0.5398 to 2.637 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Predicted (LS) mean of Sham | 2,300 | | | | |
| Predicted (LS) mean of mTBI | 1,849 | | | | |
| Difference between predicted means | 0,4515 | | | | |
| SE of difference | 0,4920 | | | | |
| 95% CI of difference | -0.5972 to 1.500 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | 1,984 | | | | |
| Mean diff, A2 - B2 | 1,193 | | | | |
| (A1 -B1) - (A2 - B2) | 0,7910 | | | | |
| 95% CI of difference | -1.306 to 2.888 | | | | |
| (B1 - A1) - (B2 - A2) | -0,7910 | | | | |
| 95% CI of difference | -2.888 to 1.306 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 1,022 | 0,5999 | Yes | ns | |
| Anderson-Darling (A2*) | 0,2116 | 0,8319 | Yes | ns | |
| Shapiro-Wilk (W) | 0,9809 | 0,9525 | Yes | ns | |
| Kolmogorov-Smirnov (distance) | 0,1041 | 0,1000 | Yes | ns | |
| | | | | | |
| Data summary | | | | | |
| Number of columns (Genotype) | 2 | | | | |
| Number of rows (Injury) | 2 | | | | |
| Number of values | 19 | | | | |

# 2way ANOVA of PA5HT pmol:mg cortex

| **Compare cell means regardless of rows and columns** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | | | | | | | |
| **Number of families** | 1 | | | | | | | |
| **Number of comparisons per family** | 6 | | | | | | | |
| **Alpha** | 0,05 | | | | | | | |
| | | | | | | | | |
| **Tukey's multiple comparisons test** | Predicted (LS) mean diff. | 95.00% CI of diff. | Below threshold? | Summary | Adjusted P Value | | | |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | -21,60 | -58.52 to 15.32 | No | ns | 0,3596 | | | |
| **Sham:WT vs. mTBI:WT** | -0,5885 | -37.51 to 36.33 | No | ns | >0.9999 | | | |
| **Sham:WT vs. mTBI:APP-SWE** | -1,388 | -40.30 to 37.53 | No | ns | 0,9996 | | | |
| **Sham:APP-SWE vs. mTBI:WT** | 21,01 | -13.80 to 55.82 | No | ns | 0,3342 | | | |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 20,21 | -16.71 to 57.13 | No | ns | 0,4143 | | | |
| **mTBI:WT vs. mTBI:APP-SWE** | -0,7990 | -37.72 to 36.12 | No | ns | >0.9999 | | | |
| | | | | | | | | |
| | | | | | | | | |
| **Test details** | Predicted (LS) mean 1 | Predicted (LS) mean 2 | Predicted (LS) mean diff. | SE of diff. | N1 | N2 | q | DF |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | 14,12 | 35,72 | -21,60 | 12,70 | 4 | 5 | 2,405 | 14,00 |
| **Sham:WT vs. mTBI:WT** | 14,12 | 14,71 | -0,5885 | 12,70 | 4 | 5 | 0,06552 | 14,00 |
| **Sham:WT vs. mTBI:APP-SWE** | 14,12 | 15,51 | -1,388 | 13,39 | 4 | 4 | 0,1466 | 14,00 |
| **Sham:APP-SWE vs. mTBI:WT** | 35,72 | 14,71 | 21,01 | 11,98 | 5 | 5 | 2,481 | 14,00 |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 35,72 | 15,51 | 20,21 | 12,70 | 5 | 4 | 2,250 | 14,00 |
| **mTBI:WT vs. mTBI:APP-SWE** | 14,71 | 15,51 | -0,7990 | 12,70 | 5 | 4 | 0,08896 | 14,00 |

## 2way ANOVA of AEA pmol:g hipp

| **Compare cell means regardless of rows and columns** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | | | | | | | |
| **Number of families** | 1 | | | | | | | |
| **Number of comparisons per family** | 6 | | | | | | | |
| **Alpha** | 0,05 | | | | | | | |
| | | | | | | | | |
| **Tukey's multiple comparisons test** | Mean Diff. | 95.00% CI of diff. | Below threshold? | Summary | Adjusted P Value | | | |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | -30,66 | -102.3 to 41.01 | No | ns | 0,6213 | | | |
| **Sham:WT vs. mTBI:WT** | 22,62 | -49.04 to 94.29 | No | ns | 0,8034 | | | |
| **Sham:WT vs. mTBI:APP-SWE** | 0,05800 | -71.61 to 71.73 | No | ns | >0.9999 | | | |
| **Sham:APP-SWE vs. mTBI:WT** | 53,29 | -18.38 to 125.0 | No | ns | 0,1866 | | | |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 30,72 | -40.95 to 102.4 | No | ns | 0,6199 | | | |
| **mTBI:WT vs. mTBI:APP-SWE** | -22,57 | -94.23 to 49.10 | No | ns | 0,8045 | | | |
| | | | | | | | | |
| | | | | | | | | |
| **Test details** | Mean 1 | Mean 2 | Mean Diff. | SE of diff. | N1 | N2 | q | DF |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | 141,4 | 172,0 | -30,66 | 25,05 | 5 | 5 | 1,731 | 16,00 |
| **Sham:WT vs. mTBI:WT** | 141,4 | 118,7 | 22,62 | 25,05 | 5 | 5 | 1,277 | 16,00 |
| **Sham:WT vs. mTBI:APP-SWE** | 141,4 | 141,3 | 0,05800 | 25,05 | 5 | 5 | 0,003274 | 16,00 |
| **Sham:APP-SWE vs. mTBI:WT** | 172,0 | 118,7 | 53,29 | 25,05 | 5 | 5 | 3,008 | 16,00 |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 172,0 | 141,3 | 30,72 | 25,05 | 5 | 5 | 1,734 | 16,00 |
| **mTBI:WT vs. mTBI:APP-SWE** | 118,7 | 141,3 | -22,57 | 25,05 | 5 | 5 | 1,274 | 16,00 |

## 2way ANOVA of 2-AG pmol:mg hipp

| **Table Analyzed** | **2-AG pmol/mg hipp** | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 2,486 | 0,2096 | ns | No | |
| **Injury** | 0,06086 | 0,8405 | ns | No | |
| **Genotype** | 74,18 | <0.0001 | **** | Yes | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 0,4322 | 1 | 0,4322 | F (1, 16) = 1.709 | P=0.2096 |
| **Injury** | 0,01058 | 1 | 0,01058 | F (1, 16) = 0.04184 | P=0.8405 |
| **Genotype** | 12,90 | 1 | 12,90 | F (1, 16) = 51.00 | P<0.0001 |
| **Residual** | 4,046 | 16 | 0,2529 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Mean of WT** | 0,7840 | | | | |
| **Mean of APP-SWE** | 2,390 | | | | |
| **Difference between means** | -1,606 | | | | |
| **SE of difference** | 0,2249 | | | | |
| **95% CI of difference** | -2.083 to -1.129 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of Sham** | 1,564 | | | | |
| **Mean of mTBI** | 1,610 | | | | |
| **Difference between means** | -0,04600 | | | | |
| **SE of difference** | 0,2249 | | | | |
| **95% CI of difference** | -0.5227 to 0.4307 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | -1,312 | | | | |
| **Mean diff, A2 - B2** | -1,900 | | | | |
| **(A1 -B1) - (A2 - B2)** | 0,5880 | | | | |
| **95% CI of difference** | -0.3655 to 1.541 | | | | |
| **(B1 - A1) - (B2 - A2)** | -0,5880 | | | | |
| **95% CI of difference** | -1.541 to 0.3655 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 1,023 | 0,5996 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,1955 | 0,8754 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,9736 | 0,8275 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,08118 | 0,1000 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| **Number of values** | 20 |  |  |  |  |

## 2way ANOVA of PEA pmol:mg hipp

| Table Analyzed | PEA pmol/mg hipp | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 1,210 | 0,5559 | ns | No | |
| Injury | 3,706 | 0,3085 | ns | No | |
| Genotype | 47,27 | 0,0019 | ** | Yes | |
| | | | | | |
| ANOVA table | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| Interaction | 0,03012 | 1 | 0,03012 | F (1, 15) = 0.3628 | P=0.5559 |
| Injury | 0,09224 | 1 | 0,09224 | F (1, 15) = 1.111 | P=0.3085 |
| Genotype | 1,176 | 1 | 1,176 | F (1, 15) = 14.17 | P=0.0019 |
| Residual | 1,245 | 15 | 0,08301 | | |
| | | | | | |
| Difference between column means | | | | | |
| Predicted (LS) mean of WT | 0,8100 | | | | |
| Predicted (LS) mean of APP-SWE | 0,3100 | | | | |
| Difference between predicted means | 0,5000 | | | | |
| SE of difference | 0,1328 | | | | |
| 95% CI of difference | 0.2169 to 0.7831 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Predicted (LS) mean of Sham | 0,6300 | | | | |
| Predicted (LS) mean of mTBI | 0,4900 | | | | |
| Difference between predicted means | 0,1400 | | | | |
| SE of difference | 0,1328 | | | | |
| 95% CI of difference | -0.1431 to 0.4231 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | 0,5800 | | | | |
| Mean diff, A2 - B2 | 0,4200 | | | | |
| (A1 -B1) - (A2 - B2) | 0,1600 | | | | |
| 95% CI of difference | -0.4062 to 0.7262 | | | | |
| (B1 - A1) - (B2 - A2) | -0,1600 | | | | |
| 95% CI of difference | -0.7262 to 0.4062 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 17,52 | 0,0002 | No | *** | |
| Anderson-Darling (A2*) | 0,9630 | 0,0118 | No | * | |
| Shapiro-Wilk (W) | 0,8426 | 0,0051 | No | ** | |
| Kolmogorov-Smirnov (distance) | 0,2446 | 0,0040 | No | ** | |
| | | | | | |
| Data summary | | | | | |
| Number of columns (Genotype) | 2 | | | | |
| Number of rows (Injury) | 2 | | | | |
| Number of values | 19 | | | | |

## 2way ANOVA of OEA pmol:mg hipp

| **Compare cell means regardless of rows and columns** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | | | | | | | |
| **Number of families** | 1 | | | | | | | |
| **Number of comparisons per family** | 6 | | | | | | | |
| **Alpha** | 0,05 | | | | | | | |
| | | | | | | | | |
| **Tukey's multiple comparisons test** | Mean Diff. | 95.00% CI of diff. | Below threshold? | Summary | Adjusted P Value | | | |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | -0,3400 | -0.6965 to 0.01650 | No | ns | 0,0643 | | | |
| **Sham:WT vs. mTBI:WT** | -0,02800 | -0.3845 to 0.3285 | No | ns | 0,9958 | | | |
| **Sham:WT vs. mTBI:APP-SWE** | -0,1200 | -0.4765 to 0.2365 | No | ns | 0,7718 | | | |
| **Sham:APP-SWE vs. mTBI:WT** | 0,3120 | -0.04450 to 0.6685 | No | ns | 0,0974 | | | |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 0,2200 | -0.1365 to 0.5765 | No | ns | 0,3247 | | | |
| **mTBI:WT vs. mTBI:APP-SWE** | -0,09200 | -0.4485 to 0.2645 | No | ns | 0,8802 | | | |
| | | | | | | | | |
| | | | | | | | | |
| **Test details** | Mean 1 | Mean 2 | Mean Diff. | SE of diff. | N1 | N2 | q | DF |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | 0,4200 | 0,7600 | -0,3400 | 0,1246 | 5 | 5 | 3,859 | 16,00 |
| **Sham:WT vs. mTBI:WT** | 0,4200 | 0,4480 | -0,02800 | 0,1246 | 5 | 5 | 0,3178 | 16,00 |
| **Sham:WT vs. mTBI:APP-SWE** | 0,4200 | 0,5400 | -0,1200 | 0,1246 | 5 | 5 | 1,362 | 16,00 |
| **Sham:APP-SWE vs. mTBI:WT** | 0,7600 | 0,4480 | 0,3120 | 0,1246 | 5 | 5 | 3,541 | 16,00 |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 0,7600 | 0,5400 | 0,2200 | 0,1246 | 5 | 5 | 2,497 | 16,00 |
| **mTBI:WT vs. mTBI:APP-SWE** | 0,4480 | 0,5400 | -0,09200 | 0,1246 | 5 | 5 | 1,044 | 16,00 |

## 2way ANOVA of DHEA pmol:mg hipp

| **Compare cell means regardless of rows and columns** | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | |
| **Number of families** | 1 | | | | | | | | |
| **Number of comparisons per family** | 6 | | | | | | | | |
| **Alpha** | 0,05 | | | | | | | | |
| | | | | | | | | | |
| **Tukey's multiple comparisons test** | Mean Diff. | 95.00% CI of diff. | Below threshold? | Summary | Adjusted P Value | | | | |
| | | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | -0,2984 | -0.5937 to -0.003057 | Yes | * | 0,0472 | | | | |
| **Sham:WT vs. mTBI:WT** | 0,07800 | -0.2173 to 0.3733 | No | ns | 0,8729 | | | | |
| **Sham:WT vs. mTBI:APP-SWE** | -0,07492 | -0.3702 to 0.2204 | No | ns | 0,8854 | | | | |
| **Sham:APP-SWE vs. mTBI:WT** | 0,3764 | 0.08106 to 0.6717 | Yes | * | 0,0105 | | | | |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 0,2235 | -0.07186 to 0.5188 | No | ns | 0,1754 | | | | |
| **mTBI:WT vs. mTBI:APP-SWE** | -0,1529 | -0.4482 to 0.1424 | No | ns | 0,4706 | | | | |
| | | | | | | | | | |
| | | | | | | | | | |
| **Test details** | Mean 1 | Mean 2 | Mean Diff. | SE of diff. | N1 | N2 | q | DF | |
| | | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | 0,3640 | 0,6624 | -0,2984 | 0,1032 | 5 | 5 | 4,088 | 16,00 | |
| **Sham:WT vs. mTBI:WT** | 0,3640 | 0,2860 | 0,07800 | 0,1032 | 5 | 5 | 1,069 | 16,00 | |
| **Sham:WT vs. mTBI:APP-SWE** | 0,3640 | 0,4389 | -0,07492 | 0,1032 | 5 | 5 | 1,026 | 16,00 | |
| **Sham:APP-SWE vs. mTBI:WT** | 0,6624 | 0,2860 | 0,3764 | 0,1032 | 5 | 5 | 5,157 | 16,00 | |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 0,6624 | 0,4389 | 0,2235 | 0,1032 | 5 | 5 | 3,062 | 16,00 | |
| **mTBI:WT vs. mTBI:APP-SWE** | 0,2860 | 0,4389 | -0,1529 | 0,1032 | 5 | 5 | 2,095 | 16,00 | |

## 2way ANOVA of EPEA pmol:mg hipp

| **Compare cell means regardless of rows and columns** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | | | | | | | |
| **Number of families** | 1 | | | | | | | |
| **Number of comparisons per family** | 6 | | | | | | | |
| **Alpha** | 0,05 | | | | | | | |
| | | | | | | | | |
| **Tukey's multiple comparisons test** | Mean Diff. | 95.00% CI of diff. | Below threshold? | Summary | Adjusted P Value | | | |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | -0,001461 | -0.01513 to 0.01221 | No | ns | 0,9897 | | | |
| **Sham:WT vs. mTBI:WT** | 0,006000 | -0.007672 to 0.01967 | No | ns | 0,6024 | | | |
| **Sham:WT vs. mTBI:APP-SWE** | 0,002738 | -0.01093 to 0.01641 | No | ns | 0,9387 | | | |
| **Sham:APP-SWE vs. mTBI:WT** | 0,007461 | -0.006211 to 0.02113 | No | ns | 0,4268 | | | |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 0,004199 | -0.009473 to 0.01787 | No | ns | 0,8158 | | | |
| **mTBI:WT vs. mTBI:APP-SWE** | -0,003262 | -0.01693 to 0.01041 | No | ns | 0,9022 | | | |
| | | | | | | | | |
| | | | | | | | | |
| **Test details** | Mean 1 | Mean 2 | Mean Diff. | SE of diff. | N1 | N2 | q | DF |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | 0,02000 | 0,02146 | -0,001461 | 0,004779 | 5 | 5 | 0,4323 | 16,00 |
| **Sham:WT vs. mTBI:WT** | 0,02000 | 0,01400 | 0,006000 | 0,004779 | 5 | 5 | 1,776 | 16,00 |
| **Sham:WT vs. mTBI:APP-SWE** | 0,02000 | 0,01726 | 0,002738 | 0,004779 | 5 | 5 | 0,8103 | 16,00 |
| **Sham:APP-SWE vs. mTBI:WT** | 0,02146 | 0,01400 | 0,007461 | 0,004779 | 5 | 5 | 2,208 | 16,00 |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 0,02146 | 0,01726 | 0,004199 | 0,004779 | 5 | 5 | 1,243 | 16,00 |
| **mTBI:WT vs. mTBI:APP-SWE** | 0,01400 | 0,01726 | -0,003262 | 0,004779 | 5 | 5 | 0,9654 | 16,00 |

## 2way ANOVA of 2-DHG pmol:mg hipp

| **Compare cell means regardless of rows and columns** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | | | | | | | |
| **Number of families** | 1 | | | | | | | |
| **Number of comparisons per family** | 6 | | | | | | | |
| **Alpha** | 0,05 | | | | | | | |
| | | | | | | | | |
| **Tukey's multiple comparisons test** | Predicted (LS) mean diff. | 95.00% CI of diff. | Below threshold? | Summary | Adjusted P Value | | | |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | -14,42 | -38.98 to 10.15 | No | ns | 0,3518 | | | |
| **Sham:WT vs. mTBI:WT** | 19,33 | -5.236 to 43.89 | No | ns | 0,1463 | | | |
| **Sham:WT vs. mTBI:APP-SWE** | -5,222 | -33.19 to 22.75 | No | ns | 0,9455 | | | |
| **Sham:APP-SWE vs. mTBI:WT** | 33,74 | 10.58 to 56.90 | Yes | ** | 0,0044 | | | |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 9,193 | -17.55 to 35.94 | No | ns | 0,7471 | | | |
| **mTBI:WT vs. mTBI:APP-SWE** | -24,55 | -51.29 to 2.193 | No | ns | 0,0764 | | | |
| | | | | | | | | |
| | | | | | | | | |
| **Test details** | Predicted (LS) mean 1 | Predicted (LS) mean 2 | Predicted (LS) mean diff. | SE of diff. | N1 | N2 | q | DF |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | 39,95 | 54,36 | -14,42 | 8,370 | 4 | 5 | 2,436 | 13,00 |
| **Sham:WT vs. mTBI:WT** | 39,95 | 20,62 | 19,33 | 8,370 | 4 | 5 | 3,266 | 13,00 |
| **Sham:WT vs. mTBI:APP-SWE** | 39,95 | 45,17 | -5,222 | 9,529 | 4 | 3 | 0,7749 | 13,00 |
| **Sham:APP-SWE vs. mTBI:WT** | 54,36 | 20,62 | 33,74 | 7,891 | 5 | 5 | 6,048 | 13,00 |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 54,36 | 45,17 | 9,193 | 9,112 | 5 | 3 | 1,427 | 13,00 |
| **mTBI:WT vs. mTBI:APP-SWE** | 20,62 | 45,17 | -24,55 | 9,112 | 5 | 3 | 3,811 | 13,00 |

## 2way ANOVA of OlGly pmol:mg hipp

| Table Analyzed | OlGly pmol/mg hipp | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 21,49 | 0,0236 | * | Yes | |
| Injury | 0,09831 | 0,8661 | ns | No | |
| Genotype | 31,80 | 0,0080 | ** | Yes | |
| | | | | | |
| ANOVA table | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| Interaction | 6,413 | 1 | 6,413 | F (1, 14) = 6.447 | P=0.0236 |
| Injury | 0,02934 | 1 | 0,02934 | F (1, 14) = 0.02949 | P=0.8661 |
| Genotype | 9,490 | 1 | 9,490 | F (1, 14) = 9.539 | P=0.0080 |
| Residual | 13,93 | 14 | 0,9948 | | |
| | | | | | |
| Difference between column means | | | | | |
| Predicted (LS) mean of WT | 1,859 | | | | |
| Predicted (LS) mean of APP-SWE | 3,320 | | | | |
| Difference between predicted means | -1,461 | | | | |
| SE of difference | 0,4731 | | | | |
| 95% CI of difference | -2.476 to -0.4465 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Predicted (LS) mean of Sham | 2,630 | | | | |
| Predicted (LS) mean of mTBI | 2,549 | | | | |
| Difference between predicted means | 0,08125 | | | | |
| SE of difference | 0,4731 | | | | |
| 95% CI of difference | -0.9335 to 1.096 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | -0,2600 | | | | |
| Mean diff, A2 - B2 | -2,663 | | | | |
| (A1 -B1) - (A2 - B2) | 2,403 | | | | |
| 95% CI of difference | 0.3730 to 4.432 | | | | |
| (B1 - A1) - (B2 - A2) | -2,403 | | | | |
| 95% CI of difference | -4.432 to -0.3730 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 0,3562 | 0,8369 | Yes | ns | |
| Anderson-Darling (A2*) | 0,1425 | 0,9638 | Yes | ns | |
| Shapiro-Wilk (W) | 0,9819 | 0,9675 | Yes | ns | |
| Kolmogorov-Smirnov (distance) | 0,09085 | 0,1000 | Yes | ns | |
| | | | | | |
| Data summary | | | | | |
| Number of columns (Genotype) | 2 | | | | |
| Number of rows (Injury) | 2 | | | | |
| Number of values | 18 | | | | |

# 2way ANOVA of OA5HT pmol:mg hipp

| Table Analyzed | OA5HT pmol/mg hipp | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 37,54 | 0,0065 | ** | Yes | |
| Injury | 2,450 | 0,4280 | ns | No | |
| Genotype | 7,535 | 0,1742 | ns | No | |
| | | | | | |
| ANOVA table | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| Interaction | 11,49 | 1 | 11,49 | F (1, 14) = 10.21 | P=0.0065 |
| Injury | 0,7500 | 1 | 0,7500 | F (1, 14) = 0.6663 | P=0.4280 |
| Genotype | 2,307 | 1 | 2,307 | F (1, 14) = 2.049 | P=0.1742 |
| Residual | 15,76 | 14 | 1,126 | | |
| | | | | | |
| Difference between column means | | | | | |
| Predicted (LS) mean of WT | 0,9063 | | | | |
| Predicted (LS) mean of APP-SWE | 1,640 | | | | |
| Difference between predicted means | -0,7337 | | | | |
| SE of difference | 0,5125 | | | | |
| 95% CI of difference | -1.833 to 0.3655 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Predicted (LS) mean of Sham | 1,064 | | | | |
| Predicted (LS) mean of mTBI | 1,482 | | | | |
| Difference between predicted means | -0,4183 | | | | |
| SE of difference | 0,5125 | | | | |
| 95% CI of difference | -1.518 to 0.6809 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | 0,9040 | | | | |
| Mean diff, A2 - B2 | -2,371 | | | | |
| (A1 -B1) - (A2 - B2) | 3,275 | | | | |
| 95% CI of difference | 1.077 to 5.474 | | | | |
| (B1 - A1) - (B2 - A2) | -3,275 | | | | |
| 95% CI of difference | -5.474 to -1.077 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 1,469 | 0,4798 | Yes | ns | |
| Anderson-Darling (A2*) | 0,4308 | 0,2734 | Yes | ns | |
| Shapiro-Wilk (W) | 0,9332 | 0,2212 | Yes | ns | |
| Kolmogorov-Smirnov (distance) | 0,1795 | 0,1000 | Yes | ns | |
| | | | | | |
| Data summary | | | | | |
| Number of columns (Genotype) | 2 | | | | |
| Number of rows (Injury) | 2 | | | | |
| Number of values | 18 | | | | |

2way ANOVA of DHA5HT pmol:mg hipp

| **Compare cell means regardless of rows and columns** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | | | | | | | |
| **Number of families** | 1 | | | | | | | |
| **Number of comparisons per family** | 6 | | | | | | | |
| **Alpha** | 0,05 | | | | | | | |
| | | | | | | | | |
| **Tukey's multiple comparisons test** | Predicted (LS) mean diff. | 95.00% CI of diff. | Below threshold? | Summary | Adjusted P Value | | | |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | -0,5725 | -2.177 to 1.032 | No | ns | 0,7256 | | | |
| **Sham:WT vs. mTBI:WT** | 0,7275 | -1.099 to 2.554 | No | ns | 0,6556 | | | |
| **Sham:WT vs. mTBI:APP-SWE** | -0,9905 | -2.595 to 0.6136 | No | ns | 0,3112 | | | |
| **Sham:APP-SWE vs. mTBI:WT** | 1,300 | -0.4463 to 3.046 | No | ns | 0,1787 | | | |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | -0,4180 | -1.930 to 1.094 | No | ns | 0,8481 | | | |
| **mTBI:WT vs. mTBI:APP-SWE** | -1,718 | -3.464 to 0.02829 | No | ns | 0,0544 | | | |
| | | | | | | | | |
| | | | | | | | | |
| **Test details** | Predicted (LS) mean 1 | Predicted (LS) mean 2 | Predicted (LS) mean diff. | SE of diff. | N1 | N2 | q | DF |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | 1,498 | 2,070 | -0,5725 | 0,5465 | 4 | 5 | 1,481 | 13,00 |
| **Sham:WT vs. mTBI:WT** | 1,498 | 0,7700 | 0,7275 | 0,6222 | 4 | 3 | 1,653 | 13,00 |
| **Sham:WT vs. mTBI:APP-SWE** | 1,498 | 2,488 | -0,9905 | 0,5465 | 4 | 5 | 2,563 | 13,00 |
| **Sham:APP-SWE vs. mTBI:WT** | 2,070 | 0,7700 | 1,300 | 0,5950 | 5 | 3 | 3,090 | 13,00 |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 2,070 | 2,488 | -0,4180 | 0,5153 | 5 | 5 | 1,147 | 13,00 |
| **mTBI:WT vs. mTBI:APP-SWE** | 0,7700 | 2,488 | -1,718 | 0,5950 | 3 | 5 | 4,084 | 13,00 |

## 2way ANOVA of EPA5HT pmol:mg hipp

| Table Analyzed | EPA5HT pmol/mg hipp | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 26,17 | 0,0072 | ** | Yes | |
| Injury | 18,39 | 0,0196 | * | Yes | |
| Genotype | 22,73 | 0,0110 | * | Yes | |
| | | | | | |
| ANOVA table | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| Interaction | 211,2 | 1 | 211,2 | F (1, 14) = 9.879 | P=0.0072 |
| Injury | 148,4 | 1 | 148,4 | F (1, 14) = 6.944 | P=0.0196 |
| Genotype | 183,5 | 1 | 183,5 | F (1, 14) = 8.581 | P=0.0110 |
| Residual | 299,3 | 14 | 21,38 | | |
| | | | | | |
| Difference between column means | | | | | |
| Predicted (LS) mean of WT | 12,39 | | | | |
| Predicted (LS) mean of APP-SWE | 5,969 | | | | |
| Difference between predicted means | 6,425 | | | | |
| SE of difference | 2,193 | | | | |
| 95% CI of difference | 1.721 to 11.13 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Predicted (LS) mean of Sham | 12,07 | | | | |
| Predicted (LS) mean of mTBI | 6,292 | | | | |
| Difference between predicted means | 5,779 | | | | |
| SE of difference | 2,193 | | | | |
| 95% CI of difference | 1.075 to 10.48 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | 13,32 | | | | |
| Mean diff, A2 - B2 | -0,4685 | | | | |
| (A1 -B1) - (A2 - B2) | 13,79 | | | | |
| 95% CI of difference | 4.379 to 23.19 | | | | |
| (B1 - A1) - (B2 - A2) | -13,79 | | | | |
| 95% CI of difference | -23.19 to -4.379 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 2,396 | 0,3018 | Yes | ns | |
| Anderson-Darling (A2*) | 0,3726 | 0,3811 | Yes | ns | |
| Shapiro-Wilk (W) | 0,9436 | 0,3331 | Yes | ns | |
| Kolmogorov-Smirnov (distance) | 0,1436 | 0,1000 | Yes | ns | |
| | | | | | |
| Data summary | | | | | |
| Number of columns (Genotype) | 2 | | | | |
| Number of rows (Injury) | 2 | | | | |
| Number of values | 18 | | | | |

2way ANOVA of PA5HT pmol:mg hipp

| Table Analyzed | PA5HT pmol/mg hipp | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 3,317 | 0,2164 | ns | No | |
| Injury | 58,07 | 0,0001 | *** | Yes | |
| Genotype | 11,95 | 0,0283 | * | Yes | |
| | | | | | |
| ANOVA table | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| Interaction | 341,4 | 1 | 341,4 | F (1, 13) = 1.688 | P=0.2164 |
| Injury | 5977 | 1 | 5977 | F (1, 13) = 29.56 | P=0.0001 |
| Genotype | 1231 | 1 | 1231 | F (1, 13) = 6.085 | P=0.0283 |
| Residual | 2629 | 13 | 202,2 | | |
| | | | | | |
| Difference between column means | | | | | |
| Predicted (LS) mean of WT | 69,20 | | | | |
| Predicted (LS) mean of APP-SWE | 52,11 | | | | |
| Difference between predicted means | 17,10 | | | | |
| SE of difference | 6,930 | | | | |
| 95% CI of difference | 2.123 to 32.07 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Predicted (LS) mean of Sham | 79,50 | | | | |
| Predicted (LS) mean of mTBI | 41,82 | | | | |
| Difference between predicted means | 37,68 | | | | |
| SE of difference | 6,930 | | | | |
| 95% CI of difference | 22.71 to 52.65 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | 26,10 | | | | |
| Mean diff, A2 - B2 | 8,091 | | | | |
| (A1 -B1) - (A2 - B2) | 18,01 | | | | |
| 95% CI of difference | -11.94 to 47.95 | | | | |
| (B1 - A1) - (B2 - A2) | -18,01 | | | | |
| 95% CI of difference | -47.95 to 11.94 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 0,5143 | 0,7732 | Yes | ns | |
| Anderson-Darling (A2*) | 0,2014 | 0,8566 | Yes | ns | |
| Shapiro-Wilk (W) | 0,9778 | 0,9346 | Yes | ns | |
| Kolmogorov-Smirnov (distance) | 0,1161 | 0,1000 | Yes | ns | |
| | | | | | |
| Data summary | | | | | |
| Number of columns (Genotype) | 2 | | | | |
| Number of rows (Injury) | 2 | | | | |
| Number of values | 17 | | | | |

## 2way ANOVA of Napepld cortex

| **Table Analyzed** | **Napepld cortex** | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 49,74 | 0,0005 | *** | Yes | |
| **Injury** | 1,368 | 0,4840 | ns | No | |
| **Genotype** | 0,6904 | 0,6177 | ns | No | |
| | | | | | |
| **ANOVA table** | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 2,526 | 1 | 2,526 | F (1, 16) = 18.67 | P=0.0005 |
| **Injury** | 0,06945 | 1 | 0,06945 | F (1, 16) = 0.5133 | P=0.4840 |
| **Genotype** | 0,03506 | 1 | 0,03506 | F (1, 16) = 0.2591 | P=0.6177 |
| **Residual** | 2,165 | 16 | 0,1353 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Predicted (LS) mean of WT** | 0,5771 | | | | |
| **Predicted (LS) mean of APP-SWE** | 0,6626 | | | | |
| **Difference between predicted means** | -0,08546 | | | | |
| **SE of difference** | 0,1679 | | | | |
| **95% CI of difference** | -0.4414 to 0.2705 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Predicted (LS) mean of Sham** | 0,6800 | | | | |
| **Predicted (LS) mean of mTBI** | 0,5597 | | | | |
| **Difference between predicted means** | 0,1203 | | | | |
| **SE of difference** | 0,1679 | | | | |
| **95% CI of difference** | -0.2356 to 0.4762 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | 0,6400 | | | | |
| **Mean diff, A2 - B2** | -0,8109 | | | | |
| **(A1 -B1) - (A2 - B2)** | 1,451 | | | | |
| **95% CI of difference** | 0.7390 to 2.163 | | | | |
| **(B1 - A1) - (B2 - A2)** | -1,451 | | | | |
| **95% CI of difference** | -2.163 to -0.7390 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 4,212 | 0,1217 | Yes | ns | |
| **Anderson-Darling (A2*)** | 1,024 | 0,0084 | No | ** | |
| **Shapiro-Wilk (W)** | 0,8864 | 0,0231 | No | * | |
| **Kolmogorov-Smirnov (distance)** | 0,1895 | 0,0579 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of values** | 20 | | | | |

# 2way ANOVA of Gde1 cortex

| **Table Analyzed** | **Gde1 cortex** | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 35,19 | <0.0001 | **** | Yes | |
| **Injury** | 27,25 | <0.0001 | **** | Yes | |
| **Genotype** | 43,36 | <0.0001 | **** | Yes | |
| | | | | | |
| **ANOVA table** | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 24,81 | 1 | 24,81 | F (1, 16) = 125.2 | P<0.0001 |
| **Injury** | 19,21 | 1 | 19,21 | F (1, 16) = 96.94 | P<0.0001 |
| **Genotype** | 30,57 | 1 | 30,57 | F (1, 16) = 154.2 | P<0.0001 |
| **Residual** | 3,171 | 16 | 0,1982 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Predicted (LS) mean of WT** | 0,8636 | | | | |
| **Predicted (LS) mean of APP-SWE** | 3,387 | | | | |
| **Difference between predicted means** | -2,524 | | | | |
| **SE of difference** | 0,2032 | | | | |
| **95% CI of difference** | -2.954 to -2.093 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Predicted (LS) mean of Sham** | 1,125 | | | | |
| **Predicted (LS) mean of mTBI** | 3,126 | | | | |
| **Difference between predicted means** | -2,001 | | | | |
| **SE of difference** | 0,2032 | | | | |
| **95% CI of difference** | -2.432 to -1.570 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | -0,2502 | | | | |
| **Mean diff, A2 - B2** | -4,797 | | | | |
| **(A1 -B1) - (A2 - B2)** | 4,547 | | | | |
| **95% CI of difference** | 3.685 to 5.409 | | | | |
| **(B1 - A1) - (B2 - A2)** | -4,547 | | | | |
| **95% CI of difference** | -5.409 to -3.685 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 1,533 | 0,4645 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,4298 | 0,2786 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,9350 | 0,1928 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1782 | 0,0959 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| **Number of values** | 20 |  |  |  |  |

## 2way ANOVA of Faah cortex

| Table Analyzed | Faah cortex | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 12,25 | 0,1362 | ns | No | |
| **Injury** | 8,710 | 0,2045 | ns | No | |
| **Genotype** | 2,832 | 0,4616 | ns | No | |
| | | | | | |
| **ANOVA table** | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 0,4663 | 1 | 0,4663 | F (1, 16) = 2.462 | P=0.1362 |
| **Injury** | 0,3315 | 1 | 0,3315 | F (1, 16) = 1.750 | P=0.2045 |
| **Genotype** | 0,1078 | 1 | 0,1078 | F (1, 16) = 0.5691 | P=0.4616 |
| **Residual** | 3,031 | 16 | 0,1894 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Predicted (LS) mean of WT** | 0,9756 | | | | |
| **Predicted (LS) mean of APP-SWE** | 0,8257 | | | | |
| **Difference between predicted means** | 0,1499 | | | | |
| **SE of difference** | 0,1987 | | | | |
| **95% CI of difference** | -0.2713 to 0.5710 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Predicted (LS) mean of Sham** | 0,7692 | | | | |
| **Predicted (LS) mean of mTBI** | 1,032 | | | | |
| **Difference between predicted means** | -0,2628 | | | | |
| **SE of difference** | 0,1987 | | | | |
| **95% CI of difference** | -0.6839 to 0.1583 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | 0,4615 | | | | |
| **Mean diff, A2 - B2** | -0,1618 | | | | |
| **(A1 -B1) - (A2 - B2)** | 0,6234 | | | | |
| **95% CI of difference** | -0.2189 to 1.466 | | | | |
| **(B1 - A1) - (B2 - A2)** | -0,6234 | | | | |
| **95% CI of difference** | -1.466 to 0.2189 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 5,369 | 0,0683 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,6148 | 0,0944 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,8996 | 0,0406 | No | * | |
| **Kolmogorov-Smirnov (distance)** | 0,1602 | 0,1000 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| **Number of values** | 20 |  |  |  |  |

## 2way ANOVA of Dagla cortex

| Table Analyzed | Dagla cortex | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 2,434 | <0.0001 | **** | Yes | |
| **Injury** | 2,195 | <0.0001 | **** | Yes | |
| **Genotype** | 95,00 | <0.0001 | **** | Yes | |
| | | | | | |
| **ANOVA table** | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 21,14 | 1 | 21,14 | F (1, 16) = 34.14 | P<0.0001 |
| **Injury** | 19,07 | 1 | 19,07 | F (1, 16) = 30.80 | P<0.0001 |
| **Genotype** | 825,1 | 1 | 825,1 | F (1, 16) = 1333 | P<0.0001 |
| **Residual** | 9,905 | 16 | 0,6190 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Predicted (LS) mean of WT** | 0,9473 | | | | |
| **Predicted (LS) mean of APP-SWE** | 14,06 | | | | |
| **Difference between predicted means** | -13,11 | | | | |
| **SE of difference** | 0,3591 | | | | |
| **95% CI of difference** | -13.87 to -12.35 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Predicted (LS) mean of Sham** | 6,506 | | | | |
| **Predicted (LS) mean of mTBI** | 8,499 | | | | |
| **Difference between predicted means** | -1,993 | | | | |
| **SE of difference** | 0,3591 | | | | |
| **95% CI of difference** | -2.754 to -1.232 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | -11,01 | | | | |
| **Mean diff, A2 - B2** | -15,21 | | | | |
| **(A1 -B1) - (A2 - B2)** | 4,197 | | | | |
| **95% CI of difference** | 2.674 to 5.720 | | | | |
| **(B1 - A1) - (B2 - A2)** | -4,197 | | | | |
| **95% CI of difference** | -5.720 to -2.674 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 6,119 | 0,0469 | No | * | |
| **Anderson-Darling (A2*)** | 0,6032 | 0,1012 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,9119 | 0,0694 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1615 | 0,1000 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| **Number of values** | 20 |  |  |  |  |

## 2way ANOVA of Magl cortex

| **Table Analyzed** | **Magl cortex** | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 0,1597 | 0,8188 | ns | No | |
| **Injury** | 4,694 | 0,2249 | ns | No | |
| **Genotype** | 47,46 | 0,0010 | ** | Yes | |
| | | | | | |
| **ANOVA table** | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 0,008658 | 1 | 0,008658 | F (1, 16) = 0.05423 | P=0.8188 |
| **Injury** | 0,2544 | 1 | 0,2544 | F (1, 16) = 1.594 | P=0.2249 |
| **Genotype** | 2,573 | 1 | 2,573 | F (1, 16) = 16.12 | P=0.0010 |
| **Residual** | 2,555 | 16 | 0,1597 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Predicted (LS) mean of WT** | 0,8636 | | | | |
| **Predicted (LS) mean of APP-SWE** | 0,1315 | | | | |
| **Difference between predicted means** | 0,7321 | | | | |
| **SE of difference** | 0,1824 | | | | |
| **95% CI of difference** | 0.3455 to 1.119 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Predicted (LS) mean of Sham** | 0,6127 | | | | |
| **Predicted (LS) mean of mTBI** | 0,3825 | | | | |
| **Difference between predicted means** | 0,2302 | | | | |
| **SE of difference** | 0,1824 | | | | |
| **95% CI of difference** | -0.1564 to 0.6169 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | 0,7746 | | | | |
| **Mean diff, A2 - B2** | 0,6897 | | | | |
| **(A1 -B1) - (A2 - B2)** | 0,08494 | | | | |
| **95% CI of difference** | -0.6883 to 0.8582 | | | | |
| **(B1 - A1) - (B2 - A2)** | -0,08494 | | | | |
| **95% CI of difference** | -0.8582 to 0.6883 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 3,295 | 0,1926 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,5824 | 0,1145 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,9167 | 0,0857 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1859 | 0,0685 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |
| **Number of values** | 20 | | | | |

2way ANOVA of Cb1 cortex

| Table Analyzed | Cb1 cortex | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 3,506 | <0.0001 | **** | Yes | |
| **Injury** | 4,554 | <0.0001 | **** | Yes | |
| **Genotype** | 92,18 | <0.0001 | **** | Yes | |
| | | | | | |
| **ANOVA table** | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 5,278 | 1 | 5,278 | F (1, 16) = 51.32 | P<0.0001 |
| **Injury** | 6,856 | 1 | 6,856 | F (1, 16) = 66.67 | P<0.0001 |
| **Genotype** | 138,8 | 1 | 138,8 | F (1, 16) = 1349 | P<0.0001 |
| **Residual** | 1,645 | 16 | 0,1028 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Predicted (LS) mean of WT** | 1,073 | | | | |
| **Predicted (LS) mean of APP-SWE** | 6,450 | | | | |
| **Difference between predicted means** | -5,377 | | | | |
| **SE of difference** | 0,1464 | | | | |
| **95% CI of difference** | -5.687 to -5.066 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Predicted (LS) mean of Sham** | 3,164 | | | | |
| **Predicted (LS) mean of mTBI** | 4,359 | | | | |
| **Difference between predicted means** | -1,195 | | | | |
| **SE of difference** | 0,1464 | | | | |
| **95% CI of difference** | -1.505 to -0.8848 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | -4,328 | | | | |
| **Mean diff, A2 - B2** | -6,425 | | | | |
| **(A1 -B1) - (A2 - B2)** | 2,097 | | | | |
| **95% CI of difference** | 1.477 to 2.718 | | | | |
| **(B1 - A1) - (B2 - A2)** | -2,097 | | | | |
| **95% CI of difference** | -2.718 to -1.477 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 0,2610 | 0,8777 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,1341 | 0,9744 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,9844 | 0,9774 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,09623 | 0,1000 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| **Number of values** | 20 |  |  |  |  |

# 2way ANOVA of Ppara cortex

| Table Analyzed | Ppara cortex | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 8,825 | 0,1762 | ns | No | |
| Injury | 14,12 | 0,0924 | ns | No | |
| Genotype | 0,9406 | 0,6503 | ns | No | |
| | | | | | |
| ANOVA table | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| Interaction | 1,556 | 1 | 1,556 | F (1, 16) = 2.003 | P=0.1762 |
| Injury | 2,489 | 1 | 2,489 | F (1, 16) = 3.204 | P=0.0924 |
| Genotype | 0,1658 | 1 | 0,1658 | F (1, 16) = 0.2134 | P=0.6503 |
| Residual | 12,43 | 16 | 0,7770 | | |
| | | | | | |
| Difference between column means | | | | | |
| Predicted (LS) mean of WT | 1,645 | | | | |
| Predicted (LS) mean of APP-SWE | 1,459 | | | | |
| Difference between predicted means | 0,1859 | | | | |
| SE of difference | 0,4023 | | | | |
| 95% CI of difference | -0.6670 to 1.039 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Predicted (LS) mean of Sham | 1,192 | | | | |
| Predicted (LS) mean of mTBI | 1,912 | | | | |
| Difference between predicted means | -0,7201 | | | | |
| SE of difference | 0,4023 | | | | |
| 95% CI of difference | -1.573 to 0.1328 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | -0,3835 | | | | |
| Mean diff, A2 - B2 | 0,7552 | | | | |
| (A1 -B1) - (A2 - B2) | -1,139 | | | | |
| 95% CI of difference | -2.845 to 0.5671 | | | | |
| (B1 - A1) - (B2 - A2) | 1,139 | | | | |
| 95% CI of difference | -0.5671 to 2.845 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 19,78 | <0.0001 | No | **** | |
| Anderson-Darling (A2*) | 1,100 | 0,0053 | No | ** | |
| Shapiro-Wilk (W) | 0,8246 | 0,0021 | No | ** | |
| Kolmogorov-Smirnov (distance) | 0,2176 | 0,0139 | No | * | |
| | | | | | |
| Data summary | | | | | |
| Number of columns (Genotype) | 2 | | | | |
| Number of rows (Injury) | 2 | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of values** | 20 | | | | |

## 2way ANOVA of Pparg cortex

| **Table Analyzed** | **Pparg cortex** | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 0,4335 | 0,1061 | ns | No | |
| **Injury** | 0,7067 | 0,0439 | * | Yes | |
| **Genotype** | 96,22 | <0.0001 | **** | Yes | |
| | | | | | |
| **ANOVA table** | SS (Type III) | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 0,9913 | 1 | 0,9913 | F (1, 16) = 2.934 | P=0.1061 |
| **Injury** | 1,616 | 1 | 1,616 | F (1, 16) = 4.783 | P=0.0439 |
| **Genotype** | 220,0 | 1 | 220,0 | F (1, 16) = 651.2 | P<0.0001 |
| **Residual** | 5,406 | 16 | 0,3379 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Predicted (LS) mean of WT** | 1,517 | | | | |
| **Predicted (LS) mean of APP-SWE** | 8,288 | | | | |
| **Difference between predicted means** | -6,770 | | | | |
| **SE of difference** | 0,2653 | | | | |
| **95% CI of difference** | -7.333 to -6.208 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Predicted (LS) mean of Sham** | 4,612 | | | | |
| **Predicted (LS) mean of mTBI** | 5,193 | | | | |
| **Difference between predicted means** | -0,5802 | | | | |
| **SE of difference** | 0,2653 | | | | |
| **95% CI of difference** | -1.143 to -0.01778 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | -7,225 | | | | |
| **Mean diff, A2 - B2** | -6,316 | | | | |
| **(A1 -B1) - (A2 - B2)** | -0,9089 | | | | |
| **95% CI of difference** | -2.034 to 0.2160 | | | | |
| **(B1 - A1) - (B2 - A2)** | 0,9089 | | | | |
| **95% CI of difference** | -0.2160 to 2.034 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 1,309 | 0,5196 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,7500 | 0,0424 | No | * | |
| **Shapiro-Wilk (W)** | 0,9321 | 0,1692 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1812 | 0,0841 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| **Number of values** | 20 |  |  |  |  |

## 2way ANOVA of Napepld hipp

| Table Analyzed | Napepld hipp | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 0,1377 | 0,8208 | ns | No | |
| **Injury** | 13,99 | 0,0379 | * | Yes | |
| **Genotype** | 55,04 | 0,0006 | *** | Yes | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 0,004567 | 1 | 0,004567 | F (1, 12) = 0.05358 | P=0.8208 |
| **Injury** | 0,4638 | 1 | 0,4638 | F (1, 12) = 5.442 | P=0.0379 |
| **Genotype** | 1,825 | 1 | 1,825 | F (1, 12) = 21.41 | P=0.0006 |
| **Residual** | 1,023 | 12 | 0,08524 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Mean of WT** | 0,8466 | | | | |
| **Mean of APP-SWE** | 1,522 | | | | |
| **Difference between means** | -0,6755 | | | | |
| **SE of difference** | 0,1460 | | | | |
| **95% CI of difference** | -0.9936 to -0.3575 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of Sham** | 1,355 | | | | |
| **Mean of mTBI** | 1,014 | | | | |
| **Difference between means** | 0,3405 | | | | |
| **SE of difference** | 0,1460 | | | | |
| **95% CI of difference** | 0.02247 to 0.6586 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | -0,7093 | | | | |
| **Mean diff, A2 - B2** | -0,6417 | | | | |
| **(A1 -B1) - (A2 - B2)** | -0,06758 | | | | |
| **95% CI of difference** | -0.7037 to 0.5685 | | | | |
| **(B1 - A1) - (B2 - A2)** | 0,06758 | | | | |
| **95% CI of difference** | -0.5685 to 0.7037 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 10,79 | 0,0045 | No | ** | |
| **Anderson-Darling (A2*)** | 0,6631 | 0,0676 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,8681 | 0,0254 | No | * | |
| **Kolmogorov-Smirnov (distance)** | 0,2134 | 0,0498 | No | * | |
| | | | | | |
| **Data summary** | | | | | |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| **Number of columns (Genotype)** | 2 |  |  |  |  |
| **Number of rows (Injury)** | 2 |  |  |  |  |
| **Number of values** | 16 |  |  |  |  |

2way ANOVA of Gde1 hipp

| **Table Analyzed** | **Gde1 hipp** | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 1,771 | 0,2159 | ns | No | |
| **Injury** | 0,05964 | 0,8146 | ns | No | |
| **Genotype** | 85,72 | <0.0001 | **** | Yes | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 0,06592 | 1 | 0,06592 | F (1, 12) = 1.707 | P=0.2159 |
| **Injury** | 0,002220 | 1 | 0,002220 | F (1, 12) = 0.05747 | P=0.8146 |
| **Genotype** | 3,191 | 1 | 3,191 | F (1, 12) = 82.60 | P<0.0001 |
| **Residual** | 0,4635 | 12 | 0,03863 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Mean of WT** | 0,9240 | | | | |
| **Mean of APP-SWE** | 1,817 | | | | |
| **Difference between means** | -0,8931 | | | | |
| **SE of difference** | 0,09827 | | | | |
| **95% CI of difference** | -1.107 to -0.6790 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of Sham** | 1,382 | | | | |
| **Mean of mTBI** | 1,359 | | | | |
| **Difference between means** | 0,02356 | | | | |
| **SE of difference** | 0,09827 | | | | |
| **95% CI of difference** | -0.1906 to 0.2377 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | -0,7647 | | | | |
| **Mean diff, A2 - B2** | -1,021 | | | | |
| **(A1 -B1) - (A2 - B2)** | 0,2568 | | | | |
| **95% CI of difference** | -0.1715 to 0.6850 | | | | |
| **(B1 - A1) - (B2 - A2)** | -0,2568 | | | | |
| **95% CI of difference** | -0.6850 to 0.1715 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 1,874 | 0,3918 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,3199 | 0,5039 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,9477 | 0,4537 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1508 | 0,1000 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |
| **Number of columns (Genotype)** | 2 | | | | |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| **Number of rows (Injury)** | 2 |  |  |  |  |
| **Number of values** | 16 |  |  |  |  |

# 2way ANOVA of Faah hipp

| **Table Analyzed** | **Faah hipp** | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 7,260 | 0,1554 | ns | No | |
| **Injury** | 4,677 | 0,2471 | ns | No | |
| **Genotype** | 50,16 | 0,0018 | ** | Yes | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 0,1243 | 1 | 0,1243 | F (1, 12) = 2.298 | P=0.1554 |
| **Injury** | 0,08007 | 1 | 0,08007 | F (1, 12) = 1.481 | P=0.2471 |
| **Genotype** | 0,8586 | 1 | 0,8586 | F (1, 12) = 15.88 | P=0.0018 |
| **Residual** | 0,6489 | 12 | 0,05408 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Mean of WT** | 0,9826 | | | | |
| **Mean of APP-SWE** | 1,446 | | | | |
| **Difference between means** | -0,4633 | | | | |
| **SE of difference** | 0,1163 | | | | |
| **95% CI of difference** | -0.7166 to -0.2100 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of Sham** | 1,144 | | | | |
| **Mean of mTBI** | 1,285 | | | | |
| **Difference between means** | -0,1415 | | | | |
| **SE of difference** | 0,1163 | | | | |
| **95% CI of difference** | -0.3948 to 0.1119 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | -0,2870 | | | | |
| **Mean diff, A2 - B2** | -0,6396 | | | | |
| **(A1 -B1) - (A2 - B2)** | 0,3525 | | | | |
| **95% CI of difference** | -0.1541 to 0.8592 | | | | |
| **(B1 - A1) - (B2 - A2)** | -0,3525 | | | | |
| **95% CI of difference** | -0.8592 to 0.1541 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 8,786 | 0,0124 | No | * | |
| **Anderson-Darling (A2*)** | 0,8020 | 0,0294 | No | * | |
| **Shapiro-Wilk (W)** | 0,8714 | 0,0285 | No | * | |
| **Kolmogorov-Smirnov (distance)** | 0,2111 | 0,0550 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |
| **Number of values** | 16 | | | | |

## 2way ANOVA of Dagla hipp

| **Table Analyzed** | **Dagla hipp** | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 0,2469 | 0,7057 | ns | No | |
| **Injury** | 5,343 | 0,0972 | ns | No | |
| **Genotype** | 74,60 | <0.0001 | **** | Yes | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 0,01094 | 1 | 0,01094 | F (1, 12) = 0.1496 | P=0.7057 |
| **Injury** | 0,2368 | 1 | 0,2368 | F (1, 12) = 3.237 | P=0.0972 |
| **Genotype** | 3,306 | 1 | 3,306 | F (1, 12) = 45.19 | P<0.0001 |
| **Residual** | 0,8780 | 12 | 0,07317 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Mean of WT** | 0,9045 | | | | |
| **Mean of APP-SWE** | 1,814 | | | | |
| **Difference between means** | -0,9092 | | | | |
| **SE of difference** | 0,1352 | | | | |
| **95% CI of difference** | -1.204 to -0.6145 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of Sham** | 1,481 | | | | |
| **Mean of mTBI** | 1,237 | | | | |
| **Difference between means** | 0,2433 | | | | |
| **SE of difference** | 0,1352 | | | | |
| **95% CI of difference** | -0.05136 to 0.5380 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | -0,9615 | | | | |
| **Mean diff, A2 - B2** | -0,8569 | | | | |
| **(A1 -B1) - (A2 - B2)** | -0,1046 | | | | |
| **95% CI of difference** | -0.6940 to 0.4847 | | | | |
| **(B1 - A1) - (B2 - A2)** | 0,1046 | | | | |
| **95% CI of difference** | -0.4847 to 0.6940 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 1,250 | 0,5354 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,2495 | 0,6999 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,9758 | 0,9214 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1239 | 0,1000 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |
| **Number of values** | 16 | | | | |

# 2way ANOVA of Magl hipp

| Table Analyzed | Magl hipp | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 0,4712 | 0,7848 | ns | No | |
| **Injury** | 9,465 | 0,2346 | ns | No | |
| **Genotype** | 17,53 | 0,1143 | ns | No | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 0,07526 | 1 | 0,07526 | F (1, 12) = 0.07797 | P=0.7848 |
| **Injury** | 1,512 | 1 | 1,512 | F (1, 12) = 1.566 | P=0.2346 |
| **Genotype** | 2,800 | 1 | 2,800 | F (1, 12) = 2.901 | P=0.1143 |
| **Residual** | 11,58 | 12 | 0,9653 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Mean of WT** | 0,7612 | | | | |
| **Mean of APP-SWE** | 1,598 | | | | |
| **Difference between means** | -0,8367 | | | | |
| **SE of difference** | 0,4913 | | | | |
| **95% CI of difference** | -1.907 to 0.2336 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of Sham** | 1,487 | | | | |
| **Mean of mTBI** | 0,8722 | | | | |
| **Difference between means** | 0,6147 | | | | |
| **SE of difference** | 0,4913 | | | | |
| **95% CI of difference** | -0.4556 to 1.685 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | -0,9739 | | | | |
| **Mean diff, A2 - B2** | -0,6995 | | | | |
| **(A1 -B1) - (A2 - B2)** | -0,2743 | | | | |
| **95% CI of difference** | -2.415 to 1.866 | | | | |
| **(B1 - A1) - (B2 - A2)** | 0,2743 | | | | |
| **95% CI of difference** | -1.866 to 2.415 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 6,711 | 0,0349 | No | * | |
| **Anderson-Darling (A2*)** | 0,5627 | 0,1211 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,9214 | 0,1779 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1835 | 0,1000 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |
| **Number of values** | 16 | | | | |

## 2way ANOVA of Cb1 hipp

| Table Analyzed | Cb1 hipp | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 4,508 | 0,2359 | ns | No | |
| Injury | 15,35 | 0,0400 | * | Yes | |
| Genotype | 45,40 | 0,0019 | ** | Yes | |
| | | | | | |
| ANOVA table | SS | DF | MS | F (DFn, DFd) | P value |
| Interaction | 0,03596 | 1 | 0,03596 | F (1, 12) = 1.557 | P=0.2359 |
| Injury | 0,1225 | 1 | 0,1225 | F (1, 12) = 5.303 | P=0.0400 |
| Genotype | 0,3622 | 1 | 0,3622 | F (1, 12) = 15.68 | P=0.0019 |
| Residual | 0,2771 | 12 | 0,02309 | | |
| | | | | | |
| Difference between column means | | | | | |
| Mean of WT | 0,8651 | | | | |
| Mean of APP-SWE | 1,166 | | | | |
| Difference between means | -0,3009 | | | | |
| SE of difference | 0,07598 | | | | |
| 95% CI of difference | -0.4665 to -0.1354 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Mean of Sham | 1,103 | | | | |
| Mean of mTBI | 0,9281 | | | | |
| Difference between means | 0,1750 | | | | |
| SE of difference | 0,07598 | | | | |
| 95% CI of difference | 0.009419 to 0.3405 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | -0,2061 | | | | |
| Mean diff, A2 - B2 | -0,3957 | | | | |
| (A1 -B1) - (A2 - B2) | 0,1896 | | | | |
| 95% CI of difference | -0.1415 to 0.5207 | | | | |
| (B1 - A1) - (B2 - A2) | -0,1896 | | | | |
| 95% CI of difference | -0.5207 to 0.1415 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 2,271 | 0,3212 | Yes | ns | |
| Anderson-Darling (A2*) | 0,2881 | 0,5711 | Yes | ns | |
| Shapiro-Wilk (W) | 0,9509 | 0,5042 | Yes | ns | |
| Kolmogorov-Smirnov (distance) | 0,1363 | 0,1000 | Yes | ns | |
| | | | | | |
| Data summary | | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |
| **Number of values** | 16 | | | | |

## 2way ANOVA of Ppara hipp

| **Table Analyzed** | **Ppara hipp** | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 20,73 | 0,0037 | ** | Yes | |
| **Injury** | 2,152 | 0,2703 | ns | No | |
| **Genotype** | 57,79 | <0.0001 | **** | Yes | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 0,3246 | 1 | 0,3246 | F (1, 12) = 12.86 | P=0.0037 |
| **Injury** | 0,03370 | 1 | 0,03370 | F (1, 12) = 1.336 | P=0.2703 |
| **Genotype** | 0,9050 | 1 | 0,9050 | F (1, 12) = 35.87 | P<0.0001 |
| **Residual** | 0,3028 | 12 | 0,02523 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Mean of WT** | 0,8117 | | | | |
| **Mean of APP-SWE** | 0,3360 | | | | |
| **Difference between means** | 0,4757 | | | | |
| **SE of difference** | 0,07942 | | | | |
| **95% CI of difference** | 0.3026 to 0.6487 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of Sham** | 0,6197 | | | | |
| **Mean of mTBI** | 0,5280 | | | | |
| **Difference between means** | 0,09179 | | | | |
| **SE of difference** | 0,07942 | | | | |
| **95% CI of difference** | -0.08125 to 0.2648 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | 0,7605 | | | | |
| **Mean diff, A2 - B2** | 0,1908 | | | | |
| **(A1 -B1) - (A2 - B2)** | 0,5697 | | | | |
| **95% CI of difference** | 0.2236 to 0.9158 | | | | |
| **(B1 - A1) - (B2 - A2)** | -0,5697 | | | | |
| **95% CI of difference** | -0.9158 to -0.2236 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 0,6883 | 0,7088 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,1990 | 0,8610 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,9820 | 0,9775 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1107 | 0,1000 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| **Number of columns (Genotype)** | 2 |  |  |  |  |
| **Number of rows (Injury)** | 2 |  |  |  |  |
| **Number of values** | 16 |  |  |  |  |

## 2way ANOVA of Pparg hipp

| Table Analyzed | Pparg hipp | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 8,959 | <0.0001 | **** | Yes | |
| Injury | 3,234 | 0,0030 | ** | Yes | |
| Genotype | 84,99 | <0.0001 | **** | Yes | |
| | | | | | |
| ANOVA table | SS | DF | MS | F (DFn, DFd) | P value |
| Interaction | 2,061 | 1 | 2,061 | F (1, 12) = 38.19 | P<0.0001 |
| Injury | 0,7442 | 1 | 0,7442 | F (1, 12) = 13.79 | P=0.0030 |
| Genotype | 19,56 | 1 | 19,56 | F (1, 12) = 362.3 | P<0.0001 |
| Residual | 0,6478 | 12 | 0,05398 | | |
| | | | | | |
| Difference between column means | | | | | |
| Mean of WT | 0,8567 | | | | |
| Mean of APP-SWE | 3,068 | | | | |
| Difference between means | -2,211 | | | | |
| SE of difference | 0,1162 | | | | |
| 95% CI of difference | -2.464 to -1.958 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Mean of Sham | 1,747 | | | | |
| Mean of mTBI | 2,178 | | | | |
| Difference between means | -0,4313 | | | | |
| SE of difference | 0,1162 | | | | |
| 95% CI of difference | -0.6844 to -0.1782 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | -1,493 | | | | |
| Mean diff, A2 - B2 | -2,929 | | | | |
| (A1 -B1) - (A2 - B2) | 1,436 | | | | |
| 95% CI of difference | 0.9295 to 1.942 | | | | |
| (B1 - A1) - (B2 - A2) | -1,436 | | | | |
| 95% CI of difference | -1.942 to -0.9295 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 2,233 | 0,3274 | Yes | ns | |
| Anderson-Darling (A2*) | 0,4595 | 0,2270 | Yes | ns | |
| Shapiro-Wilk (W) | 0,9378 | 0,3224 | Yes | ns | |
| Kolmogorov-Smirnov (distance) | 0,1669 | 0,1000 | Yes | ns | |
| | | | | | |
| Data summary | | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |
| **Number of values** | 16 | | | | |

# 2way ANOVA of 5HT cortex

| **Table Analyzed** | **5HT cortex** | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 0,2273 | 0,7059 | ns | No | |
| **Injury** | 51,79 | 0,0004 | *** | Yes | |
| **Genotype** | 36,10 | 0,0012 | ** | Yes | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 21194834 | 1 | 21194834 | F (1, 8) = 0.1530 | P=0.7059 |
| **Injury** | 4830254644 | 1 | 4830254644 | F (1, 8) = 34.86 | P=0.0004 |
| **Genotype** | 3366372064 | 1 | 3366372064 | F (1, 8) = 24.30 | P=0.0012 |
| **Residual** | 1108371191 | 8 | 138546399 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Mean of WT** | 98341 | | | | |
| **Mean of APP-SWE** | 64842 | | | | |
| **Difference between means** | 33498 | | | | |
| **SE of difference** | 6796 | | | | |
| **95% CI of difference** | 17827 to 49169 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of Sham** | 101654 | | | | |
| **Mean of mTBI** | 61529 | | | | |
| **Difference between means** | 40126 | | | | |
| **SE of difference** | 6796 | | | | |
| **95% CI of difference** | 24455 to 55797 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | 30840 | | | | |
| **Mean diff, A2 - B2** | 36156 | | | | |
| **(A1 -B1) - (A2 - B2)** | -5316 | | | | |
| **95% CI of difference** | -36658 to 26026 | | | | |
| **(B1 - A1) - (B2 - A2)** | 5316 | | | | |
| **95% CI of difference** | -26026 to 36658 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 2,403 | 0,3008 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,3764 | 0,3513 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,9222 | 0,3044 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1711 | 0,1000 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |
| **Number of values** | 12 | | | | |

## 2way ANOVA of 5HT hipp

| **Table Analyzed** | **5HT hipp** | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 12,70 | 0,0914 | ns | No | |
| **Injury** | 10,67 | 0,1168 | ns | No | |
| **Genotype** | 49,01 | 0,0055 | ** | Yes | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 2733073668 | 1 | 2733073668 | F (1, 8) = 3.678 | P=0.0914 |
| **Injury** | 2296419101 | 1 | 2296419101 | F (1, 8) = 3.091 | P=0.1168 |
| **Genotype** | 10546404413 | 1 | 10546404413 | F (1, 8) = 14.19 | P=0.0055 |
| **Residual** | 5944130395 | 8 | 743016299 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Mean of WT** | 116963 | | | | |
| **Mean of APP-SWE** | 176254 | | | | |
| **Difference between means** | -59291 | | | | |
| **SE of difference** | 15738 | | | | |
| **95% CI of difference** | -95582 to -23000 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of Sham** | 160442 | | | | |
| **Mean of mTBI** | 132775 | | | | |
| **Difference between means** | 27667 | | | | |
| **SE of difference** | 15738 | | | | |
| **95% CI of difference** | -8624 to 63958 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | -89475 | | | | |
| **Mean diff, A2 - B2** | -29108 | | | | |
| **(A1 -B1) - (A2 - B2)** | -60366 | | | | |
| **95% CI of difference** | -132948 to 12216 | | | | |
| **(B1 - A1) - (B2 - A2)** | 60366 | | | | |
| **95% CI of difference** | -12216 to 132948 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 1,393 | 0,4982 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,2786 | 0,5815 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,9451 | 0,5673 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1469 | 0,1000 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |
| **Number of values** | 12 | | | | |

# 2way ANOVA of 5HIAA cortex

| **Compare cell means regardless of rows and columns** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | | | | | | | |
| **Number of families** | 1 | | | | | | | |
| **Number of comparisons per family** | 6 | | | | | | | |
| **Alpha** | 0,05 | | | | | | | |
| | | | | | | | | |
| **Tukey's multiple comparisons test** | Mean Diff. | 95.00% CI of diff. | Below threshold? | Summary | Adjusted P Value | | | |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | 2718 | -1751 to 7187 | No | ns | 0,2824 | | | |
| **Sham:WT vs. mTBI:WT** | 760,8 | -3708 to 5230 | No | ns | 0,9453 | | | |
| **Sham:WT vs. mTBI:APP-SWE** | 7200 | 2731 to 11669 | Yes | ** | 0,0038 | | | |
| **Sham:APP-SWE vs. mTBI:WT** | -1957 | -6427 to 2512 | No | ns | 0,5315 | | | |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 4481 | 12.29 to 8950 | Yes | * | 0,0494 | | | |
| **mTBI:WT vs. mTBI:APP-SWE** | 6439 | 1970 to 10908 | Yes | ** | 0,0075 | | | |
| | | | | | | | | |
| | | | | | | | | |
| **Test details** | Mean 1 | Mean 2 | Mean Diff. | SE of diff. | N1 | N2 | q | DF |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | 12371 | 9653 | 2718 | 1396 | 3 | 3 | 2,755 | 8,000 |
| **Sham:WT vs. mTBI:WT** | 12371 | 11610 | 760,8 | 1396 | 3 | 3 | 0,7710 | 8,000 |
| **Sham:WT vs. mTBI:APP-SWE** | 12371 | 5171 | 7200 | 1396 | 3 | 3 | 7,296 | 8,000 |
| **Sham:APP-SWE vs. mTBI:WT** | 9653 | 11610 | -1957 | 1396 | 3 | 3 | 1,984 | 8,000 |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 9653 | 5171 | 4481 | 1396 | 3 | 3 | 4,541 | 8,000 |
| **mTBI:WT vs. mTBI:APP-SWE** | 11610 | 5171 | 6439 | 1396 | 3 | 3 | 6,525 | 8,000 |

## 2way ANOVA of 5HIAA hipp

| **Compare cell means regardless of rows and columns** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | | | | | | | |
| **Number of families** | 1 | | | | | | | |
| **Number of comparisons per family** | 6 | | | | | | | |
| **Alpha** | 0,05 | | | | | | | |
| | | | | | | | | |
| **Tukey's multiple comparisons test** | Mean Diff. | 95.00% CI of diff. | Below threshold? | Summary | Adjusted P Value | | | |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | -15237 | -23328 to -7146 | Yes | ** | 0,0014 | | | |
| **Sham:WT vs. mTBI:WT** | -9070 | -17161 to -979.3 | Yes | * | 0,0291 | | | |
| **Sham:WT vs. mTBI:APP-SWE** | -3921 | -12012 to 4170 | No | ns | 0,4537 | | | |
| **Sham:APP-SWE vs. mTBI:WT** | 6167 | -1924 to 14258 | No | ns | 0,1460 | | | |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 11316 | 3225 to 19407 | Yes | ** | 0,0089 | | | |
| **mTBI:WT vs. mTBI:APP-SWE** | 5150 | -2942 to 13241 | No | ns | 0,2513 | | | |
| | | | | | | | | |
| | | | | | | | | |
| **Test details** | Mean 1 | Mean 2 | Mean Diff. | SE of diff. | N1 | N2 | q | DF |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | 28276 | 43513 | -15237 | 2527 | 3 | 3 | 8,529 | 8,000 |
| **Sham:WT vs. mTBI:WT** | 28276 | 37346 | -9070 | 2527 | 3 | 3 | 5,077 | 8,000 |
| **Sham:WT vs. mTBI:APP-SWE** | 28276 | 32197 | -3921 | 2527 | 3 | 3 | 2,195 | 8,000 |
| **Sham:APP-SWE vs. mTBI:WT** | 43513 | 37346 | 6167 | 2527 | 3 | 3 | 3,452 | 8,000 |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 43513 | 32197 | 11316 | 2527 | 3 | 3 | 6,334 | 8,000 |
| **mTBI:WT vs. mTBI:APP-SWE** | 37346 | 32197 | 5150 | 2527 | 3 | 3 | 2,882 | 8,000 |

## 2way ANOVA of OA5HT cortex MSI

| **Table Analyzed** | **OA5HT cortex MSI** | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 7,126 | 0,0787 | ns | No | |
| **Injury** | 28,58 | 0,0038 | ** | Yes | |
| **Genotype** | 50,26 | 0,0007 | *** | Yes | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 398747 | 1 | 398747 | F (1, 8) = 4.061 | P=0.0787 |
| **Injury** | 1598982 | 1 | 1598982 | F (1, 8) = 16.28 | P=0.0038 |
| **Genotype** | 2812067 | 1 | 2812067 | F (1, 8) = 28.64 | P=0.0007 |
| **Residual** | 785589 | 8 | 98199 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Mean of WT** | 1910 | | | | |
| **Mean of APP-SWE** | 941,6 | | | | |
| **Difference between means** | 968,2 | | | | |
| **SE of difference** | 180,9 | | | | |
| **95% CI of difference** | 551.0 to 1385 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of Sham** | 1061 | | | | |
| **Mean of mTBI** | 1791 | | | | |
| **Difference between means** | -730,1 | | | | |
| **SE of difference** | 180,9 | | | | |
| **95% CI of difference** | -1147 to -312.9 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | 603,6 | | | | |
| **Mean diff, A2 - B2** | 1333 | | | | |
| **(A1 -B1) - (A2 - B2)** | -729,2 | | | | |
| **95% CI of difference** | -1564 to 105.3 | | | | |
| **(B1 - A1) - (B2 - A2)** | 729,2 | | | | |
| **95% CI of difference** | -105.3 to 1564 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 0,06299 | 0,9690 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,1739 | 0,9034 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,9736 | 0,9448 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1111 | 0,1000 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| **Number of columns (Genotype)** | 2 |  |  |  |  |
| **Number of rows (Injury)** | 2 |  |  |  |  |
| **Number of values** | 12 |  |  |  |  |

2way ANOVA of OA5HT hipp MSI

| **Table Analyzed** | **OA5HT hipp MSI** | | | | |
|---|---|---|---|---|---|
| | | | | | |
| **Two-way ANOVA** | Ordinary | | | | |
| **Alpha** | 0,05 | | | | |
| | | | | | |
| **Source of Variation** | % of total variation | P value | P value summary | Significant? | |
| **Interaction** | 3,522 | 0,3953 | ns | No | |
| **Injury** | 0,8273 | 0,6748 | ns | No | |
| **Genotype** | 60,73 | 0,0058 | ** | Yes | |
| | | | | | |
| **ANOVA table** | SS | DF | MS | F (DFn, DFd) | P value |
| **Interaction** | 62538 | 1 | 62538 | F (1, 8) = 0.8068 | P=0.3953 |
| **Injury** | 14690 | 1 | 14690 | F (1, 8) = 0.1895 | P=0.6748 |
| **Genotype** | 1078354 | 1 | 1078354 | F (1, 8) = 13.91 | P=0.0058 |
| **Residual** | 620144 | 8 | 77518 | | |
| | | | | | |
| **Difference between column means** | | | | | |
| **Mean of WT** | 1762 | | | | |
| **Mean of APP-SWE** | 1163 | | | | |
| **Difference between means** | 599,5 | | | | |
| **SE of difference** | 160,7 | | | | |
| **95% CI of difference** | 228.9 to 970.2 | | | | |
| | | | | | |
| **Difference between row means** | | | | | |
| **Mean of Sham** | 1497 | | | | |
| **Mean of mTBI** | 1428 | | | | |
| **Difference between means** | 69,98 | | | | |
| **SE of difference** | 160,7 | | | | |
| **95% CI of difference** | -300.7 to 440.7 | | | | |
| | | | | | |
| **Interaction CI** | | | | | |
| **Mean diff, A1 - B1** | 455,2 | | | | |
| **Mean diff, A2 - B2** | 743,9 | | | | |
| **(A1 -B1) - (A2 - B2)** | -288,8 | | | | |
| **95% CI of difference** | -1030 to 452.6 | | | | |
| **(B1 - A1) - (B2 - A2)** | 288,8 | | | | |
| **95% CI of difference** | -452.6 to 1030 | | | | |
| | | | | | |
| **Normality of Residuals** | | | | | |
| **Test name** | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| **D'Agostino-Pearson omnibus (K2)** | 2,457 | 0,2928 | Yes | ns | |
| **Anderson-Darling (A2*)** | 0,5893 | 0,0977 | Yes | ns | |
| **Shapiro-Wilk (W)** | 0,8684 | 0,0624 | Yes | ns | |
| **Kolmogorov-Smirnov (distance)** | 0,1512 | 0,1000 | Yes | ns | |
| | | | | | |
| **Data summary** | | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |
| **Number of values** | 12 | | | | |

## 2way ANOVA of Gene 5HT2a cortex

| Table Analyzed | Gene 5HT2a cortex | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 13,14 | 0,0043 | ** | Yes | |
| Injury | 41,68 | 0,0001 | *** | Yes | |
| Genotype | 38,40 | 0,0001 | *** | Yes | |
| | | | | | |
| ANOVA table | SS | DF | MS | F (DFn, DFd) | P value |
| Interaction | 0,08100 | 1 | 0,08100 | F (1, 8) = 15.49 | P=0.0043 |
| Injury | 0,2569 | 1 | 0,2569 | F (1, 8) = 49.15 | P=0.0001 |
| Genotype | 0,2367 | 1 | 0,2367 | F (1, 8) = 45.28 | P=0.0001 |
| Residual | 0,04182 | 8 | 0,005227 | | |
| | | | | | |
| Difference between column means | | | | | |
| Mean of WT | 0,9358 | | | | |
| Mean of APP-SWE | 1,217 | | | | |
| Difference between means | -0,2809 | | | | |
| SE of difference | 0,04174 | | | | |
| 95% CI of difference | -0.3772 to -0.1846 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Mean of Sham | 1,223 | | | | |
| Mean of mTBI | 0,9300 | | | | |
| Difference between means | 0,2926 | | | | |
| SE of difference | 0,04174 | | | | |
| 95% CI of difference | 0.1964 to 0.3889 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | -0,4452 | | | | |
| Mean diff, A2 - B2 | -0,1166 | | | | |
| (A1 -B1) - (A2 - B2) | -0,3286 | | | | |
| 95% CI of difference | -0.5211 to -0.1361 | | | | |
| (B1 - A1) - (B2 - A2) | 0,3286 | | | | |
| 95% CI of difference | 0.1361 to 0.5211 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 2,032 | 0,3621 | Yes | ns | |
| Anderson-Darling (A2*) | 0,3245 | 0,4732 | Yes | ns | |
| Shapiro-Wilk (W) | 0,9307 | 0,3873 | Yes | ns | |
| Kolmogorov-Smirnov (distance) | 0,1690 | 0,1000 | Yes | ns | |
| | | | | | |
| Data summary | | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |
| **Number of values** | 12 | | | | |

## 2way ANOVA of Gene 5HT2a hipp

| **Compare cell means regardless of rows and columns** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | | | | | | | |
| **Number of families** | 1 | | | | | | | |
| **Number of comparisons per family** | 6 | | | | | | | |
| **Alpha** | 0,05 | | | | | | | |
| | | | | | | | | |
| **Tukey's multiple comparisons test** | Predicted (LS) mean diff. | 95.00% CI of diff. | Below threshold? | Summary | Adjusted P Value | | | |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | 0,4285 | -0.1428 to 0.9998 | No | ns | 0,1845 | | | |
| **Sham:WT vs. mTBI:WT** | 0,05278 | -0.5917 to 0.6973 | No | ns | 0,9955 | | | |
| **Sham:WT vs. mTBI:APP-SWE** | 0,4716 | -0.09973 to 1.043 | No | ns | 0,1275 | | | |
| **Sham:APP-SWE vs. mTBI:WT** | -0,3757 | -0.9470 to 0.1956 | No | ns | 0,2799 | | | |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 0,04307 | -0.4441 to 0.5303 | No | ns | 0,9943 | | | |
| **mTBI:WT vs. mTBI:APP-SWE** | 0,4188 | -0.1525 to 0.9901 | No | ns | 0,1999 | | | |
| | | | | | | | | |
| | | | | | | | | |
| **Test details** | Predicted (LS) mean 1 | Predicted (LS) mean 2 | Predicted (LS) mean diff. | SE of diff. | N1 | N2 | q | DF |
| | | | | | | | | |
| **Sham:WT vs. Sham:APP-SWE** | 1,000 | 0,5715 | 0,4285 | 0,2021 | 4 | 7 | 2,998 | 18,00 |
| **Sham:WT vs. mTBI:WT** | 1,000 | 0,9472 | 0,05278 | 0,2280 | 4 | 4 | 0,3273 | 18,00 |
| **Sham:WT vs. mTBI:APP-SWE** | 1,000 | 0,5284 | 0,4716 | 0,2021 | 4 | 7 | 3,299 | 18,00 |
| **Sham:APP-SWE vs. mTBI:WT** | 0,5715 | 0,9472 | -0,3757 | 0,2021 | 7 | 4 | 2,629 | 18,00 |
| **Sham:APP-SWE vs. mTBI:APP-SWE** | 0,5715 | 0,5284 | 0,04307 | 0,1724 | 7 | 7 | 0,3533 | 18,00 |
| **mTBI:WT vs. mTBI:APP-SWE** | 0,9472 | 0,5284 | 0,4188 | 0,2021 | 4 | 7 | 2,930 | 18,00 |

# 2way ANOVA of 5HT2a:CB1 cortex

| Table Analyzed | 5HT2a/CB1 cortex | | | | |
|---|---|---|---|---|---|
| | | | | | |
| Two-way ANOVA | Ordinary | | | | |
| Alpha | 0,05 | | | | |
| | | | | | |
| Source of Variation | % of total variation | P value | P value summary | Significant? | |
| Interaction | 38,99 | <0.0001 | **** | Yes | |
| Injury | 32,34 | <0.0001 | **** | Yes | |
| Genotype | 28,37 | <0.0001 | **** | Yes | |
| | | | | | |
| ANOVA table | SS | DF | MS | F (DFn, DFd) | P value |
| Interaction | 2,444 | 1 | 2,444 | F (1, 4) = 505.4 | P<0.0001 |
| Injury | 2,027 | 1 | 2,027 | F (1, 4) = 419.3 | P<0.0001 |
| Genotype | 1,778 | 1 | 1,778 | F (1, 4) = 367.7 | P<0.0001 |
| Residual | 0,01934 | 4 | 0,004835 | | |
| | | | | | |
| Difference between column means | | | | | |
| Mean of WT | 0,9507 | | | | |
| Mean of APP-SWE | 1,894 | | | | |
| Difference between means | -0,9429 | | | | |
| SE of difference | 0,04917 | | | | |
| 95% CI of difference | -1.079 to -0.8064 | | | | |
| | | | | | |
| Difference between row means | | | | | |
| Mean of Sham | 0,9188 | | | | |
| Mean of mTBI | 1,926 | | | | |
| Difference between means | -1,007 | | | | |
| SE of difference | 0,04917 | | | | |
| 95% CI of difference | -1.143 to -0.8703 | | | | |
| | | | | | |
| Interaction CI | | | | | |
| Mean diff, A1 - B1 | 0,1625 | | | | |
| Mean diff, A2 - B2 | -2,048 | | | | |
| (A1 -B1) - (A2 - B2) | 2,211 | | | | |
| 95% CI of difference | 1.938 to 2.484 | | | | |
| (B1 - A1) - (B2 - A2) | -2,211 | | | | |
| 95% CI of difference | -2.484 to -1.938 | | | | |
| | | | | | |
| Normality of Residuals | | | | | |
| Test name | Statistics | P value | Passed normality test (alpha=0.05)? | P value summary | |
| D'Agostino-Pearson omnibus (K2) | 0,3762 | 0,8285 | Yes | ns | |
| Anderson-Darling (A2*) | 0,3009 | 0,5018 | Yes | ns | |
| Shapiro-Wilk (W) | 0,9121 | 0,3693 | Yes | ns | |
| Kolmogorov-Smirnov (distance) | 0,1518 | 0,1000 | Yes | ns | |
| | | | | | |
| Data summary | | | | | |

| | | | | | |
|---|---|---|---|---|---|
| **Number of columns (Genotype)** | 2 | | | | |
| **Number of rows (Injury)** | 2 | | | | |
| **Number of values** | 8 | | | | |