

Absolute Winding Number by fx Probe Day d8

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Aim

We examine whether APOE2, APOE3, and APOE4 carriers use a hippocampal or caudate based spatial navigation strategy.

Day d8 Probe by fx Vol

```
## [1] "fx: Probe d8 AWN VOL"
## [1] "omnibus test"

## model term    df1 df2 F.ratio p.value
## Genotype      2  17  13.984  0.0003
## Sex            1  17   0.201  0.6598
## Genotype:Sex   2  17   1.296  0.2993

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype   2  17  17.285  0.0001
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype   2  17   4.369  0.0294

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.737  0.4026
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
```

```

## Sex          1  17   0.067  0.7995
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex          1  17   2.032  0.1721

## [1] "anova: males and females"

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## fx              1  33.797   33.797  10.6143  0.004632 **
## Genotype        2 161.668   80.834  25.3865  7.849e-06 ***
## Sex              1  13.696   13.696   4.3012  0.053591 .
## fx:Genotype     2   15.842    7.921   2.4876  0.112822
## fx:Sex           1    1.986    1.986   0.6239  0.440494
## Genotype:Sex    2   13.422    6.711   2.1077  0.152152
## fx:Genotype:Sex 2    5.257    2.628   0.8255  0.454848
## Residuals      17  54.130    3.184
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "females"

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## fx              1   0.080    0.080   0.0222  0.88586
## Genotype        2  87.676   43.838  12.2180  0.00521 **
## fx:Genotype     2  24.485   12.242   3.4121  0.09239 .
## Residuals       7  25.116    3.588
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "males"

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## fx              1  63.959   63.959  22.0440  0.0008478 ***
## Genotype        2  44.669   22.334   7.6977  0.0094671 **
## fx:Genotype     2   0.394    0.197   0.0680  0.9347212
## Residuals      10  29.014    2.901
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "pairwise-sidak adjustments"

## Genotype = APOE22:
## contrast      estimate    SE df t.ratio p.value
## female - male  -1.607  1.87 17  -0.858  0.4026
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male   0.366  1.42 17   0.258  0.7995

```

```

##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male    2.566 1.80 17    1.425  0.1721

## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    1.08 1.51 17    0.715  0.7579
## APOE22 - APOE44   -6.07 1.31 17   -4.654  0.0006
## APOE33 - APOE44   -7.16 1.41 17   -5.087  0.0003
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    3.06 1.80 17    1.702  0.2332
## APOE22 - APOE44   -1.90 2.24 17   -0.847  0.6797
## APOE33 - APOE44   -4.96 1.81 17   -2.738  0.0355
##
## P value adjustment: tukey method for comparing a family of 3 estimates
## [1] "slopes"

## $emtrends
## Genotype fx.trend    SE df lower.CL upper.CL
## APOE22    -103273 47518 17   -203528    -3019
## APOE33    -10276 35343 17    -84843    64291
## APOE44     -3771 43198 17    -94910    87368
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33   -92997 59221 17   -1.570  0.2849
## APOE22 - APOE44   -99502 64218 17   -1.549  0.2938
## APOE33 - APOE44   -6505 55814 17   -0.117  0.9925
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates
##
## $emtrends
## Sex = female:
## Genotype fx.trend    SE df lower.CL upper.CL
## APOE22    -119057 54731 17   -234528    -3585
## APOE33     48727 31082 17    -16850    114305
## APOE44     40836 33744 17    -30358    112029
##
## Sex = male:
## Genotype fx.trend    SE df lower.CL upper.CL
## APOE22    -87490 77694 17   -251410    76430
## APOE33    -69280 63485 17   -203222    64662
## APOE44    -48378 79533 17   -216178    119422
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:

```

```
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33 -167784  62941 17  -2.666  0.0410
## APOE22 - APOE44 -159892  64297 17  -2.487  0.0582
## APOE33 - APOE44   7892  45878 17   0.172  0.9838
##
## Sex = male:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33 -18210 100333 17  -0.181  0.9820
## APOE22 - APOE44 -39112 111184 17  -0.352  0.9343
## APOE33 - APOE44 -20902 101764 17  -0.205  0.9770
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Day d8 Probe By fx FA

```
## [1] "fx: Probe d8 AWN FA"
## [1] "omnibus test"

## model term    df1 df2 F.ratio p.value
## Genotype      2  17  14.976  0.0002
## Sex           1  17   0.508  0.4855
## Genotype:Sex   2  17   0.306  0.7402

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype   2  17   6.642  0.0074
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype   2  17   9.076  0.0021

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.961  0.3408
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.026  0.8742
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.229  0.6383

## [1] "anova: males and females"

## Analysis of Variance Table
##
## Response: Probe_d8
##          Df Sum Sq Mean Sq F value    Pr(>F)
## fx         1  22.551   22.551   5.3877  0.03296 *
## Genotype    2 196.795   98.398  23.5089 1.274e-05 ***
## Sex         1   3.213    3.213   0.7677  0.39313
## fx:Genotype  2   1.398    0.699   0.1670  0.84756
## fx:Sex       1   0.682    0.682   0.1630  0.69149
## Genotype:Sex  2   3.762    1.881   0.4494  0.64538
```

```

## fx:Genotype:Sex  2    0.242    0.121    0.0290    0.97151
## Residuals      17   71.154    4.186
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "females"

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## fx           1  16.330   16.330   3.3885  0.10822
## Genotype      2  87.028   43.514   9.0294  0.01152 *
## fx:Genotype   2   0.265    0.132   0.0275  0.97301
## Residuals     7  33.734    4.819
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "males"

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## fx           1   0.181    0.181   0.0484  0.830368
## Genotype      2  99.909   49.955  13.3497  0.001502 **
## fx:Genotype   2   0.526    0.263   0.0702  0.932639
## Residuals    10  37.420    3.742
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "pairwise-sidak adjustments"

## Genotype = APOE22:
## contrast      estimate    SE df t.ratio p.value
## female - male      1.74 1.78 17   0.980  0.3408
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male    -0.31 1.93 17  -0.161  0.8742
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male      0.74 1.55 17   0.479  0.6383
##
## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33     4.16 2.10 17   1.980  0.1475
## APOE22 - APOE44    -3.04 1.80 17  -1.694  0.2362
## APOE33 - APOE44    -7.20 1.98 17  -3.630  0.0056
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33     2.11 1.57 17   1.350  0.3881
## APOE22 - APOE44    -4.04 1.52 17  -2.653  0.0421
## APOE33 - APOE44    -6.15 1.47 17  -4.175  0.0017
##

```

```
## P value adjustment: tukey method for comparing a family of 3 estimates
## [1] "slopes"
## $emtrends
##      Genotype fx.trend      SE df lower.CL upper.CL
##      APOE22      -29.8  45.2 17      -125      65.4
##      APOE33      -52.5 121.0 17      -308     202.7
##      APOE44      -13.6  44.7 17      -108      80.7
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
##      contrast      estimate      SE df t.ratio p.value
##      APOE22 - APOE33      22.7 129.1 17      0.175  0.9832
##      APOE22 - APOE44     -16.3  63.5 17     -0.256  0.9645
##      APOE33 - APOE44     -38.9 129.0 17     -0.302  0.9511
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates
## $emtrends
## Sex = female:
##      Genotype fx.trend      SE df lower.CL upper.CL
##      APOE22      -49.3  79.2 17      -216     117.8
##      APOE33      -57.6  33.4 17      -128      12.9
##      APOE44      -44.4  41.1 17      -131      42.4
##
## Sex = male:
##      Genotype fx.trend      SE df lower.CL upper.CL
##      APOE22      -10.4  43.4 17      -102      81.2
##      APOE33      -47.5 239.6 17      -553     458.1
##      APOE44       17.2  79.3 17      -150     184.5
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##      contrast      estimate      SE df t.ratio p.value
##      APOE22 - APOE33       8.25  85.9 17      0.096  0.9949
##      APOE22 - APOE44     -4.93  89.2 17     -0.055  0.9983
##      APOE33 - APOE44    -13.18  53.0 17     -0.249  0.9665
##
## Sex = male:
##      contrast      estimate      SE df t.ratio p.value
##      APOE22 - APOE33     37.07 243.5 17      0.152  0.9873
##      APOE22 - APOE44    -27.64  90.4 17     -0.306  0.9499
##      APOE33 - APOE44    -64.71 252.4 17     -0.256  0.9645
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Day d8 Probe By fx DEG

```
## [1] "fx: Probe d8 AWN DEG"
```

```

## [1] "omnibus test"

## model term    df1 df2 F.ratio p.value
## Genotype      2  17  19.965 <.0001
## Sex           1  17   2.786  0.1134
## Genotype:Sex   2  17   0.227  0.7992

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype   2  17   8.665  0.0025
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype   2  17  11.939  0.0006

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex        1  17   1.918  0.1840
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.420  0.5255
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.649  0.4316

## [1] "anova: males and females"

## Analysis of Variance Table
##
## Response: Probe_d8
##          Df Sum Sq Mean Sq F value    Pr(>F)
## fx          1  20.768   20.768   5.3493  0.03352 *
## Genotype     2 188.692   94.346  24.3013 1.035e-05 ***
## Sex          1  12.573   12.573   3.2384  0.08971 .
## fx:Genotype   2   3.110    1.555   0.4005  0.67612
## fx:Sex        1   4.607    4.607   1.1866  0.29122
## Genotype:Sex   2   3.088    1.544   0.3977  0.67793
## fx:Genotype:Sex 2   0.961    0.480   0.1237  0.88441
## Residuals    17  66.000    3.882
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "females"

## Analysis of Variance Table
##
## Response: Probe_d8
##          Df Sum Sq Mean Sq F value    Pr(>F)
## fx          1  28.647   28.647   6.3306  0.04004 *
## Genotype     2  75.763   37.882   8.3713  0.01392 *
## fx:Genotype   2   1.270    0.635   0.1404  0.87144
## Residuals     7  31.676    4.525
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "males"

```

```

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## fx           1  1.550    1.550   0.4514 0.516871
## Genotype      2 99.418   49.709  14.4825 0.001113 **
## fx:Genotype   2  2.745    1.373   0.3999 0.680655
## Residuals    10 34.324    3.432
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "pairwise-sidak adjustments"

## Genotype = APOE22:
## contrast      estimate    SE df t.ratio p.value
## female - male    2.330 1.68 17   1.385  0.1840
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male    0.986 1.52 17   0.648  0.5255
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male    1.040 1.29 17   0.806  0.4316
##
## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    3.41 1.81 17   1.879  0.1750
## APOE22 - APOE44   -2.86 1.67 17  -1.709  0.2307
## APOE33 - APOE44   -6.26 1.51 17  -4.155  0.0018
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    2.07 1.36 17   1.516  0.3084
## APOE22 - APOE44   -4.15 1.30 17  -3.178  0.0144
## APOE33 - APOE44   -6.21 1.31 17  -4.753  0.0005
##
## P value adjustment: tukey method for comparing a family of 3 estimates

## [1] "slopes"

## $emtrends
## Genotype fx.trend      SE df  lower.CL upper.CL
## APOE22    3.85e-04 0.000392 17 -0.000442 0.001211
## APOE33    1.76e-04 0.000338 17 -0.000537 0.000889
## APOE44   -3.21e-05 0.000205 17 -0.000464 0.000400
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33 0.000209 0.000517 17   0.403  0.9146
## APOE22 - APOE44 0.000417 0.000442 17   0.943  0.6215
## APOE33 - APOE44 0.000208 0.000395 17   0.526  0.8596
##

```



```

## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
## Sex = female:
##      Genotype  fx.trend      SE df  lower.CL upper.CL
##      APOE22    5.28e-04 0.000455 17 -4.32e-04 0.001488
##      APOE33    2.71e-04 0.000161 17 -6.81e-05 0.000609
##      APOE44    2.43e-04 0.000220 17 -2.21e-04 0.000707
##
## Sex = male:
##      Genotype  fx.trend      SE df  lower.CL upper.CL
##      APOE22    2.42e-04 0.000638 17 -1.10e-03 0.001587
##      APOE33    8.12e-05 0.000657 17 -1.30e-03 0.001466
##      APOE44   -3.07e-04 0.000345 17 -1.04e-03 0.000421
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##      contrast      estimate      SE df t.ratio p.value
##      APOE22 - APOE33 2.57e-04 0.000483 17   0.533  0.8566
##      APOE22 - APOE44 2.84e-04 0.000505 17   0.562  0.8415
##      APOE33 - APOE44 2.73e-05 0.000272 17   0.100  0.9945
##
## Sex = male:
##      contrast      estimate      SE df t.ratio p.value
##      APOE22 - APOE33 1.61e-04 0.000915 17   0.175  0.9832
##      APOE22 - APOE44 5.49e-04 0.000725 17   0.757  0.7334
##      APOE33 - APOE44 3.89e-04 0.000742 17   0.524  0.8608
##
## P value adjustment: tukey method for comparing a family of 3 estimates

```

Day d8 Probe By fx CLUS

```

## [1] "fx: Probe d8 AWN CLUSTERING"
## [1] "omnibus test"

##      model term   df1 df2 F.ratio p.value
##      Genotype      2  17  19.354 <.0001
##      Sex            1  17   1.959  0.1796
##      Genotype:Sex    2  17   0.181  0.8359

## Sex = female:
##      model term df1 df2 F.ratio p.value
##      Genotype    2  17   8.473  0.0028
##
## Sex = male:
##      model term df1 df2 F.ratio p.value
##      Genotype    2  17  11.283  0.0008

## Genotype = APOE22:
##      model term df1 df2 F.ratio p.value
##      Sex         1  17   1.240  0.2811
##

```

```

## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex          1  17   0.334  0.5711
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex          1  17   0.439  0.5166

## model term      df1 df2 F.ratio p.value
## fx              1  17   0.316  0.5811
## Genotype        2  17  11.959  0.0006
## Sex              1  17   2.231  0.1536
## fx:Genotype      2  17   0.149  0.8630
## fx:Sex            1  17   1.154  0.2977
## Genotype:Sex      2  17   0.083  0.9208
## fx:Genotype:Sex   2  17   0.112  0.8945

## [1] "anova: males and females"

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## fx              1  19.022   19.022   4.8544  0.04166 *
## Genotype        2 188.277   94.139  24.0239 1.113e-05 ***
## Sex              1  13.295   13.295   3.3929  0.08299 .
## fx:Genotype      2   1.508    0.754   0.1925  0.82669
## fx:Sex            1   7.047    7.047   1.7983  0.19756
## Genotype:Sex      2   3.153    1.577   0.4023  0.67495
## fx:Genotype:Sex   2   0.879    0.440   0.1122  0.89451
## Residuals       17  66.615    3.919
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "females"

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## fx              1  29.730   29.730   6.4842  0.03830 *
## Genotype        2  75.324   37.662   8.2143  0.01458 *
## fx:Genotype      2   0.208    0.104   0.0226  0.97769
## Residuals       7  32.095    4.585
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "males"

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## fx              1   1.552    1.552   0.4496  0.517707
## Genotype        2 100.703   50.352  14.5860 0.001084 **
## fx:Genotype      2   1.260    0.630   0.1826  0.835854
## Residuals      10  34.520    3.452

```

```

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

## [1] "pairwise-sidak adjustments"

## Genotype = APOE22:
## contrast      estimate    SE df t.ratio p.value
## female - male    2.218 1.99 17   1.113  0.2811
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male    0.897 1.55 17   0.578  0.5711
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male    0.863 1.30 17   0.662  0.5166

## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    3.17 1.90 17   1.672  0.2441
## APOE22 - APOE44   -3.03 1.76 17  -1.726  0.2246
## APOE33 - APOE44   -6.20 1.51 17  -4.100  0.0020
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    1.85 1.67 17   1.107  0.5227
## APOE22 - APOE44   -4.39 1.61 17  -2.732  0.0360
## APOE33 - APOE44   -6.24 1.35 17  -4.624  0.0007
##
## P value adjustment: tukey method for comparing a family of 3 estimates

## [1] "slopes"

## $emtrends
## Genotype fx.trend      SE df lower.CL upper.CL
## APOE22    0.06938 0.1505 17   -0.248    0.387
## APOE33    0.03644 0.0783 17   -0.129    0.202
## APOE44   -0.00414 0.0625 17   -0.136    0.128
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    0.0329 0.170 17   0.194  0.9794
## APOE22 - APOE44    0.0735 0.163 17   0.451  0.8945
## APOE33 - APOE44    0.0406 0.100 17   0.405  0.9140
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
## Sex = female:
## Genotype fx.trend      SE df lower.CL upper.CL
## APOE22    0.1207 0.1445 17  -0.1842    0.426
## APOE33    0.0855 0.0505 17  -0.0211    0.192
## APOE44    0.0896 0.0690 17  -0.0559    0.235

```

```

##
## Sex = male:
## Genotype fx.trend      SE df lower.CL upper.CL
## APOE22      0.0180 0.2639 17  -0.5388   0.575
## APOE33     -0.0126 0.1482 17  -0.3253   0.300
## APOE44     -0.0979 0.1043 17  -0.3180   0.122
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33  0.03523 0.1531 17   0.230  0.9713
## APOE22 - APOE44  0.03108 0.1601 17   0.194  0.9795
## APOE33 - APOE44 -0.00416 0.0855 17  -0.049  0.9987
##
## Sex = male:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33  0.03065 0.3027 17   0.101  0.9944
## APOE22 - APOE44  0.11597 0.2838 17   0.409  0.9125
## APOE33 - APOE44  0.08532 0.1812 17   0.471  0.8858
##
## P value adjustment: tukey method for comparing a family of 3 estimates
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```

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##
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```

