Winding_by_Hc

alexandra badea

10/4/2021

Contents

Aim **8**

Day 5 Probe by Hc Vol **8**

List of 7 . . . 10
$ panel.grid :List of 6 . . . 11
..$ colour : chr “grey85” . . . 11
..$ size : num 0.5 . . . 11
..$ linetype : num 1 . . . 11
..$ lineend : chr “butt” . . . 11
..$ arrow : logi FALSE . . . 11
..$ inherit.blank: logi FALSE . . . 11
..- attr(*, “class”)= chr [1:2] “element_line” “element” . . . 11
$ panel.grid.major : NULL . . . 11
$ panel.grid.minor :List of 6 . . . 11
..$ colour : chr “grey85” . . . 11
..$ size : num 0.2 . . . 11
..$ linetype : num 1 . . . 11
..$ lineend : chr “butt” . . . 11
..$ arrow : logi FALSE . . . 11
..$ inherit.blank: logi FALSE . . . 11
..- attr(*, “class”)= chr [1:2] “element_line” “element” . . . 11
$ panel.grid.major.x: NULL . . . 11
$ panel.grid.major.y: NULL . . . 11
$ panel.grid.minor.x: list() . . . 11
..- attr(*, “class”)= chr [1:2] “element_blank” “element” . . . 11
$ panel.grid.minor.y: list() . . . 11
..- attr(*, “class”)= chr [1:2] “element_blank” “element” . . . 11
- attr(*, “class”)= chr [1:2] “theme” “gg” . . . 11
- attr(*, “complete”)= logi FALSE . . . 11
- attr(*, “validate”)= logi TRUE . . . 11
. . . 11
Call: . . . 11
lm(formula = Probe_d5 ~ Hc * Genotype * Sex, data = geno_combined_FA) . . . 11
. . . 11
Residuals: . . . 11
Min 1Q Median 3Q Max . . . 12
-4.7884 -1.6344 -0.6007 0.9028 11.8871 . . . 12
. . . 12
Coefficients: . . . 12
Estimate Std. Error t value Pr(>|t|) . . . 12

(Intercept) 79.1555 65.0064 1.218 0.240 12
Hc -222.1334 242.7476 -0.915 0.373 12
GenotypeAPOE33 11.1811 80.4063 0.139 0.891 12
GenotypeAPOE44 0.1215 81.2783 0.001 0.999 12
Sexmale -52.3686 84.4278 -0.620 0.543 12
Hc:GenotypeAPOE33 -64.9119 307.5279 -0.211 0.835 12
Hc:GenotypeAPOE44 13.9267 311.6158 0.045 0.965 12
Hc:Sexmale 195.5625 318.1092 0.615 0.547 12
GenotypeAPOE33:Sexmale 8.7780 159.1224 0.055 0.957 12
GenotypeAPOE44:Sexmale -34.4001 124.5997 -0.276 0.786 12
Hc:GenotypeAPOE33:Sexmale -20.6269 612.5697 -0.034 0.974 12
Hc:GenotypeAPOE44:Sexmale 124.8552 478.4404 0.261 0.797 12
. 12
Residual standard error: 4.041 on 17 degrees of freedom 12
Multiple R-squared: 0.567, Adjusted R-squared: 0.2869 12
F-statistic: 2.024 on 11 and 17 DF, p-value: 0.09275 12
. 12
Call: 12
lm(formula = Probe_d5 ~ Hc * Genotype, data = combo_f_FA) 12
. 12
Residuals: 12
Min 1Q Median 3Q Max 12
-4.7884 -1.0771 -0.8191 -0.0791 11.8871 12
. 12
Coefficients: 12
Estimate Std. Error t value Pr(>|t|) 13
(Intercept) 79.1555 84.6466 0.935 0.381 13
Hc -222.1334 316.0879 -0.703 0.505 13
GenotypeAPOE33 11.1811 104.6991 0.107 0.918 13
GenotypeAPOE44 0.1215 105.8346 0.001 0.999 13
Hc:GenotypeAPOE33 -64.9119 400.4401 -0.162 0.876 13
Hc:GenotypeAPOE44 13.9267 405.7631 0.034 0.974 13
. 13
Residual standard error: 5.262 on 7 degrees of freedom 13
Multiple R-squared: 0.5857, Adjusted R-squared: 0.2897 13
F-statistic: 1.979 on 5 and 7 DF, p-value: 0.1991 13
. 13
Call: 13
lm(formula = Probe_d5 ~ Hc * Genotype, data = combo_m_FA) 13
. 13
Residuals: 13
Min 1Q Median 3Q Max 13
-3.6807 -1.7185 -0.5574 1.0024 5.0419 13
. 13
Coefficients: 13
Estimate Std. Error t value Pr(>|t|) 13
(Intercept) 26.79 38.59 0.694 0.503 13
Hc -26.57 147.27 -0.180 0.860 13
GenotypeAPOE33 19.96 98.36 0.203 0.843 13
GenotypeAPOE44 -34.28 67.65 -0.507 0.623 13
Hc:GenotypeAPOE33 -85.54 379.50 -0.225 0.826 13
Hc:GenotypeAPOE44 138.78 260.06 0.534 0.605 13
. 13
Residual standard error: 2.895 on 10 degrees of freedom 13

Multiple R-squared: 0.3253, Adjusted R-squared: -0.01205 . . . 13
F-statistic: 0.9643 on 5 and 10 DF, p-value: 0.4831 . . . 14
Analysis of Variance Table . . . 14
. . . 14
Response: Probe_d5 . . . 14
Df Sum Sq Mean Sq F value Pr(>F) . . . 14
Hc 1 118.580 118.580 7.2625 0.01534 * . . . 14
Genotype 2 170.837 85.419 5.2315 0.01696 * . . . 14
Sex 1 16.903 16.903 1.0353 0.32319 . . . 14
Hc:Genotype 2 2.652 1.326 0.0812 0.92235 . . . 14
Hc:Sex 1 24.879 24.879 1.5237 0.23385 . . . 14
Genotype:Sex 2 28.290 14.145 0.8663 0.43825 . . . 14
Hc:Genotype:Sex 2 1.396 0.698 0.0427 0.95826 . . . 14
Residuals 17 277.571 16.328 . . . 14
— . . . 14
Signif. codes: 0 ‘’ ***0.001*** ’’ *0.01* ’’ 0.05 ‘.’ 0.1 ’ ’ 1 . . . 14
Analysis of Variance Table . . . 14
. . . 14
Response: Probe_d5 . . . 14
Df Sum Sq Mean Sq F value Pr(>F) . . . 14
Hc 1 132.222 132.222 4.7761 0.06512 . . . 14
Genotype 2 140.176 70.088 2.5317 0.14883 . . . 14
Hc:Genotype 2 1.527 0.763 0.0276 0.97291 . . . 14
Residuals 7 193.789 27.684 . . . 14
— . . . 14
Signif. codes: 0 ‘’ ***0.001*** ’’ *0.01* ’’ 0.05 ‘.’ 0.1 ’ ’ 1 . . . 14
Analysis of Variance Table . . . 14
. . . 14
Response: Probe_d5 . . . 14
Df Sum Sq Mean Sq F value Pr(>F) . . . 15
Hc 1 0.126 0.1256 0.0150 0.9050 . . . 15
Genotype 2 36.850 18.4248 2.1991 0.1616 . . . 15
Hc:Genotype 2 3.420 1.7099 0.2041 0.8187 . . . 15
Residuals 10 83.782 8.3782 . . . 15
List of 7 . . . 15
$ panel.grid :List of 6 . . . 15
..$ colour : chr “grey85” . . . 15
..$ size : num 0.5 . . . 15
..$ linetype : num 1 . . . 15
..$ lineend : chr “butt” . . . 15
..$ arrow : logi FALSE . . . 15
..$ inherit.blank: logi FALSE . . . 15
..- attr(*, “class”)= chr [1:2] “element_line” “element” . . . 15
$ panel.grid.major : NULL . . . 15
$ panel.grid.minor :List of 6 . . . 15
..$ colour : chr “grey85” . . . 15
..$ size : num 0.2 . . . 15
..$ linetype : num 1 . . . 15
..$ lineend : chr “butt” . . . 15
..$ arrow : logi FALSE . . . 15
..$ inherit.blank: logi FALSE . . . 15
..- attr(*, “class”)= chr [1:2] “element_line” “element” . . . 15
$ panel.grid.major.x: NULL . . . 15
$ panel.grid.major.y: NULL . . . 15

$ panel.grid.minor.x: list() . . . 15
..- attr(*, “class”)= chr [1:2] “element_blank” “element” . . . 16
$ panel.grid.minor.y: list() . . . 16
..- attr(*, “class”)= chr [1:2] “element_blank” “element” . . . 16
- attr(*, “class”)= chr [1:2] “theme” “gg” . . . 16
- attr(*, “complete”)= logi FALSE . . . 16
- attr(*, “validate”)= logi TRUE . . . 16
. . . 16
Call: . . . 16
lm(formula = Probe_d5 ~ Hc * Genotype * Sex, data = geno_combined_DEG) . . . 16
. . . 16
Residuals: . . . 16
Min 1Q Median 3Q Max . . . 16
-5.7704 -1.6278 -0.1620 0.5598 10.4695 . . . 16
. . . 16
Coefficients: . . . 16
Estimate Std. Error t value Pr(>|t|) . . . 16
(Intercept) -5.022e+01 6.771e+01 -0.742 0.468 . . . 16
Hc 1.925e-04 1.864e-04 1.033 0.316 . . . 16
GenotypeAPOE33 3.987e+01 6.991e+01 0.570 0.576 . . . 16
GenotypeAPOE44 1.174e+02 7.300e+01 1.608 0.126 . . . 16
Sexmale 5.328e+01 8.181e+01 0.651 0.524 . . . 16
Hc:GenotypeAPOE33 -1.231e-04 1.910e-04 -0.644 0.528 . . . 16
Hc:GenotypeAPOE44 -2.955e-04 1.992e-04 -1.483 0.156 . . . 16
Hc:Sexmale -1.488e-04 2.215e-04 -0.672 0.511 . . . 16
GenotypeAPOE33:Sexmale 4.565e+00 8.665e+01 0.053 0.959 . . . 16
GenotypeAPOE44:Sexmale -9.077e+01 9.002e+01 -1.008 0.327 . . . 16
Hc:GenotypeAPOE33:Sexmale 1.070e-05 2.313e-04 0.046 0.964 . . . 16
Hc:GenotypeAPOE44:Sexmale 2.318e-04 2.409e-04 0.962 0.349 . . . 16
. . . 16
Residual standard error: 3.75 on 17 degrees of freedom . . . 16
Multiple R-squared: 0.6272, Adjusted R-squared: 0.3859 . . . 17
F-statistic: 2.6 on 11 and 17 DF, p-value: 0.03746 . . . 17
. . . 17
Call: . . . 17
lm(formula = Probe_d5 ~ Hc * Genotype, data = combo_f_DEG) . . . 17
. . . 17
Residuals: . . . 17
Min 1Q Median 3Q Max . . . 17
-5.7704 -1.2366 -0.1620 0.4741 10.4695 . . . 17
. . . 17
Coefficients: . . . 17
Estimate Std. Error t value Pr(>|t|) . . . 17
(Intercept) -5.022e+01 9.144e+01 -0.549 0.600 . . . 17
Hc 1.925e-04 2.517e-04 0.765 0.469 . . . 17
GenotypeAPOE33 3.987e+01 9.441e+01 0.422 0.686 . . . 17
GenotypeAPOE44 1.174e+02 9.858e+01 1.191 0.273 . . . 17
Hc:GenotypeAPOE33 -1.231e-04 2.579e-04 -0.477 0.648 . . . 17
Hc:GenotypeAPOE44 -2.955e-04 2.690e-04 -1.098 0.308 . . . 17
. . . 17
Residual standard error: 5.064 on 7 degrees of freedom . . . 17
Multiple R-squared: 0.6163, Adjusted R-squared: 0.3421 . . . 17
F-statistic: 2.248 on 5 and 7 DF, p-value: 0.1602 . . . 17
. . . 17

Call: . . . 17
lm(formula = Probe_d5 ~ Hc * Genotype, data = combo_m_DEG) . . . 17
. . . 17
Residuals: . . . 17
Min 1Q Median 3Q Max . . . 17
-3.0103 -1.6504 -0.2215 0.8732 5.0438 . . . 17
. . . 18
Coefficients: . . . 18
Estimate Std. Error t value Pr(>|t|) . . . 18
(Intercept) 3.059e+00 2.988e+01 0.102 0.920 . . . 18
Hc 4.371e-05 7.785e-05 0.561 0.587 . . . 18
GenotypeAPOE33 4.443e+01 3.331e+01 1.334 0.212 . . . 18
GenotypeAPOE44 2.661e+01 3.428e+01 0.776 0.456 . . . 18
Hc:GenotypeAPOE33 -1.124e-04 8.491e-05 -1.323 0.215 . . . 18
Hc:GenotypeAPOE44 -6.365e-05 8.816e-05 -0.722 0.487 . . . 18
. . . 18
Residual standard error: 2.44 on 10 degrees of freedom . . . 18
Multiple R-squared: 0.5206, Adjusted R-squared: 0.2809 . . . 18
F-statistic: 2.172 on 5 and 10 DF, p-value: 0.1389 . . . 18
Analysis of Variance Table . . . 18
. . . 18
Response: Probe_d5 . . . 18
Df Sum Sq Mean Sq F value Pr(>F) . . . 18
Hc 1 15.305 15.305 1.0885 0.31141 . . . 18
Genotype 2 195.804 97.902 6.9632 0.00618 ** . . . 18
Sex 1 28.919 28.919 2.0569 0.16966 . . . 18
Hc:Genotype 2 69.296 34.648 2.4643 0.11487 . . . 18
Hc:Sex 1 11.482 11.482 0.8166 0.37880 . . . 18
Genotype:Sex 2 28.221 14.111 1.0036 0.38727 . . . 18
Hc:Genotype:Sex 2 53.062 26.531 1.8870 0.18193 . . . 18
Residuals 17 239.020 14.060 . . . 18
— . . . 18
Signif. codes: 0 ‘’ ***0.001*** ’’ *0.01* ’’ 0.05 ‘.’ 0.1 ’ ’ 1 . . . 18
Analysis of Variance Table . . . 18
. . . 18
Response: Probe_d5 . . . 19
Df Sum Sq Mean Sq F value Pr(>F) . . . 19
Hc 1 6.659 6.659 0.2597 0.62599 . . . 19
Genotype 2 208.055 104.027 4.0571 0.06761 . . . 19
Hc:Genotype 2 73.515 36.758 1.4336 0.30073 . . . 19
Residuals 7 179.485 25.641 . . . 19
— . . . 19
Signif. codes: 0 ‘’ ***0.001*** ’’ *0.01* ’’ 0.05 ‘.’ 0.1 ’ ’ 1 . . . 19
Analysis of Variance Table . . . 19
. . . 19
Response: Probe_d5 . . . 19
Df Sum Sq Mean Sq F value Pr(>F) . . . 19
Hc 1 27.464 27.4636 4.6131 0.05728 . . . 19
Genotype 2 24.642 12.3212 2.0696 0.17696 . . . 19
Hc:Genotype 2 12.537 6.2683 1.0529 0.38462 . . . 19
Residuals 10 59.534 5.9534 . . . 19
— . . . 19
Signif. codes: 0 ‘’ ***0.001*** ’’ *0.01* ’’ 0.05 ‘.’ 0.1 ’ ’ 1 . . . 19
List of 7 . . . 19

$ panel.grid :List of 6 . . . 19
..$ colour : chr “grey85” . . . 19
..$ size : num 0.5 . . . 19
..$ linetype : num 1 . . . 19
..$ lineend : chr “butt” . . . 19
..$ arrow : logi FALSE . . . 19
..$ inherit.blank: logi FALSE . . . 19
..- attr(*, “class”)= chr [1:2] “element_line” “element” . . . 19
$ panel.grid.major : NULL . . . 20
$ panel.grid.minor :List of 6 . . . 20
..$ colour : chr “grey85” . . . 20
..$ size : num 0.2 . . . 20
..$ linetype : num 1 . . . 20
..$ lineend : chr “butt” . . . 20
..$ arrow : logi FALSE . . . 20
..$ inherit.blank: logi FALSE . . . 20
..- attr(*, “class”)= chr [1:2] “element_line” “element” . . . 20
$ panel.grid.major.x: NULL . . . 20
$ panel.grid.major.y: NULL . . . 20
$ panel.grid.minor.x: list() . . . 20
..- attr(*, “class”)= chr [1:2] “element_blank” “element” . . . 20
$ panel.grid.minor.y: list() . . . 20
..- attr(*, “class”)= chr [1:2] “element_blank” “element” . . . 20
- attr(*, “class”)= chr [1:2] “theme” “gg” . . . 20
- attr(*, “complete”)= logi FALSE . . . 20
- attr(*, “validate”)= logi TRUE . . . 20
. . . 20
Call: . . . 20
lm(formula = Probe_d8 ~ Hc * Genotype * Sex, data = geno_combined_CLUS) . . . 20
. . . 20
Residuals: . . . 20
Min 1Q Median 3Q Max . . . 20
-3.4072 -0.7136 -0.4157 0.6722 3.1713 . . . 20
. . . 20
Coefficients: . . . 20
Estimate Std. Error t value Pr(>|t|) . . . 20
(Intercept) 0.154247 32.563320 0.005 0.996 . . . 20
Hc 0.043727 0.073570 0.594 0.560 . . . 20
GenotypeAPOE33 5.834486 33.281779 0.175 0.863 . . . 21
GenotypeAPOE44 12.249771 33.655104 0.364 0.720 . . . 21
Sexmale 16.235909 37.728063 0.430 0.672 . . . 21
Hc:GenotypeAPOE33 -0.021319 0.074681 -0.285 0.779 . . . 21
Hc:GenotypeAPOE44 -0.020105 0.075575 -0.266 0.793 . . . 21
Hc:Sexmale -0.039901 0.083820 -0.476 0.640 . . . 21
GenotypeAPOE33:Sexmale 5.186597 39.939181 0.130 0.898 . . . 21
GenotypeAPOE44:Sexmale -9.118977 40.047248 -0.228 0.823 . . . 21
Hc:GenotypeAPOE33:Sexmale -0.003435 0.087384 -0.039 0.969 . . . 21
Hc:GenotypeAPOE44:Sexmale 0.022244 0.088023 0.253 0.804 . . . 21
. . . 21
Residual standard error: 1.971 on 17 degrees of freedom . . . 21
Multiple R-squared: 0.7797, Adjusted R-squared: 0.6372 . . . 21
F-statistic: 5.47 on 11 and 17 DF, p-value: 0.0009722 . . . 21
. . . 21
Call: . . . 21

lm(formula = Probe_d8 ~ Hc * Genotype, data = combo_f_CLUS) . . . 21
. . . 21
Residuals: . . . 21
Min 1Q Median 3Q Max . . . 21
-3.4072 -0.5681 -0.4157 1.4910 2.9049 . . . 21
. . . 21
Coefficients: . . . 21
Estimate Std. Error t value Pr(>|t|) . . . 21
(Intercept) 0.15425 35.43554 0.004 0.997 . . . 21
Hc 0.04373 0.08006 0.546 0.602 . . . 21
GenotypeAPOE33 5.83449 36.21737 0.161 0.877 . . . 21
GenotypeAPOE44 12.24977 36.62362 0.334 0.748 . . . 21
Hc:GenotypeAPOE33 -0.02132 0.08127 -0.262 0.801 . . . 21
Hc:GenotypeAPOE44 -0.02011 0.08224 -0.244 0.814 . . . 21
. . . 21
Residual standard error: 2.145 on 7 degrees of freedom . . . 22
Multiple R-squared: 0.7655, Adjusted R-squared: 0.5981 . . . 22
F-statistic: 4.571 on 5 and 7 DF, p-value: 0.03584 . . . 22
. . . 22
Call: . . . 22
lm(formula = Probe_d8 ~ Hc * Genotype, data = combo_m_CLUS) . . . 22
. . . 22
Residuals: . . . 22
Min 1Q Median 3Q Max . . . 22
-1.9007 -1.0347 -0.4135 0.5060 3.1713 . . . 22
. . . 22
Coefficients: . . . 22
Estimate Std. Error t value Pr(>|t|) . . . 22
(Intercept) 16.390156 17.782857 0.922 0.378 . . . 22
Hc 0.003826 0.037485 0.102 0.921 . . . 22
GenotypeAPOE33 11.021083 20.606118 0.535 0.604 . . . 22
GenotypeAPOE44 3.130794 20.257696 0.155 0.880 . . . 22
Hc:GenotypeAPOE33 -0.024754 0.042347 -0.585 0.572 . . . 22
Hc:GenotypeAPOE44 0.002138 0.042119 0.051 0.961 . . . 22
. . . 22
Residual standard error: 1.84 on 10 degrees of freedom . . . 22
Multiple R-squared: 0.7548, Adjusted R-squared: 0.6323 . . . 22
F-statistic: 6.158 on 5 and 10 DF, p-value: 0.007379 . . . 22
Analysis of Variance Table . . . 22
. . . 22
Response: Probe_d8 . . . 22
Df Sum Sq Mean Sq F value Pr(>F) . . . 22
Hc 1 0.956 0.956 0.2460 0.62624 . . . 22
Genotype 2 200.220 100.110 25.7680 7.137e-06 *** . . . 22
Sex 1 17.562 17.562 4.5204 0.04844 * . . . 23
Hc:Genotype 2 0.418 0.209 0.0538 0.94779 . . . 23
Hc:Sex 1 8.179 8.179 2.1052 0.16500 . . . 23
Genotype:Sex 2 4.459 2.230 0.5739 0.57388 . . . 23
Hc:Genotype:Sex 2 1.959 0.979 0.2521 0.78002 . . . 23
Residuals 17 66.046 3.885 . . . 23
— . . . 23
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1 . . . 23
Analysis of Variance Table . . . 23
. . . 23

Response: Probe_d8 . . . 23
Df Sum Sq Mean Sq F value Pr(>F) . . . 23
Hc 1 13.038 13.038 2.8339 0.136169 . . . 23
Genotype 2 91.795 45.898 9.9764 0.008928 ** . . . 23
Hc:Genotype 2 0.319 0.160 0.0347 0.966038 . . . 23
Residuals 7 32.204 4.601 . . . 23
— . . . 23
Signif. codes: 0 ‘’ ***0.001*** ’’ *0.01* ’’ 0.05 ‘.’ 0.1 ’ ’ 1 . . . 23
Analysis of Variance Table . . . 23
. . . 23
Response: Probe_d8 . . . 23
Df Sum Sq Mean Sq F value Pr(>F) . . . 23
Hc 1 2.891 2.891 0.8544 0.377084 . . . 23
Genotype 2 97.815 48.907 14.4520 0.001122 ** . . . 23
Hc:Genotype 2 3.488 1.744 0.5154 0.612307 . . . 23
Residuals 10 33.841 3.384 . . . 23
— . . . 23
Signif. codes: 0 ‘’ ***0.001*** ’’ *0.01* ’’ 0.05 ‘.’ 0.1 ’ ’ 1 . . . 23

Aim

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

Day 5 Probe by Hc Vol

```
## List of 7
##  $ panel.grid        :List of 6
##   ..$ colour       : chr "grey85"
##   ..$ size         : num 0.5
##   ..$ linetype     : num 1
##   ..$ lineend      : chr "butt"
##   ..$ arrow        : logi FALSE
##   ..$ inherit.blank: logi FALSE
##   ..- attr(*, "class")= chr [1:2] "element_line" "element"
##  $ panel.grid.major  : NULL
##  $ panel.grid.minor  :List of 6
##   ..$ colour       : chr "grey85"
##   ..$ size         : num 0.2
##   ..$ linetype     : num 1
##   ..$ lineend      : chr "butt"
##   ..$ arrow        : logi FALSE
##   ..$ inherit.blank: logi FALSE
##   ..- attr(*, "class")= chr [1:2] "element_line" "element"
##  $ panel.grid.major.x: NULL
##  $ panel.grid.major.y: NULL
##  $ panel.grid.minor.x: list()
##   ..- attr(*, "class")= chr [1:2] "element_blank" "element"
##  $ panel.grid.minor.y: list()
##   ..- attr(*, "class")= chr [1:2] "element_blank" "element"
##  - attr(*, "class")= chr [1:2] "theme" "gg"
```

```
##  - attr(*, "complete")= logi FALSE
##  - attr(*, "validate")= logi TRUE
```

```
##
## Call:
## lm(formula = Probe_d5 ~ Hc * Genotype * Sex, data = geno_combined_VOL)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.9045 -2.2851  0.2789  0.7352 11.9846
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  -216.2      335.8  -0.644    0.528
## Hc                           7466.1    10627.7   0.703    0.492
## GenotypeAPOE33                365.5      513.0   0.713    0.486
## GenotypeAPOE44                211.1      345.9   0.610    0.550
## Sexmale                       287.3      377.1   0.762    0.457
## Hc:GenotypeAPOE33          -11624.7    16274.5  -0.714    0.485
## Hc:GenotypeAPOE44           -6449.3    10944.7  -0.589    0.563
## Hc:Sexmale                  -9052.3    11882.8  -0.762    0.457
## GenotypeAPOE33:Sexmale       -233.7      573.9  -0.407    0.689
## GenotypeAPOE44:Sexmale       -210.3      406.2  -0.518    0.611
## Hc:GenotypeAPOE33:Sexmale   7513.3    18108.7   0.415    0.683
## Hc:GenotypeAPOE44:Sexmale   6488.5    12767.3   0.508    0.618
##
## Residual standard error: 4.305 on 17 degrees of freedom
## Multiple R-squared:  0.5087, Adjusted R-squared:  0.1907
## F-statistic:   1.6 on 11 and 17 DF,  p-value: 0.1859
```

```
##
## Call:
## lm(formula = Probe_d5 ~ Hc * Genotype, data = combo_f_VOL)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.9045 -2.6844 -1.4808  0.4536 11.9846
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)          -216.2      465.9  -0.464    0.657
## Hc                   7466.1    14745.2   0.506    0.628
## GenotypeAPOE33        365.5      711.7   0.514    0.623
## GenotypeAPOE44        211.1      480.0   0.440    0.673
## Hc:GenotypeAPOE33 -11624.7    22579.8  -0.515    0.623
## Hc:GenotypeAPOE44  -6449.3    15185.1  -0.425    0.684
##
## Residual standard error: 5.972 on 7 degrees of freedom
## Multiple R-squared:  0.4662, Adjusted R-squared:  0.08484
## F-statistic: 1.223 on 5 and 7 DF,  p-value: 0.3895
```

```
##
## Call:
## lm(formula = Probe_d5 ~ Hc * Genotype, data = combo_m_VOL)
##
```

```
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.2968 -1.3665  0.3588  0.9100  4.4142
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)          71.0777   101.9763   0.697    0.502
## Hc                -1586.1443  3155.9047  -0.503    0.626
## GenotypeAPOE33      131.8214   152.8389   0.862    0.409
## GenotypeAPOE44        0.8303   126.4182   0.007    0.995
## Hc:GenotypeAPOE33 -4111.4365  4715.0413  -0.872    0.404
## Hc:GenotypeAPOE44    39.2137  3903.1279   0.010    0.992
##
## Residual standard error: 2.556 on 10 degrees of freedom
## Multiple R-squared:  0.474,  Adjusted R-squared:  0.211
## F-statistic: 1.802 on 5 and 10 DF,  p-value: 0.2001
```

```
## Analysis of Variance Table
##
## Response: Probe_d5
##                 Df  Sum Sq Mean Sq F value  Pr(>F)
## Hc               1   9.084   9.084  0.4902 0.49329
## Genotype         2 216.414 108.207  5.8397 0.01173 *
## Sex              1  14.908  14.908  0.8046 0.38226
## Hc:Genotype      2  16.190   8.095  0.4369 0.65311
## Hc:Sex           1  38.755  38.755  2.0915 0.16630
## Genotype:Sex     2  25.643  12.822  0.6919 0.51416
## Hc:Genotype:Sex  2   5.109   2.554  0.1379 0.87219
## Residuals       17 315.005  18.530
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Analysis of Variance Table
##
## Response: Probe_d5
##             Df  Sum Sq Mean Sq F value Pr(>F)
## Hc           1  35.942  35.942  1.0077 0.3489
## Genotype     2 172.057  86.028  2.4118 0.1597
## Hc:Genotype  2  10.030   5.015  0.1406 0.8712
## Residuals    7 249.685  35.669
```

```
## Analysis of Variance Table
##
## Response: Probe_d5
##             Df Sum Sq Mean Sq F value  Pr(>F)
## Hc           1 13.040 13.0402  1.9964 0.18804
## Genotype     2 38.705 19.3525  2.9627 0.09762 .
## Hc:Genotype  2  7.112  3.5561  0.5444 0.59644
## Residuals   10 65.320  6.5320
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Day 5 Probe By Hc FA
```

List of 7

$ panel.grid :List of 6

..$ colour : chr “grey85”

..$ size : num 0.5

..$ linetype : num 1

..$ lineend : chr “butt”

..$ arrow : logi FALSE

..$ inherit.blank: logi FALSE

..- attr(*, “class”)= chr [1:2] “element_line” “element”

$ panel.grid.major : NULL

$ panel.grid.minor :List of 6

..$ colour : chr “grey85”

..$ size : num 0.2

..$ linetype : num 1

..$ lineend : chr “butt”

..$ arrow : logi FALSE

..$ inherit.blank: logi FALSE

..- attr(*, “class”)= chr [1:2] “element_line” “element”

$ panel.grid.major.x: NULL

$ panel.grid.major.y: NULL

$ panel.grid.minor.x: list()

..- attr(*, “class”)= chr [1:2] “element_blank” “element”

$ panel.grid.minor.y: list()

..- attr(*, “class”)= chr [1:2] “element_blank” “element”

- attr(*, “class”)= chr [1:2] “theme” “gg”

- attr(*, “complete”)= logi FALSE

- attr(*, “validate”)= logi TRUE

Call:

lm(formula = Probe_d5 ~ Hc * Genotype * Sex, data = geno_combined_FA)

Residuals:

Min 1Q Median 3Q Max
-4.7884 -1.6344 -0.6007 0.9028 11.8871

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 79.1555 65.0064 1.218 0.240
Hc -222.1334 242.7476 -0.915 0.373
GenotypeAPOE33 11.1811 80.4063 0.139 0.891
GenotypeAPOE44 0.1215 81.2783 0.001 0.999
Sexmale -52.3686 84.4278 -0.620 0.543
Hc:GenotypeAPOE33 -64.9119 307.5279 -0.211 0.835
Hc:GenotypeAPOE44 13.9267 311.6158 0.045 0.965
Hc:Sexmale 195.5625 318.1092 0.615 0.547
GenotypeAPOE33:Sexmale 8.7780 159.1224 0.055 0.957
GenotypeAPOE44:Sexmale -34.4001 124.5997 -0.276 0.786
Hc:GenotypeAPOE33:Sexmale -20.6269 612.5697 -0.034 0.974
Hc:GenotypeAPOE44:Sexmale 124.8552 478.4404 0.261 0.797

Residual standard error: 4.041 on 17 degrees of freedom
Multiple R-squared: 0.567, Adjusted R-squared: 0.2869
F-statistic: 2.024 on 11 and 17 DF, p-value: 0.09275

Call:
lm(formula = Probe_d5 ~ Hc * Genotype, data = combo_f_FA)

Residuals:
Min 1Q Median 3Q Max
-4.7884 -1.0771 -0.8191 -0.0791 11.8871

Coefficients:

Estimate Std. Error t value Pr(>|t|)
(Intercept) 79.1555 84.6466 0.935 0.381
Hc -222.1334 316.0879 -0.703 0.505
GenotypeAPOE33 11.1811 104.6991 0.107 0.918
GenotypeAPOE44 0.1215 105.8346 0.001 0.999
Hc:GenotypeAPOE33 -64.9119 400.4401 -0.162 0.876
Hc:GenotypeAPOE44 13.9267 405.7631 0.034 0.974

Residual standard error: 5.262 on 7 degrees of freedom
Multiple R-squared: 0.5857, Adjusted R-squared: 0.2897
F-statistic: 1.979 on 5 and 7 DF, p-value: 0.1991

Call:
lm(formula = Probe_d5 ~ Hc * Genotype, data = combo_m_FA)

Residuals:
Min 1Q Median 3Q Max
-3.6807 -1.7185 -0.5574 1.0024 5.0419

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 26.79 38.59 0.694 0.503
Hc -26.57 147.27 -0.180 0.860
GenotypeAPOE33 19.96 98.36 0.203 0.843
GenotypeAPOE44 -34.28 67.65 -0.507 0.623
Hc:GenotypeAPOE33 -85.54 379.50 -0.225 0.826
Hc:GenotypeAPOE44 138.78 260.06 0.534 0.605

Residual standard error: 2.895 on 10 degrees of freedom
Multiple R-squared: 0.3253, Adjusted R-squared: -0.01205

F-statistic: 0.9643 on 5 and 10 DF, p-value: 0.4831

Analysis of Variance Table

Response: Probe_d5
Df Sum Sq Mean Sq F value Pr(>F)
Hc 1 118.580 118.580 7.2625 0.01534 *
Genotype 2 170.837 85.419 5.2315 0.01696 *
Sex 1 16.903 16.903 1.0353 0.32319
Hc:Genotype 2 2.652 1.326 0.0812 0.92235
Hc:Sex 1 24.879 24.879 1.5237 0.23385
Genotype:Sex 2 28.290 14.145 0.8663 0.43825
Hc:Genotype:Sex 2 1.396 0.698 0.0427 0.95826
Residuals 17 277.571 16.328
—
Signif. codes: 0 ‘’ *0.001* ’’ *0.01* ’’ 0.05 ‘.’ 0.1 ’ ’ 1

Analysis of Variance Table

Response: Probe_d5
Df Sum Sq Mean Sq F value Pr(>F)
Hc 1 132.222 132.222 4.7761 0.06512 .
Genotype 2 140.176 70.088 2.5317 0.14883
Hc:Genotype 2 1.527 0.763 0.0276 0.97291
Residuals 7 193.789 27.684
—
Signif. codes: 0 ‘’ *0.001* ’’ *0.01* ’’ 0.05 ‘.’ 0.1 ’ ’ 1

Analysis of Variance Table

Response: Probe_d5

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

Hc 1 0.126 0.1256 0.0150 0.9050

Genotype 2 36.850 18.4248 2.1991 0.1616

Hc:Genotype 2 3.420 1.7099 0.2041 0.8187

Residuals 10 83.782 8.3782

```
# Degree of Connectivity

# Day 5 Probe By Hc DEG
```

List of 7

$ panel.grid :List of 6

..$ colour : chr “grey85”

..$ size : num 0.5

..$ linetype : num 1

..$ lineend : chr “butt”

..$ arrow : logi FALSE

..$ inherit.blank: logi FALSE

..- attr(*, “class”)= chr [1:2] “element_line” “element”

$ panel.grid.major : NULL

$ panel.grid.minor :List of 6

..$ colour : chr “grey85”

..$ size : num 0.2

..$ linetype : num 1

..$ lineend : chr “butt”

..$ arrow : logi FALSE

..$ inherit.blank: logi FALSE

..- attr(*, “class”)= chr [1:2] “element_line” “element”

$ panel.grid.major.x: NULL

$ panel.grid.major.y: NULL

$ panel.grid.minor.x: list()

..- attr(*, “class”)= chr [1:2] “element_blank” “element”

$ panel.grid.minor.y: list()

..- attr(*, “class”)= chr [1:2] “element_blank” “element”

- attr(*, “class”)= chr [1:2] “theme” “gg”

- attr(*, “complete”)= logi FALSE

- attr(*, “validate”)= logi TRUE

Call:

lm(formula = Probe_d5 ~ Hc * Genotype * Sex, data = geno_combined_DEG)

Residuals:

Min 1Q Median 3Q Max

-5.7704 -1.6278 -0.1620 0.5598 10.4695

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) -5.022e+01 6.771e+01 -0.742 0.468

Hc 1.925e-04 1.864e-04 1.033 0.316

GenotypeAPOE33 3.987e+01 6.991e+01 0.570 0.576

GenotypeAPOE44 1.174e+02 7.300e+01 1.608 0.126

Sexmale 5.328e+01 8.181e+01 0.651 0.524

Hc:GenotypeAPOE33 -1.231e-04 1.910e-04 -0.644 0.528

Hc:GenotypeAPOE44 -2.955e-04 1.992e-04 -1.483 0.156

Hc:Sexmale -1.488e-04 2.215e-04 -0.672 0.511

GenotypeAPOE33:Sexmale 4.565e+00 8.665e+01 0.053 0.959

GenotypeAPOE44:Sexmale -9.077e+01 9.002e+01 -1.008 0.327

Hc:GenotypeAPOE33:Sexmale 1.070e-05 2.313e-04 0.046 0.964

Hc:GenotypeAPOE44:Sexmale 2.318e-04 2.409e-04 0.962 0.349

Residual standard error: 3.75 on 17 degrees of freedom

Multiple R-squared: 0.6272, Adjusted R-squared: 0.3859
F-statistic: 2.6 on 11 and 17 DF, p-value: 0.03746

Call:
lm(formula = Probe_d5 ~ Hc * Genotype, data = combo_f_DEG)

Residuals:
Min 1Q Median 3Q Max
-5.7704 -1.2366 -0.1620 0.4741 10.4695

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) -5.022e+01 9.144e+01 -0.549 0.600
Hc 1.925e-04 2.517e-04 0.765 0.469
GenotypeAPOE33 3.987e+01 9.441e+01 0.422 0.686
GenotypeAPOE44 1.174e+02 9.858e+01 1.191 0.273
Hc:GenotypeAPOE33 -1.231e-04 2.579e-04 -0.477 0.648
Hc:GenotypeAPOE44 -2.955e-04 2.690e-04 -1.098 0.308

Residual standard error: 5.064 on 7 degrees of freedom
Multiple R-squared: 0.6163, Adjusted R-squared: 0.3421
F-statistic: 2.248 on 5 and 7 DF, p-value: 0.1602

Call:
lm(formula = Probe_d5 ~ Hc * Genotype, data = combo_m_DEG)

Residuals:
Min 1Q Median 3Q Max
-3.0103 -1.6504 -0.2215 0.8732 5.0438

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 3.059e+00 2.988e+01 0.102 0.920

Hc 4.371e-05 7.785e-05 0.561 0.587

GenotypeAPOE33 4.443e+01 3.331e+01 1.334 0.212

GenotypeAPOE44 2.661e+01 3.428e+01 0.776 0.456

Hc:GenotypeAPOE33 -1.124e-04 8.491e-05 -1.323 0.215

Hc:GenotypeAPOE44 -6.365e-05 8.816e-05 -0.722 0.487

Residual standard error: 2.44 on 10 degrees of freedom

Multiple R-squared: 0.5206, Adjusted R-squared: 0.2809

F-statistic: 2.172 on 5 and 10 DF, p-value: 0.1389

Analysis of Variance Table

Response: Probe_d5

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

Hc 1 15.305 15.305 1.0885 0.31141

Genotype 2 195.804 97.902 6.9632 0.00618 **

Sex 1 28.919 28.919 2.0569 0.16966

Hc:Genotype 2 69.296 34.648 2.4643 0.11487

Hc:Sex 1 11.482 11.482 0.8166 0.37880

Genotype:Sex 2 28.221 14.111 1.0036 0.38727

Hc:Genotype:Sex 2 53.062 26.531 1.8870 0.18193

Residuals 17 239.020 14.060

—

Signif. codes: 0 ‘’ *0.001* ’’ *0.01* ” 0.05 ‘.’ 0.1 ’ ’ 1

Analysis of Variance Table

Response: Probe_d5

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

Hc 1 6.659 6.659 0.2597 0.62599

Genotype 2 208.055 104.027 4.0571 0.06761 .

Hc:Genotype 2 73.515 36.758 1.4336 0.30073

Residuals 7 179.485 25.641

—

Signif. codes: 0 ‘’ *0.001* ’’ *0.01* ” 0.05 ‘.’ 0.1 ’ ’ 1

Analysis of Variance Table

Response: Probe_d5

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

Hc 1 27.464 27.4636 4.6131 0.05728 .

Genotype 2 24.642 12.3212 2.0696 0.17696

Hc:Genotype 2 12.537 6.2683 1.0529 0.38462

Residuals 10 59.534 5.9534

—

Signif. codes: 0 ‘’ *0.001* ’’ *0.01* ” 0.05 ‘.’ 0.1 ’ ’ 1

```
# Day 8 Probe By Hc CLUS
```

List of 7

$ panel.grid :List of 6

..$ colour : chr “grey85”

..$ size : num 0.5

..$ linetype : num 1

..$ lineend : chr “butt”

..$ arrow : logi FALSE

..$ inherit.blank: logi FALSE

..- attr(*, “class”)= chr [1:2] “element_line” “element”

$ panel.grid.major : NULL

$ panel.grid.minor :List of 6

..$ colour : chr “grey85”

..$ size : num 0.2

..$ linetype : num 1

..$ lineend : chr “butt”

..$ arrow : logi FALSE

..$ inherit.blank: logi FALSE

..- attr(*, “class”)= chr [1:2] “element_line” “element”

$ panel.grid.major.x: NULL

$ panel.grid.major.y: NULL

$ panel.grid.minor.x: list()

..- attr(*, “class”)= chr [1:2] “element_blank” “element”

$ panel.grid.minor.y: list()

..- attr(*, “class”)= chr [1:2] “element_blank” “element”

- attr(*, “class”)= chr [1:2] “theme” “gg”

- attr(*, “complete”)= logi FALSE

- attr(*, “validate”)= logi TRUE

Call:

lm(formula = Probe_d8 ~ Hc * Genotype * Sex, data = geno_combined_CLUS)

Residuals:

Min 1Q Median 3Q Max

-3.4072 -0.7136 -0.4157 0.6722 3.1713

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 0.154247 32.563320 0.005 0.996

Hc 0.043727 0.073570 0.594 0.560

GenotypeAPOE33 5.834486 33.281779 0.175 0.863
GenotypeAPOE44 12.249771 33.655104 0.364 0.720
Sexmale 16.235909 37.728063 0.430 0.672
Hc:GenotypeAPOE33 -0.021319 0.074681 -0.285 0.779
Hc:GenotypeAPOE44 -0.020105 0.075575 -0.266 0.793
Hc:Sexmale -0.039901 0.083820 -0.476 0.640
GenotypeAPOE33:Sexmale 5.186597 39.939181 0.130 0.898
GenotypeAPOE44:Sexmale -9.118977 40.047248 -0.228 0.823
Hc:GenotypeAPOE33:Sexmale -0.003435 0.087384 -0.039 0.969
Hc:GenotypeAPOE44:Sexmale 0.022244 0.088023 0.253 0.804

Residual standard error: 1.971 on 17 degrees of freedom
Multiple R-squared: 0.7797, Adjusted R-squared: 0.6372
F-statistic: 5.47 on 11 and 17 DF, p-value: 0.0009722

Call:
lm(formula = Probe_d8 ~ Hc * Genotype, data = combo_f_CLUS)

Residuals:
Min 1Q Median 3Q Max
-3.4072 -0.5681 -0.4157 1.4910 2.9049

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.15425 35.43554 0.004 0.997
Hc 0.04373 0.08006 0.546 0.602
GenotypeAPOE33 5.83449 36.21737 0.161 0.877
GenotypeAPOE44 12.24977 36.62362 0.334 0.748
Hc:GenotypeAPOE33 -0.02132 0.08127 -0.262 0.801
Hc:GenotypeAPOE44 -0.02011 0.08224 -0.244 0.814

Residual standard error: 2.145 on 7 degrees of freedom
Multiple R-squared: 0.7655, Adjusted R-squared: 0.5981
F-statistic: 4.571 on 5 and 7 DF, p-value: 0.03584

Call:
lm(formula = Probe_d8 ~ Hc * Genotype, data = combo_m_CLUS)

Residuals:
Min 1Q Median 3Q Max
-1.9007 -1.0347 -0.4135 0.5060 3.1713

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 16.390156 17.782857 0.922 0.378
Hc 0.003826 0.037485 0.102 0.921
GenotypeAPOE33 11.021083 20.606118 0.535 0.604
GenotypeAPOE44 3.130794 20.257696 0.155 0.880
Hc:GenotypeAPOE33 -0.024754 0.042347 -0.585 0.572
Hc:GenotypeAPOE44 0.002138 0.042119 0.051 0.961

Residual standard error: 1.84 on 10 degrees of freedom
Multiple R-squared: 0.7548, Adjusted R-squared: 0.6323
F-statistic: 6.158 on 5 and 10 DF, p-value: 0.007379

Analysis of Variance Table

Response: Probe_d8
Df Sum Sq Mean Sq F value Pr(>F)
Hc 1 0.956 0.956 0.2460 0.62624
Genotype 2 200.220 100.110 25.7680 7.137e-06 *

Sex 1 17.562 17.562 4.5204 0.04844 *

Hc:Genotype 2 0.418 0.209 0.0538 0.94779

Hc:Sex 1 8.179 8.179 2.1052 0.16500

Genotype:Sex 2 4.459 2.230 0.5739 0.57388

Hc:Genotype:Sex 2 1.959 0.979 0.2521 0.78002

Residuals 17 66.046 3.885

—

Signif. codes: 0 ‘’ *0.001* ’’ *0.01* ” 0.05 ‘.’ 0.1 ’ ’ 1

Analysis of Variance Table

Response: Probe_d8

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

Hc 1 13.038 13.038 2.8339 0.136169

Genotype 2 91.795 45.898 9.9764 0.008928 **

Hc:Genotype 2 0.319 0.160 0.0347 0.966038

Residuals 7 32.204 4.601

—

Signif. codes: 0 ‘’ *0.001* ’’ *0.01* ” 0.05 ‘.’ 0.1 ’ ’ 1

Analysis of Variance Table

Response: Probe_d8

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

Hc 1 2.891 2.891 0.8544 0.377084

Genotype 2 97.815 48.907 14.4520 0.001122 **

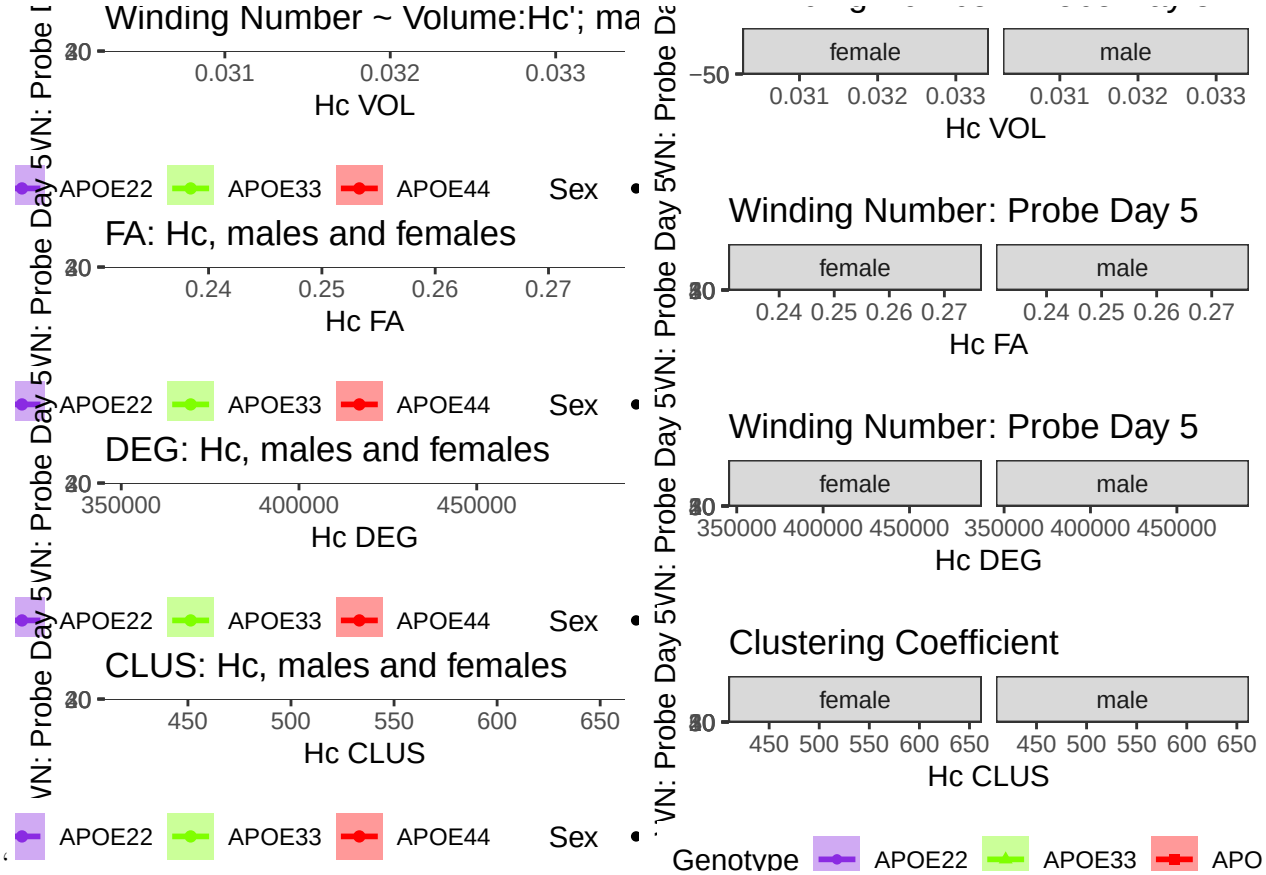
Hc:Genotype 2 3.488 1.744 0.5154 0.612307

Residuals 10 33.841 3.384

—

Signif. codes: 0 ‘’ *0.001* ’’ *0.01* ” 0.05 ‘.’ 0.1 ’ ’ 1

‘‘‘


Winding Number ~ Volume:Hc'; ma
Hc VOL
APOE22 APOE33 APOE44 Sex
FA: Hc, males and females
Hc FA
APOE22 APOE33 APOE44 Sex
DEG: Hc, males and females
Hc DEG
APOE22 APOE33 APOE44 Sex
CLUS: Hc, males and females
Hc CLUS
APOE22 APOE33 APOE44 Sex
female
male
Winding Number: Probe Day 5
Clustering Coefficient
Genotype APOE22 APOE33 APO