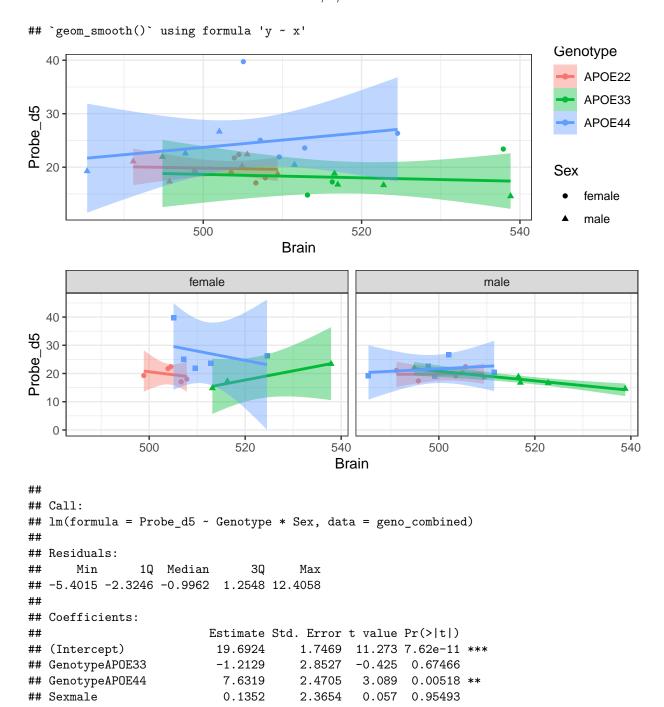
winding_by_vol

alexandra badea

10/4/2021

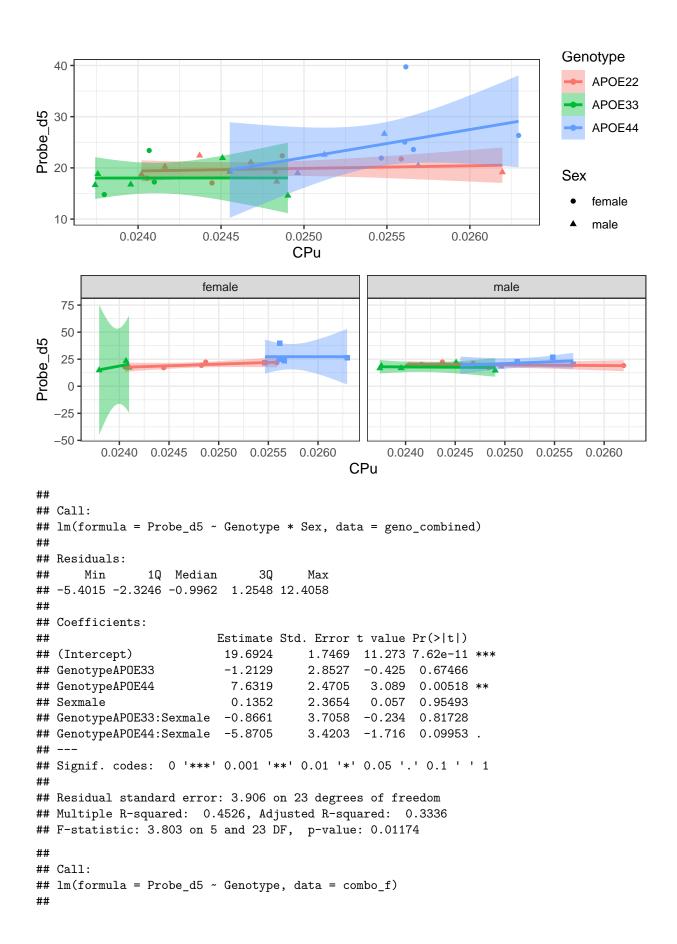


```
## GenotypeAPOE33:Sexmale -0.8661
                                      3.7058 -0.234 0.81728
                                      3.4203 -1.716 0.09953 .
## GenotypeAPOE44:Sexmale -5.8705
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 3.906 on 23 degrees of freedom
## Multiple R-squared: 0.4526, Adjusted R-squared: 0.3336
## F-statistic: 3.803 on 5 and 23 DF, p-value: 0.01174
##
## Call:
## lm(formula = Probe_d5 ~ Genotype, data = combo_f)
##
## Residuals:
     Min
             10 Median
                           3Q
                                 Max
## -5.402 -2.623 -1.232 2.046 12.406
## Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
                                       8.574 6.38e-06 ***
                   19.692
                               2.297
## (Intercept)
## GenotypeAPOE33
                   -1.213
                               3.750 -0.323
                                               0.7531
                    7.632
                                       2.350
                                               0.0407 *
## GenotypeAPOE44
                               3.248
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.136 on 10 degrees of freedom
## Multiple R-squared: 0.4361, Adjusted R-squared: 0.3233
## F-statistic: 3.867 on 2 and 10 DF, p-value: 0.05701
##
## Call:
## lm(formula = Probe_d5 ~ Genotype, data = combo_m)
##
## Residuals:
               1Q Median
##
      Min
                               3Q
                                      Max
## -3.1660 -1.4438 -0.8342 1.1177 5.0717
## Coefficients:
##
                 Estimate Std. Error t value Pr(>|t|)
                   19.828
                               1.057 18.751 8.55e-11 ***
## (Intercept)
                   -2.079
                               1.568 -1.326
                                                0.208
## GenotypeAPOE33
                    1.761
                               1.568
                                      1.123
                                                0.282
## GenotypeAPOE44
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.59 on 13 degrees of freedom
## Multiple R-squared: 0.2977, Adjusted R-squared: 0.1896
## F-statistic: 2.755 on 2 and 13 DF, p-value: 0.1006
## Analysis of Variance Table
##
## Response: Probe_d5
               Df Sum Sq Mean Sq F value
                                           Pr(>F)
                2 206.87 103.434 6.7786 0.004849 **
## Genotype
                1 33.13 33.134 2.1715 0.154148
## Sex
```

```
## Genotype:Sex 2 50.15 25.077 1.6434 0.215215
                23 350.95 15.259
## Residuals
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Analysis of Variance Table
## Response: Probe_d5
             Df Sum Sq Mean Sq F value Pr(>F)
            2 203.97 101.987 3.8669 0.05701 .
## Genotype
## Residuals 10 263.74 26.374
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Analysis of Variance Table
##
## Response: Probe_d5
##
             Df Sum Sq Mean Sq F value Pr(>F)
## Genotype 2 36.965 18.4826 2.7551 0.1006
## Residuals 13 87.212 6.7086
## `geom_smooth()` using formula 'y ~ x'
                                                                            Genotype
  40
                                                                                APOE22
                                                                                 APOE33
Probe_d5
  30
                                                                                 APOE44
  20
                                                                            Sex
                                                                                female
                                                                                male
                   0.031
                                        0.032
                                                              0.033
                                      Hc
                        female
                                                                  male
   50
Probe_d5
    0
  -50
             0.031
                          0.032
                                       0.033
                                                       0.031
                                                                    0.032
                                                                                 0.033
                                              Hc
##
## lm(formula = Probe_d5 ~ Genotype * Sex, data = geno_combined)
##
## Residuals:
##
       Min
                1Q Median
                                ЗQ
                                       Max
```

```
## -5.4015 -2.3246 -0.9962 1.2548 12.4058
##
## Coefficients:
                         Estimate Std. Error t value Pr(>|t|)
##
## (Intercept)
                          19.6924
                                      1.7469 11.273 7.62e-11 ***
## GenotypeAPOE33
                                      2.8527 -0.425 0.67466
                          -1.2129
## GenotypeAPOE44
                           7.6319
                                      2.4705
                                              3.089 0.00518 **
## Sexmale
                           0.1352
                                      2.3654
                                              0.057 0.95493
## GenotypeAPOE33:Sexmale -0.8661
                                      3.7058 -0.234 0.81728
## GenotypeAPOE44:Sexmale -5.8705
                                      3.4203 -1.716 0.09953 .
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 3.906 on 23 degrees of freedom
## Multiple R-squared: 0.4526, Adjusted R-squared: 0.3336
## F-statistic: 3.803 on 5 and 23 DF, p-value: 0.01174
##
## Call:
## lm(formula = Probe_d5 ~ Genotype, data = combo_f)
## Residuals:
     Min
             1Q Median
                           3Q
                                 Max
## -5.402 -2.623 -1.232 2.046 12.406
##
## Coefficients:
##
                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)
                   19.692
                               2.297
                                       8.574 6.38e-06 ***
                   -1.213
                               3.750 -0.323
                                               0.7531
## GenotypeAPOE33
## GenotypeAPOE44
                    7.632
                               3.248
                                       2.350
                                               0.0407 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 5.136 on 10 degrees of freedom
## Multiple R-squared: 0.4361, Adjusted R-squared: 0.3233
## F-statistic: 3.867 on 2 and 10 DF, p-value: 0.05701
##
## Call:
## lm(formula = Probe_d5 ~ Genotype, data = combo_m)
##
## Residuals:
               1Q Median
      Min
                               3Q
## -3.1660 -1.4438 -0.8342 1.1177 5.0717
##
## Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
##
## (Intercept)
                   19.828
                               1.057 18.751 8.55e-11 ***
## GenotypeAPOE33
                   -2.079
                               1.568 - 1.326
                                                0.208
## GenotypeAPOE44
                    1.761
                               1.568
                                      1.123
                                                0.282
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 2.59 on 13 degrees of freedom
## Multiple R-squared: 0.2977, Adjusted R-squared: 0.1896
```

```
## F-statistic: 2.755 on 2 and 13 DF, p-value: 0.1006
## Analysis of Variance Table
## Response: Probe_d5
              Df Sum Sq Mean Sq F value
                                        Pr(>F)
              2 206.87 103.434 6.7786 0.004849 **
## Genotype
              1 33.13 33.134 2.1715 0.154148
## Sex
## Genotype:Sex 2 50.15 25.077 1.6434 0.215215
## Residuals
             23 350.95 15.259
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Analysis of Variance Table
##
## Response: Probe_d5
            Df Sum Sq Mean Sq F value Pr(>F)
## Genotype 2 203.97 101.987 3.8669 0.05701 .
## Residuals 10 263.74 26.374
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Analysis of Variance Table
## Response: Probe d5
           Df Sum Sq Mean Sq F value Pr(>F)
## Genotype 2 36.965 18.4826 2.7551 0.1006
## Residuals 13 87.212 6.7086
## `geom_smooth()` using formula 'y ~ x'
```



```
## Residuals:
    Min
             1Q Median
                           30
                                 Max
## -5.402 -2.623 -1.232 2.046 12.406
##
## Coefficients:
##
                 Estimate Std. Error t value Pr(>|t|)
                               2.297 8.574 6.38e-06 ***
## (Intercept)
                   19.692
                               3.750 -0.323
## GenotypeAPOE33
                   -1.213
                                              0.7531
## GenotypeAPOE44
                    7.632
                               3.248
                                       2.350
                                             0.0407 *
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 5.136 on 10 degrees of freedom
## Multiple R-squared: 0.4361, Adjusted R-squared: 0.3233
## F-statistic: 3.867 on 2 and 10 DF, p-value: 0.05701
## Call:
## lm(formula = Probe_d5 ~ Genotype, data = combo_m)
##
## Residuals:
##
      Min
               1Q Median
                               3Q
                                      Max
## -3.1660 -1.4438 -0.8342 1.1177 5.0717
## Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
                               1.057 18.751 8.55e-11 ***
## (Intercept)
                   19.828
## GenotypeAPOE33
                   -2.079
                               1.568 -1.326
                                                0.208
                    1.761
                               1.568
                                       1.123
                                                0.282
## GenotypeAPOE44
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 2.59 on 13 degrees of freedom
## Multiple R-squared: 0.2977, Adjusted R-squared: 0.1896
## F-statistic: 2.755 on 2 and 13 DF, p-value: 0.1006
## Analysis of Variance Table
##
## Response: Probe_d5
               Df Sum Sq Mean Sq F value
                                          Pr(>F)
                2 206.87 103.434 6.7786 0.004849 **
## Genotype
                1 33.13 33.134 2.1715 0.154148
## Genotype:Sex 2 50.15 25.077 1.6434 0.215215
## Residuals
               23 350.95 15.259
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Analysis of Variance Table
##
## Response: Probe_d5
            Df Sum Sq Mean Sq F value Pr(>F)
## Genotype
             2 203.97 101.987 3.8669 0.05701 .
## Residuals 10 263.74 26.374
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

```
## Analysis of Variance Table
##
## Response: Probe_d5
             Df Sum Sq Mean Sq F value Pr(>F)
            2 36.965 18.4826 2.7551 0.1006
## Genotype
## Residuals 13 87.212 6.7086
## `geom_smooth()` using formula 'y ~ x'
                                                                             Genotype
  28
                                                                                 APOE22
  24
                                                                                 APOE33
                                                                                 APOE44
  20
                                                                             Sex
  16
                                                                                 female
                                                                                 male
                        500
                                               520
                                                                      540
                                     Brain
                       female
                                                                  male
  60
  40
  20
   0
                500
                              520
                                            540
                                                          500
                                                                        520
                                                                                      540
                                             Brain
##
## Call:
## lm(formula = Probe_d5 ~ Genotype * Sex, data = geno_combined)
## Residuals:
##
       Min
                1Q Median
                                ЗQ
## -5.4015 -2.3246 -0.9962 1.2548 12.4058
##
## Coefficients:
##
                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)
                           19.6924
                                       1.7469 11.273 7.62e-11 ***
## GenotypeAPOE33
                           -1.2129
                                       2.8527 -0.425 0.67466
## GenotypeAPOE44
                            7.6319
                                       2.4705
                                                3.089 0.00518 **
## Sexmale
                            0.1352
                                       2.3654
                                                0.057 0.95493
## GenotypeAPOE33:Sexmale -0.8661
                                       3.7058 -0.234 0.81728
                                       3.4203 -1.716 0.09953 .
## GenotypeAPOE44:Sexmale -5.8705
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Residual standard error: 3.906 on 23 degrees of freedom
## Multiple R-squared: 0.4526, Adjusted R-squared: 0.3336
## F-statistic: 3.803 on 5 and 23 DF, p-value: 0.01174
##
## Call:
## lm(formula = Probe d5 ~ Genotype, data = combo f)
## Residuals:
##
     Min
             1Q Median
                           3Q
                                 Max
## -5.402 -2.623 -1.232 2.046 12.406
##
## Coefficients:
##
                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)
                   19.692
                               2.297
                                       8.574 6.38e-06 ***
                   -1.213
                               3.750
                                     -0.323
                                               0.7531
## GenotypeAPOE33
                    7.632
## GenotypeAPOE44
                               3.248
                                       2.350
                                               0.0407 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.136 on 10 degrees of freedom
## Multiple R-squared: 0.4361, Adjusted R-squared: 0.3233
## F-statistic: 3.867 on 2 and 10 DF, p-value: 0.05701
## Call:
## lm(formula = Probe_d5 ~ Genotype, data = combo_m)
## Residuals:
##
               1Q Median
      Min
                               3Q
                                      Max
## -3.1660 -1.4438 -0.8342 1.1177 5.0717
##
## Coefficients:
##
                 Estimate Std. Error t value Pr(>|t|)
                   19.828
                               1.057 18.751 8.55e-11 ***
## (Intercept)
## GenotypeAPOE33
                   -2.079
                               1.568 -1.326
                                                0.208
                               1.568
                                                0.282
## GenotypeAPOE44
                    1.761
                                       1.123
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 2.59 on 13 degrees of freedom
## Multiple R-squared: 0.2977, Adjusted R-squared: 0.1896
## F-statistic: 2.755 on 2 and 13 DF, p-value: 0.1006
## Analysis of Variance Table
##
## Response: Probe_d5
               Df Sum Sq Mean Sq F value
                                           Pr(>F)
                2 206.87 103.434 6.7786 0.004849 **
## Genotype
                1 33.13 33.134 2.1715 0.154148
## Genotype:Sex 2 50.15 25.077 1.6434 0.215215
## Residuals
               23 350.95 15.259
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Analysis of Variance Table
```

```
##
## Response: Probe_d5
             Df Sum Sq Mean Sq F value Pr(>F)
## Genotype 2 203.97 101.987 3.8669 0.05701 .
## Residuals 10 263.74 26.374
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Analysis of Variance Table
##
## Response: Probe_d5
             Df Sum Sq Mean Sq F value Pr(>F)
##
            2 36.965 18.4826 2.7551 0.1006
## Genotype
## Residuals 13 87.212 6.7086
## `geom_smooth()` using formula 'y ~ x'
                                                                             Genotype
                                                                                 APOE22
  25
                                                                                 APOE33
                                                                                 APOE44
  20
                                                                             Sex
  15
                                                                                female
                                                                                 male
                                         0.032
                   0.031
                                                              0.033
                                      Hc
                        female
                                                                   male
   40 -
Probe_d8
   20
    0
  -20
              0.031
                          0.032
                                       0.033
                                                       0.031
                                                                     0.032
                                                                                 0.033
                                              Hc
##
## Call:
## lm(formula = Probe_d5 ~ Genotype * Sex, data = geno_combined)
##
## Residuals:
       Min
                1Q Median
                                3Q
## -5.4015 -2.3246 -0.9962 1.2548 12.4058
##
## Coefficients:
##
                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)
                           19.6924
                                       1.7469 11.273 7.62e-11 ***
```

```
## GenotypeAPOE33
                          -1.2129
                                      2.8527 -0.425 0.67466
## GenotypeAPOE44
                           7.6319
                                      2.4705
                                               3.089 0.00518 **
## Sexmale
                           0.1352
                                      2.3654
                                              0.057 0.95493
                                      3.7058 -0.234 0.81728
## GenotypeAPOE33:Sexmale -0.8661
## GenotypeAPOE44:Sexmale -5.8705
                                      3.4203 -1.716 0.09953 .
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.906 on 23 degrees of freedom
## Multiple R-squared: 0.4526, Adjusted R-squared: 0.3336
## F-statistic: 3.803 on 5 and 23 DF, p-value: 0.01174
##
## Call:
## lm(formula = Probe_d5 ~ Genotype, data = combo_f)
##
## Residuals:
     Min
             1Q Median
                           3Q
                                 Max
## -5.402 -2.623 -1.232 2.046 12.406
##
## Coefficients:
##
                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)
                   19.692
                               2.297
                                       8.574 6.38e-06 ***
## GenotypeAPOE33
                   -1.213
                               3.750 -0.323 0.7531
## GenotypeAPOE44
                    7.632
                               3.248
                                       2.350
                                             0.0407 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 5.136 on 10 degrees of freedom
## Multiple R-squared: 0.4361, Adjusted R-squared: 0.3233
## F-statistic: 3.867 on 2 and 10 DF, p-value: 0.05701
##
## Call:
## lm(formula = Probe_d5 ~ Genotype, data = combo_m)
##
## Residuals:
      Min
               1Q Median
                               30
                                      Max
## -3.1660 -1.4438 -0.8342 1.1177 5.0717
##
## Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)
                   19.828
                               1.057 18.751 8.55e-11 ***
                   -2.079
## GenotypeAPOE33
                               1.568 -1.326
                                                0.208
## GenotypeAPOE44
                    1.761
                               1.568
                                      1.123
                                                0.282
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 2.59 on 13 degrees of freedom
## Multiple R-squared: 0.2977, Adjusted R-squared: 0.1896
## F-statistic: 2.755 on 2 and 13 DF, p-value: 0.1006
## Analysis of Variance Table
## Response: Probe_d5
```

```
Df Sum Sq Mean Sq F value
## Genotype
                 2 206.87 103.434 6.7786 0.004849 **
                 1 33.13 33.134 2.1715 0.154148
## Genotype:Sex 2 50.15 25.077 1.6434 0.215215
## Residuals
                23 350.95 15.259
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Analysis of Variance Table
##
## Response: Probe_d5
             Df Sum Sq Mean Sq F value Pr(>F)
## Genotype 2 203.97 101.987 3.8669 0.05701 .
## Residuals 10 263.74 26.374
## ---
## 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)
## Genotype
             2 36.965 18.4826 2.7551 0.1006
## Residuals 13 87.212 6.7086
## `geom_smooth()` using formula 'y ~ x'
                                                                            Genotype
                                                                                 APOE22
  25
                                                                                 APOE33
Probe_d8
                                                                                 APOE44
  20
                                                                            Sex
  15
                                                                                 female
                                                                                 male
            0.0240
                        0.0245
                                    0.0250
                                                0.0255
                                                            0.0260
                                     CPu
                       female
                                                                  male
  30
Probe_d8
  20
  10
   0
        0.0240
               0.0245
                       0.0250
                              0.0255
                                     0.0260
                                                   0.0240 0.0245 0.0250 0.0255
                                             CPu
##
## Call:
## lm(formula = Probe_d5 ~ Genotype * Sex, data = geno_combined)
```

```
##
## Residuals:
##
      Min
                1Q Median
## -5.4015 -2.3246 -0.9962 1.2548 12.4058
## Coefficients:
                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)
                                       1.7469 11.273 7.62e-11 ***
                           19.6924
## GenotypeAPOE33
                           -1.2129
                                       2.8527 -0.425
                                                      0.67466
## GenotypeAPOE44
                           7.6319
                                       2.4705
                                                3.089
                                                      0.00518 **
## Sexmale
                            0.1352
                                       2.3654
                                                0.057
                                                       0.95493
                                              -0.234
## GenotypeAPOE33:Sexmale
                          -0.8661
                                       3.7058
                                                       0.81728
## GenotypeAPOE44:Sexmale
                          -5.8705
                                       3.4203 -1.716 0.09953 .
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.906 on 23 degrees of freedom
## Multiple R-squared: 0.4526, Adjusted R-squared: 0.3336
## F-statistic: 3.803 on 5 and 23 DF, p-value: 0.01174
##
## Call:
## lm(formula = Probe_d5 ~ Genotype, data = combo_f)
## Residuals:
##
     Min
             1Q Median
## -5.402 -2.623 -1.232 2.046 12.406
##
## Coefficients:
##
                  Estimate Std. Error t value Pr(>|t|)
                    19.692
                                2.297
                                        8.574 6.38e-06 ***
## (Intercept)
## GenotypeAPOE33
                    -1.213
                                3.750
                                       -0.323
                                                0.7531
                    7.632
                                3.248
                                        2.350
                                                0.0407 *
## GenotypeAPOE44
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 5.136 on 10 degrees of freedom
## Multiple R-squared: 0.4361, Adjusted R-squared: 0.3233
## F-statistic: 3.867 on 2 and 10 DF, p-value: 0.05701
##
## Call:
## lm(formula = Probe_d5 ~ Genotype, data = combo_m)
## Residuals:
                1Q Median
                                3Q
                                       Max
## -3.1660 -1.4438 -0.8342 1.1177
                                  5.0717
##
## Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
##
## (Intercept)
                    19.828
                                1.057
                                      18.751 8.55e-11 ***
                                1.568
                                                 0.208
## GenotypeAPOE33
                   -2.079
                                     -1.326
## GenotypeAPOE44
                     1.761
                                1.568
                                       1.123
                                                 0.282
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 2.59 on 13 degrees of freedom
## Multiple R-squared: 0.2977, Adjusted R-squared: 0.1896
## F-statistic: 2.755 on 2 and 13 DF, p-value: 0.1006
## Analysis of Variance Table
## Response: Probe_d5
               Df Sum Sq Mean Sq F value
                2 206.87 103.434 6.7786 0.004849 **
## Genotype
                1 33.13 33.134 2.1715 0.154148
## Genotype:Sex 2 50.15 25.077 1.6434 0.215215
             23 350.95 15.259
## Residuals
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Analysis of Variance Table
##
## Response: Probe_d5
            Df Sum Sq Mean Sq F value Pr(>F)
## Genotype 2 203.97 101.987 3.8669 0.05701 .
## Residuals 10 263.74 26.374
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Analysis of Variance Table
## Response: Probe_d5
            Df Sum Sq Mean Sq F value Pr(>F)
## Genotype 2 36.965 18.4826 2.7551 0.1006
## Residuals 13 87.212 6.7086
```