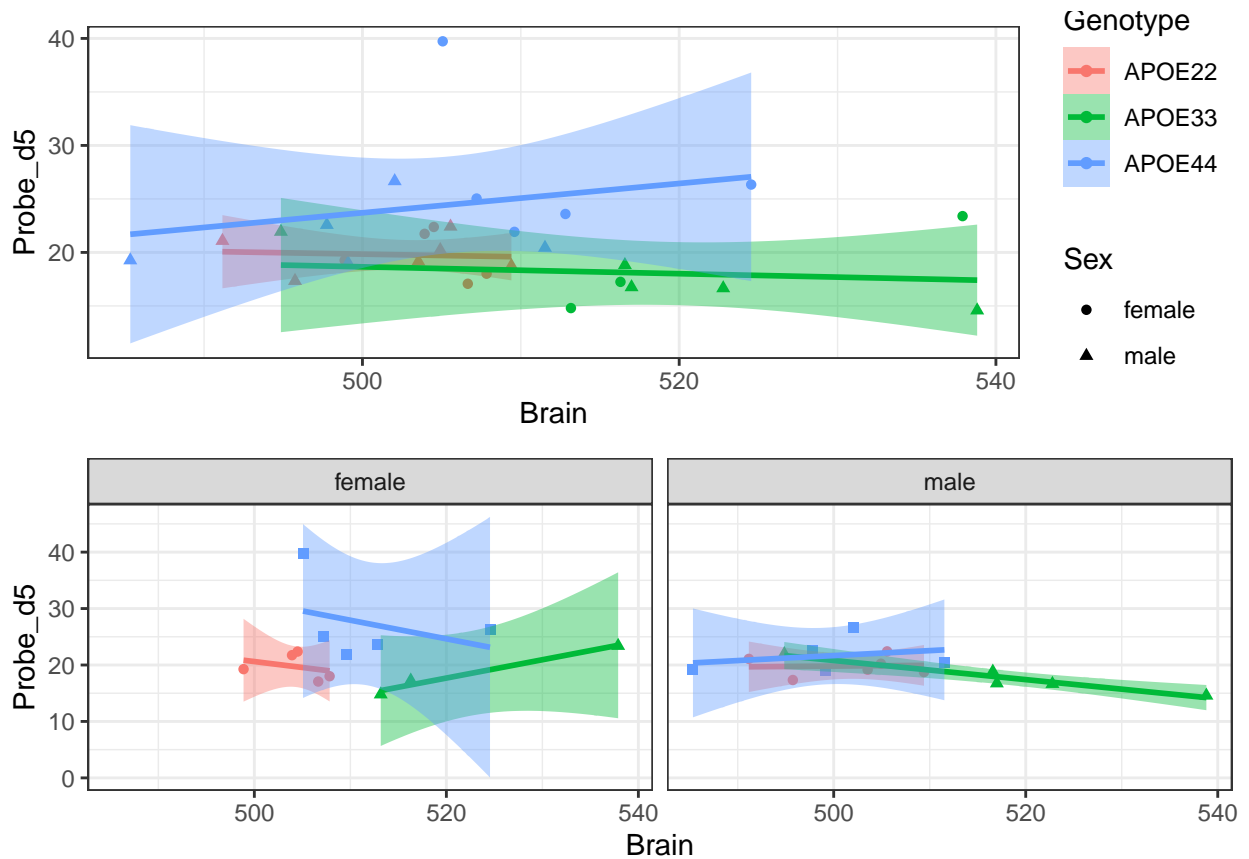


# winding\_by\_vol

alexandra badea

10/4/2021

```
## `geom_smooth()` using formula 'y ~ x'
```



```
##  
## Call:  
## lm(formula = Probe_d5 ~ Genotype * Sex, data = geno_combined)  
##  
## Residuals:  
##      Min       1Q   Median       3Q      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    -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
## 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 ***
## GenotypeAPOE33  -1.213      3.750  -0.323  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|)
## (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)
## Genotype      2  206.87  103.434    6.7786 0.004849 **
## Sex           1   33.13   33.134    2.1715 0.154148

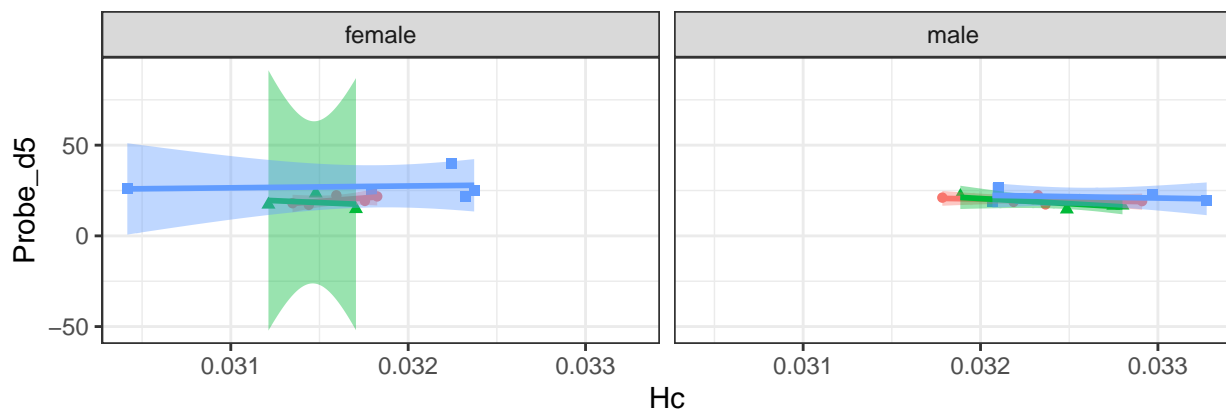
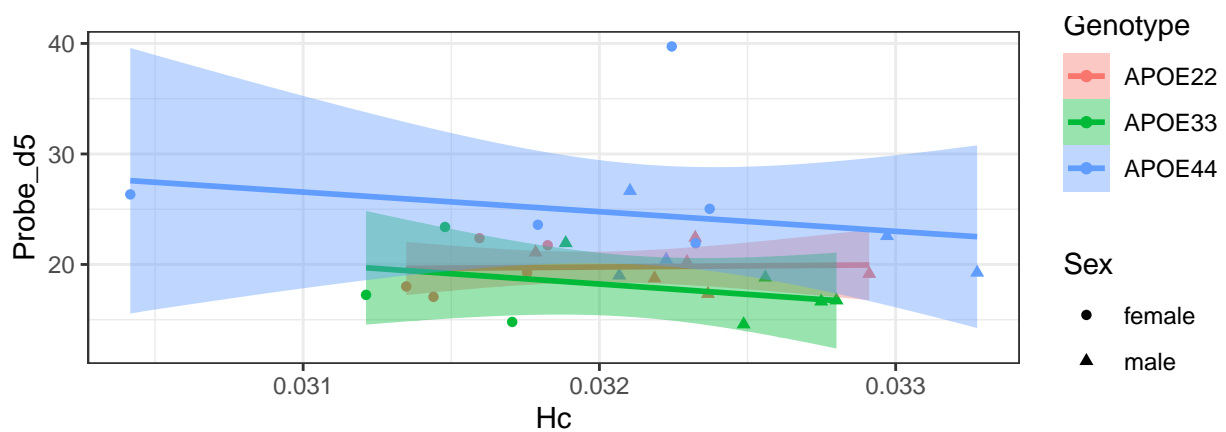
```

```
## Genotype:Sex  2  50.15  25.077  1.6434 0.215215
## Residuals    23 350.95  15.259
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 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'
```



```
##
## Call:
## lm(formula = Probe_d5 ~ Genotype * Sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
```

```

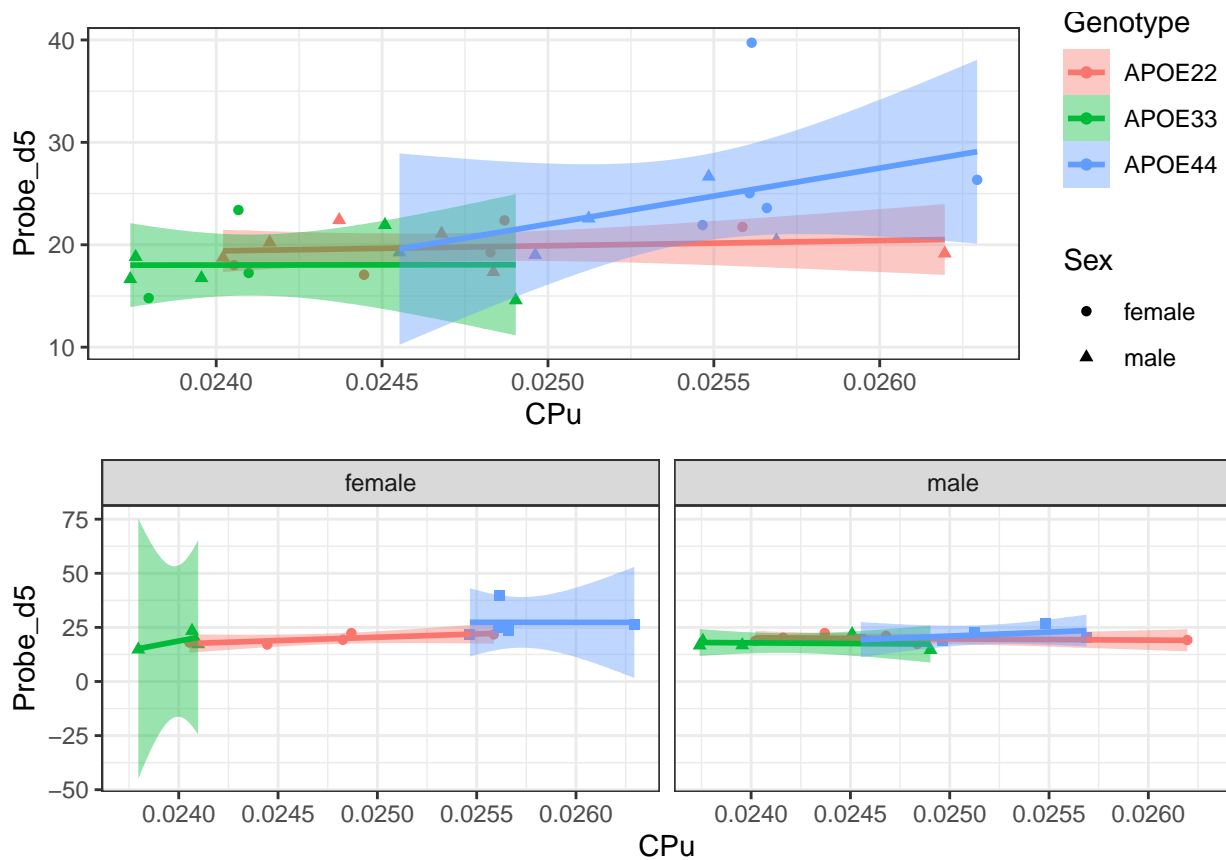
## -5.4015 -2.3246 -0.9962 1.2548 12.4058
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      19.6924      1.7469  11.273 7.62e-11 ***
## GenotypeAPOE33     -1.2129      2.8527   -0.425  0.67466
## GenotypeAPOE44       7.6319      2.4705    3.089  0.00518 **
## Sexmale            0.1352      2.3654    0.057  0.95493
## GenotypeAPOE33:Sexmale -0.8661      3.7058   -0.234  0.81728
## 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 ***
## GenotypeAPOE33     -1.213      3.750   -0.323  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|)
## (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)
## Genotype    2 206.87  103.434   6.7786 0.004849 **
## Sex          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 '**' 0.01 '*' 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'
```



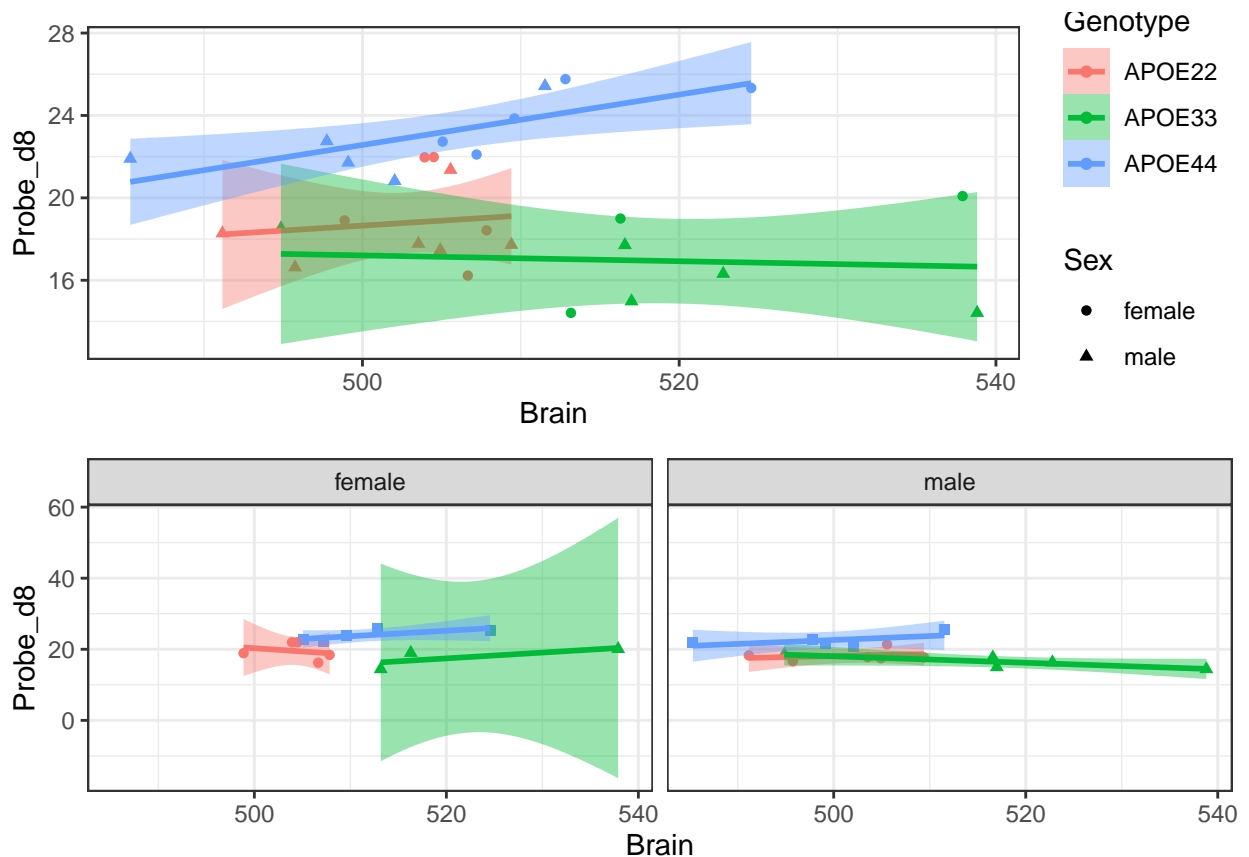
```
##
## Call:
## lm(formula = Probe_d5 ~ Genotype * Sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.4015 -2.3246 -0.9962  1.2548 12.4058
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      19.6924     1.7469  11.273 7.62e-11 ***
## GenotypeAPOE33     -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
## 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 ***
## GenotypeAPOE33  -1.213     3.750  -0.323  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|)
## (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)
## Genotype    2  206.87  103.434   6.7786 0.004849 **
## Sex          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 '**' 0.01 '*' 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'
```



```
##
## Call:
## lm(formula = Probe_d5 ~ Genotype * Sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      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    -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
## 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 ***
## GenotypeAPOE33  -1.213     3.750  -0.323  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|)
## (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

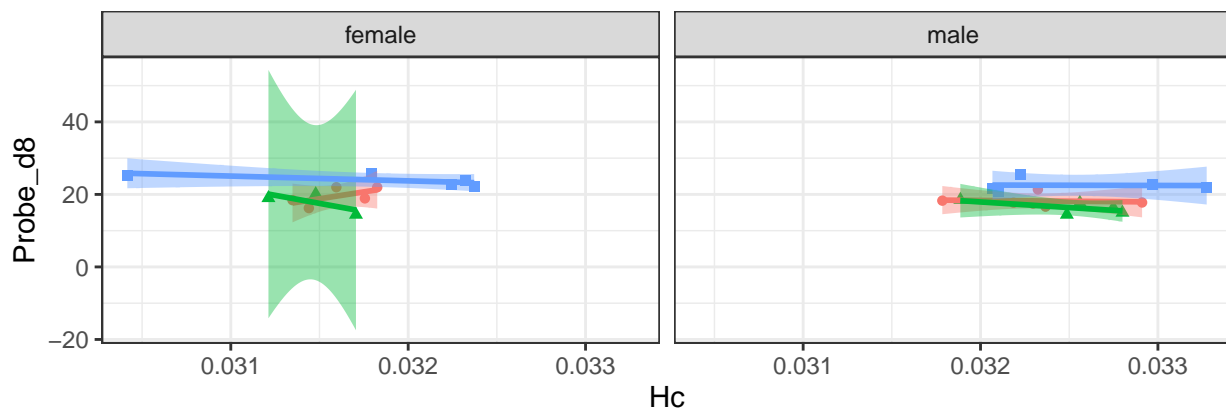
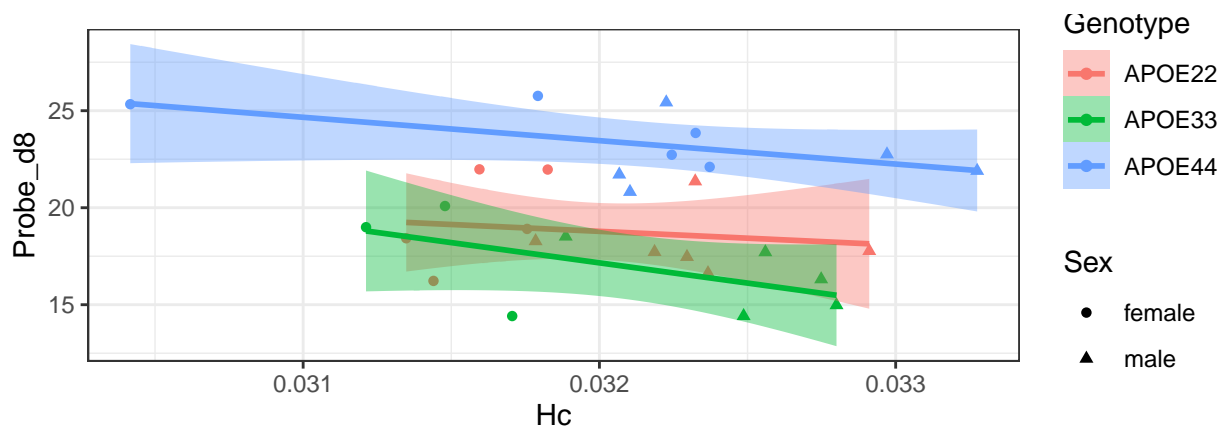
## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Genotype    2  206.87  103.434   6.7786 0.004849 **
## Sex          1   33.13   33.134   2.1715 0.154148
## Genotype:Sex  2   50.15   25.077   1.6434 0.215215
## Residuals   23  350.95   15.259
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 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'
```



```
##
## Call:
## lm(formula = Probe_d5 ~ Genotype * Sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      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      -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
## 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 ***
## GenotypeAPOE33  -1.213     3.750  -0.323  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|)
## (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

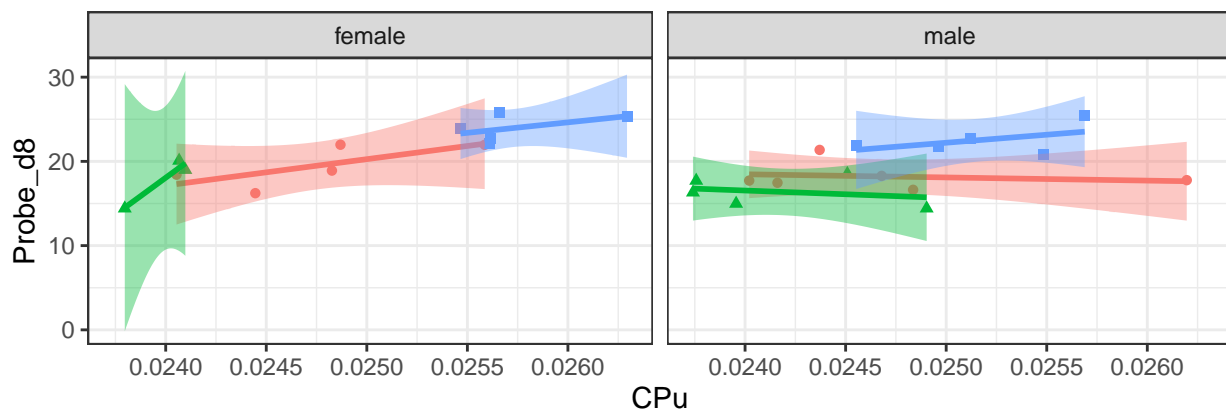
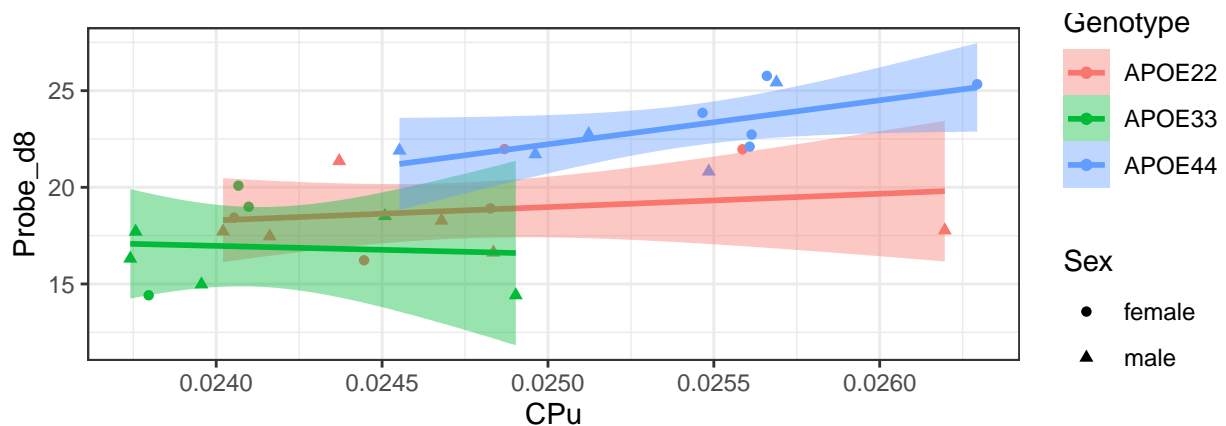
```

```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Genotype      2 206.87  103.434    6.7786 0.004849 **
## Sex           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 '**' 0.01 '*' 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'
```



```
##
## Call:
## lm(formula = Probe_d5 ~ Genotype * Sex, data = geno_combined)
```

```

##
## Residuals:
##      Min       1Q   Median       3Q      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    -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
## 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 ***
## GenotypeAPOE33    -1.213     3.750   -0.323  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|)
## (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)
## Genotype    2 206.87  103.434   6.7786 0.004849 **
## Sex          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 '**' 0.01 '*' 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

```