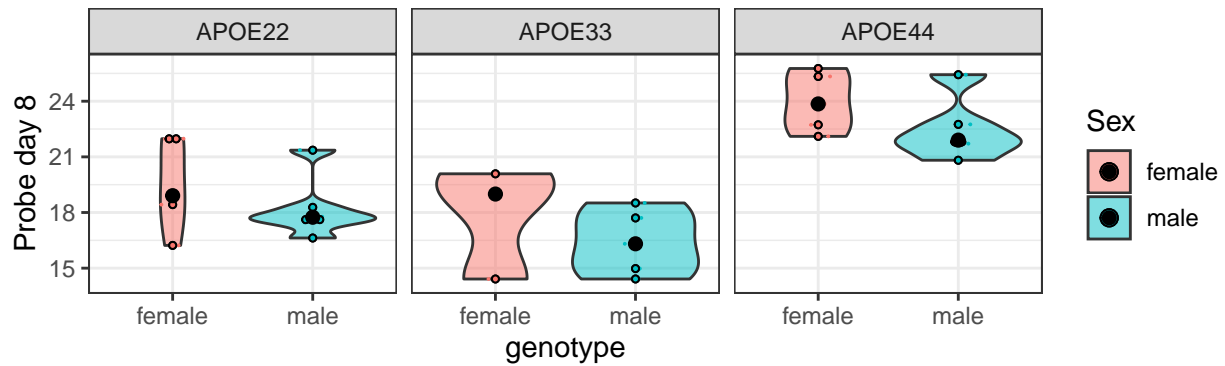
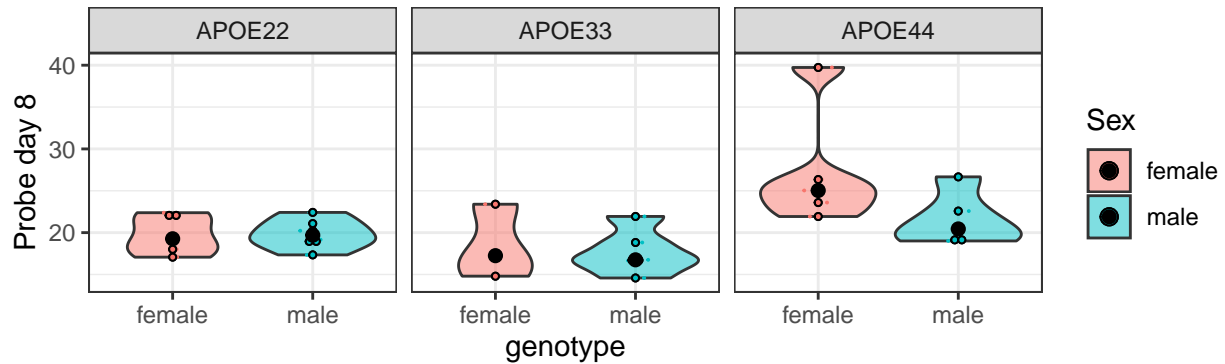


winding_by_fa

alexandra badea

10/4/2021



```
##
## 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

## Sex = female:
## contrast estimate SE df t.ratio p.value
## linear      7.63 2.47 23   3.089 0.0052
## quadratic   10.06 5.14 23   1.956 0.0628
##
## Sex = male:
## contrast estimate SE df t.ratio p.value
## linear      1.76 2.37 23   0.745 0.4640
## quadratic    5.92 4.22 23   1.403 0.1740

## Sex = female:
## contrast estimate SE df t.ratio p.value
## APOE22 - APOE33      1.21 2.85 23   0.425 0.9056
## APOE22 - APOE44     -7.63 2.47 23  -3.089 0.0138
## APOE33 - APOE44     -8.84 2.85 23  -3.100 0.0134
##
## Sex = male:
## contrast estimate SE df t.ratio p.value
## APOE22 - APOE33      2.08 2.37 23   0.879 0.6587
## APOE22 - APOE44     -1.76 2.37 23  -0.745 0.7398
## APOE33 - APOE44     -3.84 2.47 23  -1.554 0.2851
##
## P value adjustment: tukey method for comparing a family of 3 estimates

## contrast estimate SE df t.ratio p.value
## APOE22 female effect  -1.084 1.61 23  -0.674 0.6184
## APOE33 female effect  -2.297 1.99 23  -1.157 0.5182
## APOE44 female effect   6.547 1.61 23   4.072 0.0028
## APOE22 male effect    -0.949 1.50 23  -0.633 0.6184
## APOE33 male effect    -3.028 1.61 23  -1.883 0.2171
## APOE44 male effect     0.812 1.61 23   0.505 0.6184
##
## P value adjustment: fdr method for 6 tests

## Genotype = APOE22:
## contrast estimate SE df t.ratio p.value
## female - male  -0.135 2.37 23  -0.057 0.9549
##
## Genotype = APOE33:
## contrast estimate SE df t.ratio p.value
## female - male   0.731 2.85 23   0.256 0.8001
##
## Genotype = APOE44:
## contrast estimate SE df t.ratio p.value
## female - male   5.735 2.47 23   2.322 0.0295

## Sex Genotype contrast estimate SE df t.ratio p.value
## female . APOE22 - APOE33 1.213 2.85 23 0.425 1.0000
## female . APOE22 - APOE44 -7.632 2.47 23 -3.089 0.0466
## female . APOE33 - APOE44 -8.845 2.85 23 -3.100 0.0454

```

```

## male . APOE22 - APOE33 2.079 2.37 23 0.879 1.0000
## male . APOE22 - APOE44 -1.761 2.37 23 -0.745 1.0000
## male . APOE33 - APOE44 -3.840 2.47 23 -1.554 1.0000
## . APOE22 female - male -0.135 2.37 23 -0.057 1.0000
## . APOE33 female - male 0.731 2.85 23 0.256 1.0000
## . APOE44 female - male 5.735 2.47 23 2.322 0.2653
##
## P value adjustment: bonferroni method for 9 tests

## $`simple contrasts for Genotype`
## Sex = female:
## contrast estimate SE df t.ratio p.value
## APOE22 effect -2.140 1.50 23 -1.423 0.1681
## APOE33 effect -3.353 1.71 23 -1.956 0.0941
## APOE44 effect 5.492 1.50 23 3.653 0.0040
##
## Sex = male:
## contrast estimate SE df t.ratio p.value
## APOE22 effect 0.106 1.34 23 0.079 0.9379
## APOE33 effect -1.973 1.41 23 -1.403 0.2960
## APOE44 effect 1.867 1.41 23 1.328 0.2960
##
## P value adjustment: fdr method for 3 tests
##
## $`simple contrasts for Sex`
## Genotype = APOE22:
## contrast estimate SE df t.ratio p.value
## female effect -0.0676 1.18 23 -0.057 0.9549
## male effect 0.0676 1.18 23 0.057 0.9549
##
## Genotype = APOE33:
## contrast estimate SE df t.ratio p.value
## female effect 0.3655 1.43 23 0.256 0.8001
## male effect -0.3655 1.43 23 -0.256 0.8001
##
## Genotype = APOE44:
## contrast estimate SE df t.ratio p.value
## female effect 2.8677 1.24 23 2.322 0.0295
## male effect -2.8677 1.24 23 -2.322 0.0295
##
## P value adjustment: fdr method for 2 tests

## contrast estimate SE df t.ratio p.value
## APOE22 female effect -1.084 1.61 23 -0.674 0.6184
## APOE33 female effect -2.297 1.99 23 -1.157 0.5182
## APOE44 female effect 6.547 1.61 23 4.072 0.0028
## APOE22 male effect -0.949 1.50 23 -0.633 0.6184
## APOE33 male effect -3.028 1.61 23 -1.883 0.2171
## APOE44 male effect 0.812 1.61 23 0.505 0.6184
##
## P value adjustment: fdr method for 6 tests

## Genotype_poly Sex_consec estimate SE df t.ratio p.value
## linear male - female -5.87 3.42 23 -1.716 0.0995
## quadratic male - female -4.14 6.65 23 -0.622 0.5400

```

```

##      Genotype      Sex c.1 c.2
## 1   APOE22 female    1  -1
## 2   APOE33 female    0   2
## 3   APOE44 female   -1  -1
## 4   APOE22  male   -1   1
## 5   APOE33  male    0  -2
## 6   APOE44  male    1   1

## Sex = female:
## contrast estimate SE df t.ratio p.value
## linear      7.63 2.47 23   3.089 0.0052
## quadratic   10.06 5.14 23   1.956 0.0628
##
## Sex = male:
## contrast estimate SE df t.ratio p.value
## linear      1.76 2.37 23   0.745 0.4640
## quadratic    5.92 4.22 23   1.403 0.1740

## Sex = female:
## contrast estimate SE df t.ratio p.value
## APOE22 - APOE33    1.21 2.85 23   0.425 0.9056
## APOE22 - APOE44   -7.63 2.47 23  -3.089 0.0138
## APOE33 - APOE44   -8.84 2.85 23  -3.100 0.0134
##
## Sex = male:
## contrast estimate SE df t.ratio p.value
## APOE22 - APOE33    2.08 2.37 23   0.879 0.6587
## APOE22 - APOE44   -1.76 2.37 23  -0.745 0.7398
## APOE33 - APOE44   -3.84 2.47 23  -1.554 0.2851
##
## P value adjustment: tukey method for comparing a family of 3 estimates

## Sex = female:
## contrast estimate SE df t.ratio p.value
## APOE33 vs earlier  -1.21 2.85 23  -0.425 0.6747
## APOE44 vs earlier  16.48 4.51 23   3.653 0.0013
##
## Sex = male:
## contrast estimate SE df t.ratio p.value
## APOE33 vs earlier  -2.08 2.37 23  -0.879 0.3885
## APOE44 vs earlier   5.60 4.22 23   1.328 0.1973

## linear quadratic cubic quartic degree 5
## 1    -5         5    -5         1        -1
## 2    -3        -1     7        -3         5
## 3    -1        -4     4         2        -10
## 4     1        -4    -4         2         10
## 5     3        -1    -7        -3         -5
## 6     5         5     5         1          1

## contrast effect.size SE df lower.CL upper.CL
## APOE22 - APOE33    0.421 0.478 23  -0.568 1.411
## APOE22 - APOE44   -1.202 0.472 23  -2.179 -0.225
## APOE33 - APOE44   -1.624 0.539 23  -2.739 -0.508
##
## Results are averaged over the levels of: Sex

```

```

## sigma used for effect sizes: 3.906
## Confidence level used: 0.95

## contrast          effect.size      SE df lower.CL upper.CL
## (APOE22 - APOE33)      0.421 0.478 23   -0.568    1.411
## (APOE22 - APOE44)     -1.202 0.472 23   -2.179   -0.225
## (APOE33 - APOE44)     -1.624 0.539 23   -2.739   -0.508
##
## Results are averaged over the levels of: Sex
## sigma used for effect sizes: 3.906
## Confidence level used: 0.95

## $`Sex = female`
##
## Simultaneous Tests for General Linear Hypotheses
##
## Fit: lm(formula = Probe_d5 ~ Genotype * Sex, data = data)
##
## Linear Hypotheses:
##              Estimate Std. Error t value Pr(>|t|)
## APOE22 - APOE33 == 0    1.213      2.853   0.425  0.9052
## APOE22 - APOE44 == 0   -7.632      2.471  -3.089  0.0137 *
## APOE33 - APOE44 == 0   -8.845      2.853  -3.100  0.0134 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
##
##
## $`Sex = male`
##
## Simultaneous Tests for General Linear Hypotheses
##
## Fit: lm(formula = Probe_d5 ~ Genotype * Sex, data = data)
##
## Linear Hypotheses:
##              Estimate Std. Error t value Pr(>|t|)
## APOE22 - APOE33 == 0    2.079      2.365   0.879  0.659
## APOE22 - APOE44 == 0   -1.761      2.365  -0.745  0.740
## APOE33 - APOE44 == 0   -3.840      2.471  -1.554  0.285
## (Adjusted p values reported -- single-step method)
##
## 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
##
## contrast      estimate    SE df t.ratio p.value
## female - male      2.11 1.48 23   1.422 0.1686
##

```

```
## Results are averaged over the levels of: Genotype
##
## 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
##
##              2.5 %    97.5 %
## (Intercept)      16.078587 23.306186
## GenotypeAPOE33     -7.114220  4.688400
## GenotypeAPOE44       2.521180 12.742549
## Sexmale           -4.757956  5.028260
## GenotypeAPOE33:Sexmale -8.532119  6.799935
## GenotypeAPOE44:Sexmale -12.945941  1.204904
##
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33      1.65 1.85 23   0.888  0.6529
## APOE22 - APOE44     -4.70 1.71 23  -2.746  0.0298
## APOE33 - APOE44     -6.34 1.89 23  -3.361  0.0073
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates
##
## 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

##              2.5 %    97.5 %
## (Intercept)      16.078587 23.306186
## GenotypeAPOE33     -7.114220  4.688400
## GenotypeAPOE44      2.521180 12.742549
## Sexmale           -4.757956  5.028260
## GenotypeAPOE33:Sexmale -8.532119  6.799935
## GenotypeAPOE44:Sexmale -12.945941  1.204904

##
## Call:
## lm(formula = Probe_d8 ~ Genotype * Sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.4167 -1.2288 -0.4318  1.3781  3.1566
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      19.5012     0.8881  21.959 < 2e-16 ***
## GenotypeAPOE33     -1.6686     1.4502  -1.151  0.26171
## GenotypeAPOE44      4.4562     1.2559   3.548  0.00171 **
## Sexmale           -1.2979     1.2024  -1.079  0.29161
## GenotypeAPOE33:Sexmale -0.1483     1.8839  -0.079  0.93796
## GenotypeAPOE44:Sexmale -0.1366     1.7387  -0.079  0.93808
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.986 on 23 degrees of freedom
## Multiple R-squared:  0.6975, Adjusted R-squared:  0.6317
## F-statistic: 10.61 on 5 and 23 DF,  p-value: 2.242e-05

##
## Call:
## lm(formula = Probe_d8 ~ Genotype, data = combo_f)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.4167 -1.2288 -0.1041  1.8071  2.4777
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      19.501     1.026  19.000 3.54e-09 ***
## GenotypeAPOE33     -1.669     1.676  -0.996  0.3429
## GenotypeAPOE44      4.456     1.452   3.070  0.0118 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##

```



```

## Residual standard error: 2.295 on 10 degrees of freedom
## Multiple R-squared:  0.6165, Adjusted R-squared:  0.5398
## F-statistic: 8.039 on 2 and 10 DF,  p-value: 0.008292

##
## Call:
## lm(formula = Probe_d8 ~ Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.9692 -0.9598 -0.4575  0.5022  3.1566
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    18.2034     0.6982   26.072 1.31e-12 ***
## GenotypeAPOE33  -1.8169     1.0356   -1.754  0.1029
## GenotypeAPOE44   4.3196     1.0356    4.171  0.0011 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.71 on 13 degrees of freedom
## Multiple R-squared:  0.7246, Adjusted R-squared:  0.6822
## F-statistic: 17.1 on 2 and 13 DF,  p-value: 0.0002292

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Genotype    2 195.444   97.722  24.7824 1.826e-06 ***
## Sex          1  13.625   13.625   3.4554  0.07589 .
## Genotype:Sex  2   0.034    0.017   0.0043  0.99572
## Residuals   23  90.694    3.943
## ---
## 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)
## Genotype    2 84.685   42.342   8.0389 0.008292 **
## Residuals   10 52.672    5.267
## ---
## 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)
## Genotype    2 100.014   50.007  17.098 0.0002292 ***
## Residuals   13  38.022    2.925
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

{r volume, echo = FALSE, message=FALSE, quiet = TRUE }

# separating by sex

```

```

geno_combined <- data_VOL
combo_f <- geno_combined %>%
  filter(Sex == "female")
combo_m <- geno_combined %>%
  filter(Sex == "male")

p<-ggplot(data_VOL, aes(Genotype, Hc, fill = Sex)) +
  geom_violin(alpha = 0.5) +
  facet_grid(. ~ Genotype) +
  #geom_boxplot(width = 0.1, outlier.color = "red") +
  geom_jitter(size = 0.01, height = 0, width = 0.1, aes(color = Sex)) +
  geom_dotplot(binaxis='y', stackdir='center',
               position=position_dodge(1))+
  labs(title = "Hc Volume")+
  theme_minimal()+
  geom_dotplot(binaxis='y', stackdir='center',
               position=position_dodge(1))+
  stat_summary(fun.y=median, geom="point", size=2, color="black")+
  theme_bw()

#
#
plot1<-ggplot(data_VOL, aes(Sex, Hc, fill = Sex)) +
  geom_violin(alpha = 0.5) +
  facet_grid(. ~ Genotype) +
  #geom_boxplot(width = 0.1, outlier.color = "red") +
  geom_jitter(size = 0.01, height = 0, width = 0.1, aes(color = Sex)) +
  geom_dotplot(binaxis='y', stackdir='center',
               position=position_dodge(1))+
  labs(title = "Hc Volume (%)")+
  theme_minimal()+
  background_grid(major = 'xy', minor = "none") + # add thin horizontal lines
  panel_border() +
  theme_bw()+
  labs(x = "genotype", y = "Hc Volume (%)", title = "") +
  geom_dotplot(binaxis='y', stackdir='center',
               position=position_dodge(1)) +
  stat_summary(fun.y=median, geom="point", size=2, color="black") +
  theme_bw()

plot2<-ggplot(data_VOL, aes(Sex, CPu, fill = Sex)) +
  geom_violin(alpha = 0.5) +
  facet_grid(. ~ Genotype) +
  #geom_boxplot(width = 0.1, outlier.color = "red") +
  geom_jitter(size = 0.01, height = 0, width = 0.1, aes(color = Sex)) +
  geom_dotplot(binaxis='y', stackdir='center',
               position=position_dodge(1))+
  labs(title = "CPu Volume (%)")+
  theme_minimal()+
  background_grid(major = 'xy', minor = "none") + # add thin horizontal lines
  panel_border() +
  theme_bw()+

```

```

  labs(x = "genotype", y = "CPu Volume (%)", title = "") +
  geom_dotplot(binaxis='y', stackdir='center',
               position=position_dodge(1)) +
  stat_summary(fun.y=median, geom="point", size=2, color="black") +
  theme_bw()

ggdraw() +
  draw_plot(plot1, 0, .5, 1, .5) +
  draw_plot(plot2, 0, 0, 1, .5)

lm <- lm(Hc ~ Genotype*Sex, geno_combined)

summary(lm)

# emmip(lm, type ~ Genotype | Animal)
# colors <- c("red", "green", "blue")
# plot3 <-plot (emmeans(lm, ~ Genotype | Sex) ,
#               col=colors(data$Genotype), main="Probe Day5")
# draw(plot3)
#
# plot3 <-plot (emmeans(lm, ~ Genotype * Sex) , main="Probe Day5")
#
# legend("bottomright", legend = paste("Probe Day5", 1:3), col = Genotype, pch = 19, bty = "n")
#
# ggdraw(plot3)

###alex pairs
Hc.lm <- lm(Hc ~ Genotype*Sex, data = data)
warp.emm <- emmeans(Hc.lm , ~ Genotype | Sex)
contrast(warp.emm, "poly") # inherits 'by = "wool"' from warp.emm
pairs(warp.emm) # ditto
contrast(warp.emm, "eff", by = NULL) # contrasts of the 6 factor combs
pairs(warp.emm, simple = "Sex") # same as pairs(warp.emm, by = "tension")
# Do all "simple" comparisons, combined into one family
pairs(warp.emm, simple = "each", combine = TRUE)

contrast(warp.emm, simple = list("Genotype", "Sex"))

contrast(warp.emm, simple = c("Genotype", "Sex"))

tw.emm <- contrast(warp.emm, interaction = c(Genotype = "poly", Sex = "consec"),
by = NULL)
tw.emm # see the estimates
coef(tw.emm) # see the contrast coefficients

# warp.lm <- lm(breaks ~ wool*tension, data = warpbreaks)
# warp.emm <- emmeans(warp.lm, ~ tension | wool)
# contrast(warp.emm, "poly") # inherits 'by = "wool"' from warp.emm
# pairs(warp.emm) # ditto
# contrast(warp.emm, "eff", by = NULL) # contrasts of the 6 factor combs
# pairs(warp.emm, simple = "wool") # same as pairs(warp.emm, by = "tension")

```

```

# # Do all "simple" comparisons, combined into one family
# pairs(warp.emm, simple = "each", combine = TRUE)
# ###alex pairs

####
warp.lm <- lm(Hc ~ Genotype*Sex, data = data)
warp.emm <- emmeans(warp.lm, ~ Genotype | Sex)
contrast(warp.emm, "poly")

pairs(warp.emm)

### Setting up a custom contrast function
helmert.emmc <- function(levs, ...) {
  M <- as.data.frame(contr.helmert(levs))
  names(M) <- paste(levs[-1], "vs earlier")
  attr(M, "desc") <- "Helmert contrasts"
  M
}
contrast(warp.emm, "helmert")
## Not run:
# See what is used for polynomial contrasts with 6 levels
emmeans::poly.emmc(1:6)
## End(Not run)

###
####
Hc.lm <- lm(Hc ~ Genotype * Sex, data = data)
emm <- emmeans(Hc.lm, "Genotype")
eff_size(emm, sigma = sigma(Hc.lm), edf = df.residual(Hc.lm))
# or equivalently:
eff_size(pairs(emm), sigma(Hc.lm), df.residual(Hc.lm), method = "identity")
# ### Mixed model example:
# if (require(nlme)) {
#   Oats.lme <- lme(yield ~ Variety + factor(nitro),
#   random = ~ 1 | Block / Variety,
#   data = Oats)
#   # Combine variance estimates
#   VarCorr(Oats.lme)
#   totSD <- sqrt(214.4724 + 109.6931 + 162.5590)
#   # I figure edf is somewhere between 5 (Blocks df) and 51 (Resid df)
#   emmV <- emmeans(Oats.lme, ~ Variety)
#   print(eff_size(emmV, sigma = totSD, edf = 5))
#   print(eff_size(emmV, sigma = totSD, edf = 51))
# }
# Multivariate model for the same data:
# MOats.lm <- lm(yield ~ Variety, data = MOats)
# eff_size(emmeans(MOats.lm, "Variety"),
# sigma = sqrt(mean(sigma(MOats.lm)^2)), # RMS of sigma()
# edf = df.residual(MOats.lm))
# These results illustrate a sobering message that effect sizes are often
# not nearly as accurate as you may think.

summary(glht(Hc.lm, emm(pairwise ~ Genotype | Sex)))

```

```
####

lm_f <- lm(Hc ~ Genotype, combo_f)
summary(lm_f)
lm_m <- lm(Hc ~ Genotype, combo_m)
summary(lm_m)

anova(lm)
anova(lm_f)
anova(lm_m)

model<-emmeans(Hc.lm, "Sex", adjust = "Tukey")
pairs(model)
summary(lm)
confint(lm)

model<-emmeans(Hc.lm, "Genotype", adjust = "Tukey")
pairs(model)
summary(lm)
confint(lm)

lm.CPu <- lm(CPu ~ Genotype*Sex, geno_combined)
summary(lm)
lm_f <- lm(CPu ~ Genotype, combo_f)
summary(lm_f)
lm_m <- lm(CPu ~ Genotype, combo_m)
summary(lm_m)

anova(lm.CPu)
anova(lm_f)
anova(lm_m)

{r violin FA, echo = FALSE}
#volumes, FAs, DEG , CLUS plots
# separating by sex
geno_combined <- data_FA
combo_f <- geno_combined %>%
  filter(Sex == "female")
combo_m <- geno_combined %>%
  filter(Sex == "male")

plot1<-ggplot(data_FA, aes(Sex, fi, fill = Sex)) +
  geom_violin(alpha = 0.5)
  facet_grid(. ~ Genotype) +
  #geom_boxplot(width = 0.1, outlier.color = "red") +
  geom_jitter(size = 0.01, height = 0, width = 0.1, aes(color = Sex)) +
  geom_dotplot(binaxis='y', stackdir='center',
    position=position_dodge(1))+
  labs(title = "fi:FA")+

```

```

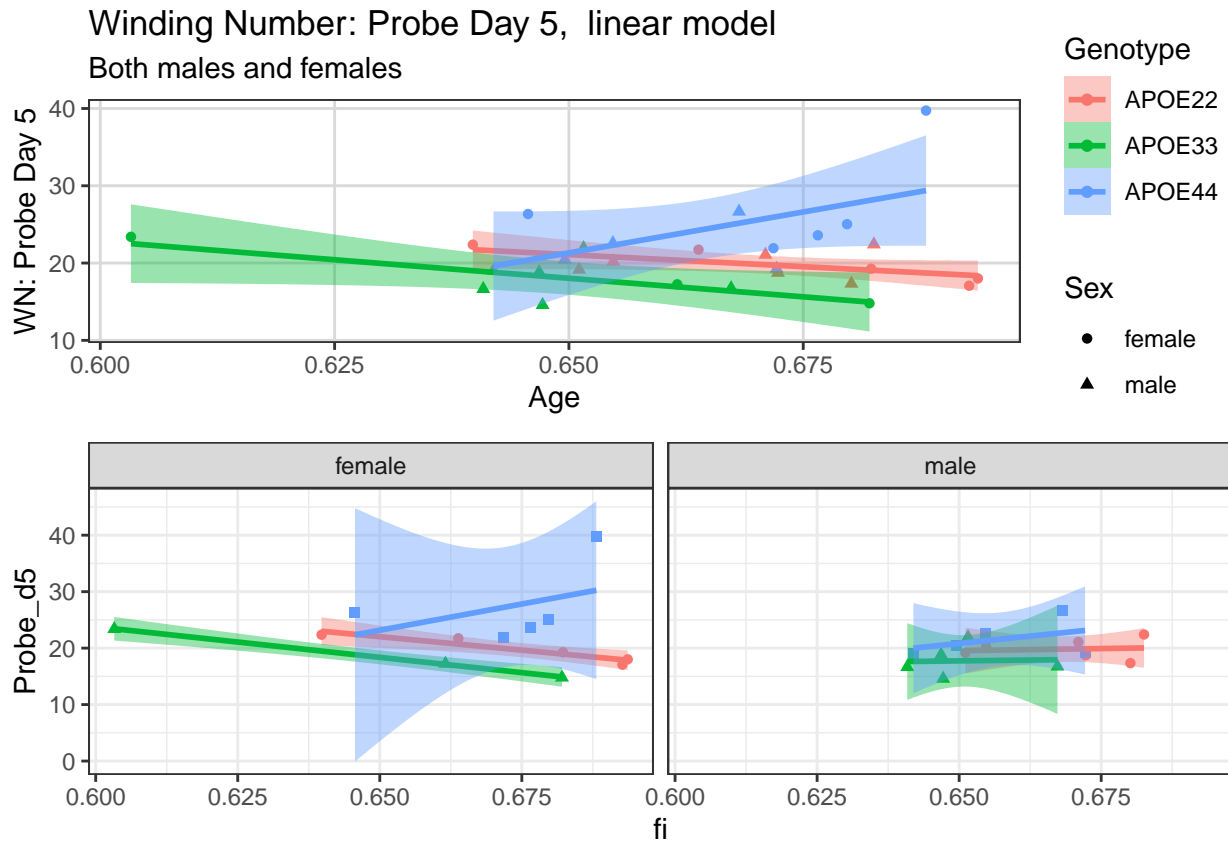
    theme_minimal()+
    background_grid(major = 'xy', minor = "none") + # add thin horizontal lines
    panel_border() +
    theme_bw()+
    labs(x = "genotype", y = "fi", title = "") +
    geom_dotplot(binaxis='y', stackdir='center',
                 position=position_dodge(1)) +
    stat_summary(fun.y=median, geom="point", size=2, color="black") +
    theme_bw()

plot2<-ggplot(data_FA, aes(Sex, ic, fill = Sex)) +
  geom_violin(alpha = 0.5) +
  facet_grid(. ~ Genotype) +
  #geom_boxplot(width = 0.1, outlier.color = "red") +
  geom_jitter(size = 0.01, height = 0, width = 0.1, aes(color = Sex)) +
  geom_dotplot(binaxis='y', stackdir='center',
               position=position_dodge(1))+
  labs(title = "ic:FA")+
  theme_minimal()+
  background_grid(major = 'xy', minor = "none") + # add thin horizontal lines
  panel_border() +
  theme_bw()+
  labs(x = "genotype", y = "fi", title = "") +
  geom_dotplot(binaxis='y', stackdir='center',
               position=position_dodge(1)) +
  stat_summary(fun.y=median, geom="point", size=2, color="black") +
  theme_bw()

ggdraw() +
  draw_plot(plot1, 0, .5, 1, .5) +
  draw_plot(plot2, 0, 0, 1, .5)

#end volume, FAs, DEG, CLUST plots
## `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:
```

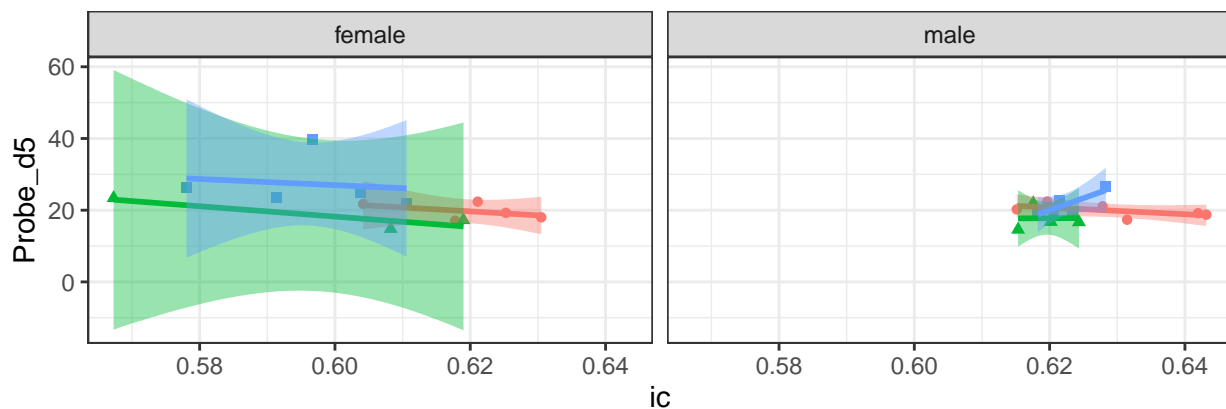
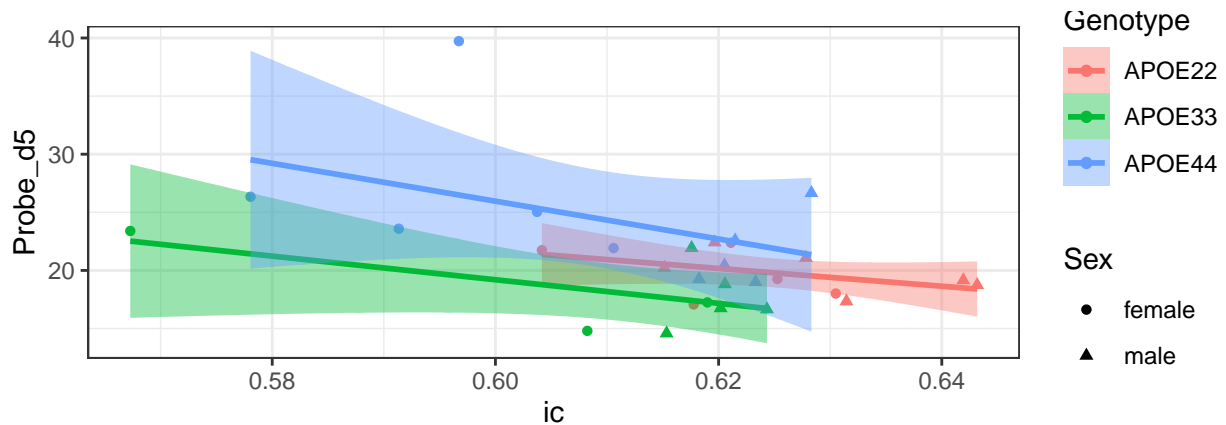
```

##      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

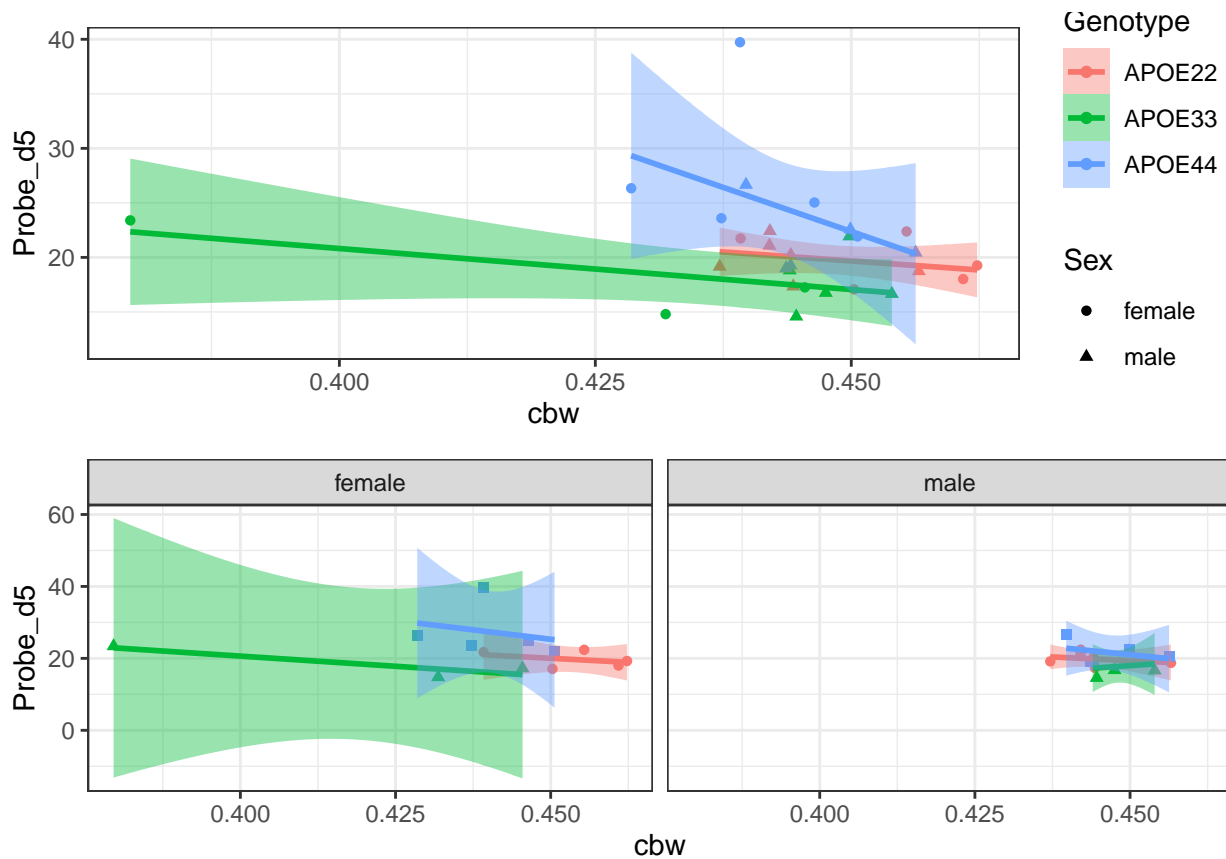
## Analysis of Variance Table
##

```

```
## 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)

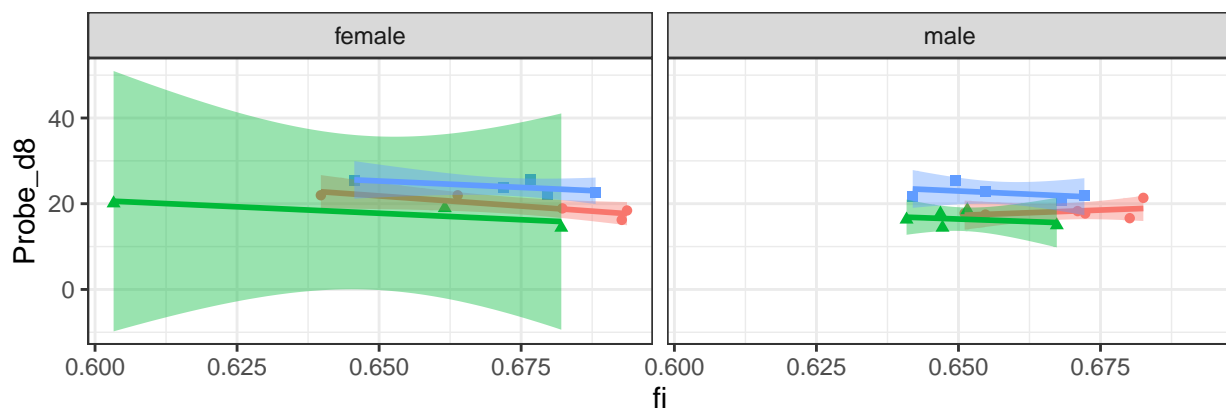
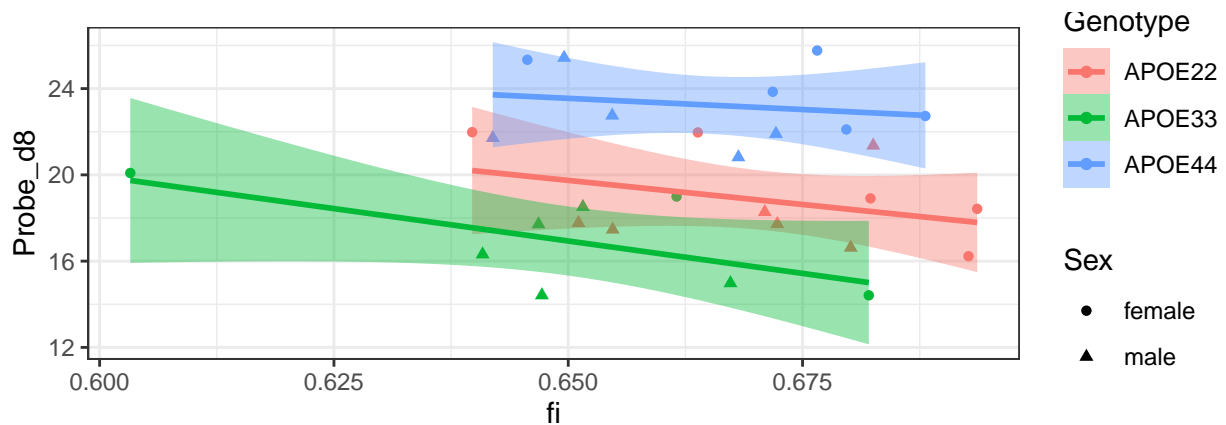
```

```
## 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

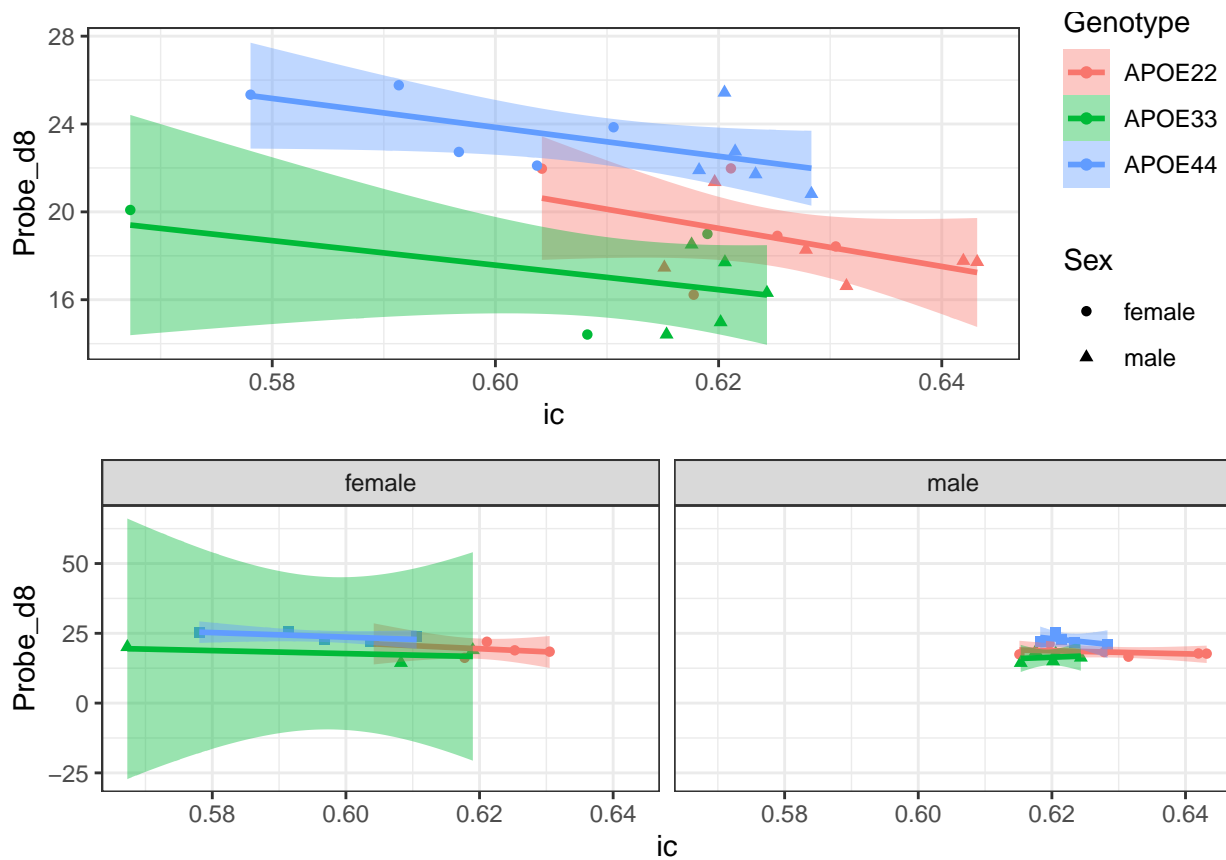
## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Genotype    2  206.87  103.434   6.7786 0.004849 **
## Sex          1   33.13   33.134   2.1715 0.154148
## Genotype:Sex  2   50.15   25.077   1.6434 0.215215
## Residuals   23  350.95   15.259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

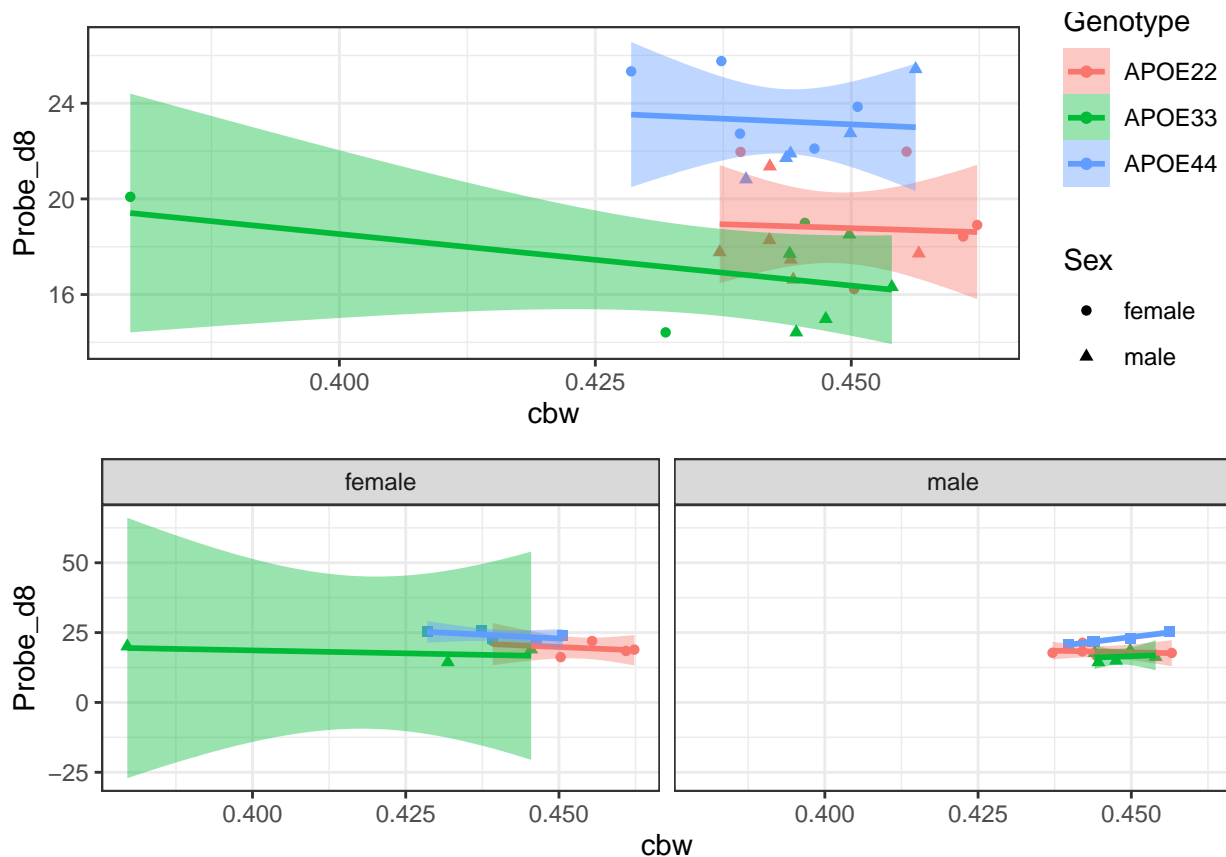


```

## 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
```